



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95445

TO: Rita Mitra
Location: 9B03
Art Unit: 1653
Monday, June 02, 2003

Case Serial Number: 643260

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Mitra, Rita
Sent: Friday, May 30, 2003 2:09 PM
To: O'Bryen, Barbara
Subject: Sequence search request 09/643260

Hi Barbara

I would like to request an expedited sequence search for application 09/643260 because this is an amended case due this biweek.

Please search commercial databases, issued patent and pending patents databases:

09/643260
SEQ ID NOs : 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 and 19

Please print out results.

Thank You.
Rita

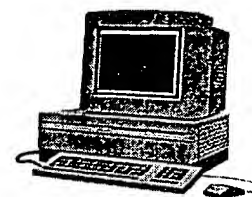


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BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSA 6
|||||
Db 2 LDWSA 7

Db |||||
1 LDWSW 5

Search completed: May 30, 2003, 15:53:16
Job time : 11.4605 secs

RESULT 14

US-09-847-946A-63
; Sequence 63, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-63

Query Match 100.0%; Score 40; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSA 6
|||||
Db 3 LDWSA 8

RESULT 15

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 90.0%; Score 36; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDWSWA 6

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	92.5	304	2 F83632	probable cytochrome
2	36	90.0	258	2 T21987	hypothetical prote
3	36	90.0	362	2 S23471	uroporphyrinogen d
4	36	90.0	374	2 B83241	conserved hypothet
5	36	90.0	409	2 T47298	probable replicati
6	36	90.0	745	1 I49101	conserved helix-lo
7	36	90.0	983	2 B45583	receptor tyrosine
8	36	90.0	983	2 A38224	protein-tyrosine k
9	36	90.0	983	2 A45583	receptor tyrosine
10	34	85.0	211	2 T03355	gene e12 protein -
11	34	85.0	411	2 E84949	tetrahydrofolylpol
12	34	85.0	433	2 T31511	hypothetical prote
13	34	85.0	616	2 T14235	NADH2 dehydrogenas
14	34	85.0	1139	2 A10379	conserved potassium
15	33	82.5	198	2 B82531	conserved hypothet
16	33	82.5	234	2 T36162	probable integral
17	33	82.5	275	2 T05922	hypothetical prote
18	33	82.5	316	2 D98351	dipeptide ABC tran
19	33	82.5	316	2 AB2931	hypothetical prote
20	33	82.5	322	2 A13395	NADH2 dehydrogenas
21	33	82.5	324	2 AB3548	vegetatible incomp
22	33	82.5	360	2 S60888	ferric exochelin b
23	33	82.5	415	2 AE1844	hypothetical prote
24	33	82.5	421	2 T31787	hypothetical prote
25	33	82.5	436	2 B69371	bile acid-inducibi
26	33	82.5	453	1 NMIV3	exo-alpha-sialidas
27	33	82.5	454	1 NMIV	exo-alpha-sialidas
28	33	82.5	464	2 S75362	hypothetical prote
29	33	82.5	492	2 S03098	aerolysin precurso

30 33 82.5 516 2 T10000 cytochrome P450 (C
31 33 82.5 524 2 T09999 cytochrome P450 -
32 33 82.5 524 2 T09944 probable cytochrom
33 33 82.5 539 2 T15256 hypothetical prote
34 33 82.5 610 2 T35222 hypothetical prote
35 33 82.5 656 2 A56975 VI polysaccharide
36 33 82.5 656 2 AF1040 VI polysaccharide
37 33 82.5 836 2 D82177 conserved hypothet
38 33 82.5 840 1 A42970 H+-exporting ATPas
39 33 82.5 885 2 C83441 two-component sens
40 33 82.5 1334 2 T50568 probable multi-dom
41 33 82.5 1575 2 T18545 lysobactin synthet
42 33 82.5 1842 2 T43409 probable fatty-aci
43 33 82.5 1842 2 T38781 fatty acid synthas
44 32 80.0 53 2 T11353 H+-transporting tw
45 32 80.0 83 2 S24712 Ig alpha chain - h

ALIGNMENTS

RESULT 1

F83632

probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aerugin
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83632

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83632

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-304 <STO>

A:Cross-references: GB:AE004449; GB:AE004091; NID:99945928; PIDN:AG03503.1; GSPDB:G
A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0113

C:Superfamily: heme O synthase

Query Match 92.5%; Score 37; DB 2; Length 304;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
Db 259 LDWSWA 264

RESULT 2

T21987

hypothetical protein F39B2.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21987

R:Dobson, R.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19498

A:Accession: T21987

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-258 <WIL>

A:Cross-references: EMBL:Z92834; PIDN:CA807386.1; GSPDB:GN00019; CESP:F39B2.5
A:Experimental source: clone F39B2

C:Genetics:

A:Gene: CESP:F39B2.5

A:Map position: 1

A:Introns: 16/2; 58/1; 97/3

Query Match 90.0%; Score 36; DB 2; Length 258;

Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWA 6
|||||
Db 21 LDWKWA 26

RESULT 3

S23471
uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YP9609.03; protein YDR047w
C:Species: *Saccharomyces cerevisiae*
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: S23471; S33965; S54033; S20190; S27348; S31312
R:Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytka, J.; Harrison, L.; Kushner, J.; Le
Eur. J. Biochem. 205, 1011-1016, 1992
A:Title: Uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence
A:Reference number: S23471; MUID:92249304; PMID:1576986
A:Accession: S23471

A:Molecule type: DNA
A:Residues: 1-362 <GAR>
A:Cross-references: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
R:Diflumeri, C.; Larocque, R.; Keng, T.
Yeast 9, 613-623, 1993
A:Title: Molecular analysis of HEM6 (HEM12) in *Saccharomyces cerevisiae*, the gene for u
A:Reference number: S33965; MUID:93348774; PMID:8346678
A:Accession: S33965

A:Molecule type: DNA
A:Residues: 1-362 <DIF>
A:Cross-references: EMBL:Z19089; NID:g4775; PIDN:CAA79514.1; PID:g4776
R:Hunt, S.; Bowman, S.; Harris, D.
Submitted to the EMBL Data Library, May 1995
A:Reference number: S54031
A:Accession: S54033

A:Molecule type: DNA
A:Residues: 1-362 <HUN>
A:Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAA99078.1; PID:g798900; MIPs:YDR047w
C:Genetics:

A:Gene: HEM12; HEM6; POP3
A:Cross-references: MIPs:YDR047w; SGD:S0002454
A:Map position: 4R
C:Superfamily: uroporphyrinogen decarboxylase
C:Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 279 LDWSW 283

RESULT 4

B83241
conserved hypothetical protein PA3230 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83241
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83241

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:

A:Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 81 DWSWA 85

RESULT 5

T47298

probable replication protein - *Arabidopsis thaliana*
N:Alternate names: protein T14K23.110

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47298

R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M
Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24458

A:Accession: T47298

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <NYA>

A:Cross-references: EMBL:AL132909

A:Experimental source: cultivar Columbia; BAC clone T14K23

C:Genetics:

A:Map position: 3

A:Introns: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3

A:Note: T14K23.110

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 409;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 190 LDWSW 194

RESULT 6

I49101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse

C:Species: *Mus musculus* (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: I49101

R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

Genomics 27, 348-351, 1995

A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromoso

A:Reference number: I49101; MUID:96044444; PMID:7558004

A:Accession: I49101

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-745 <RES>

A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493

C:Genetics:

A:Gene: CHUK

C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase hom
C:Keywords: ATP; phosphotransferase

F:13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 738 LDWSW 742

RESULT 7

B45583
receptor tyrosine kinase Cck4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: B45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A;Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse an
A;Reference number: A45583; MUID:92031278; PMID:1657122
A;Accession: B45583
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 <SAJ>
A;Cross-references: GB:M68514; NID:g454809; PIDN:AAA8666.1; PID:g211447
A;Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIP:62411)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif

Query Match 90.0%; Score 36; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
| | | | |
Db 342 LDWSW 346

RESULT 8
A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession: A38224; B38224
R;Wicks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A;Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed
A;Reference number: A38224; MUID:92179233; PMID:1311845
A;Accession: A38224
A;Molecule type: mRNA
A;Residues: 1-983 <WIC>
A;Cross-references: GB:M83941; NID:g183931; PIDN:AAA56633.1; PID:g183932
A;Experimental source: pre-B-cell leukemia cell line LK63
A;Note: sequence extracted from NCBI backbone (NCBIP:86627)
A;Accession: B38224
A;Molecule type: protein
A;Residues: 21-39;810-860 <WIC>
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F;542-565/Domain: transmembrane #status predicted <TMN>
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif
F;232,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
| | | | |
Db 343 LDWSW 347

RESULT 9
A45583
receptor tyrosine kinase Mek4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.

New Biol. 3, 769-778, 1991
A;Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A;Reference number: A45583; MUID:92031278; PMID:1657122
A;Accession: A45583
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 <SAJ>
A;Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif

Query Match 90.0%; Score 36; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
| | | | |
Db 342 LDWSW 346

RESULT 10
T03355
gene e12 protein - Lactococcus phage bIL170
C;Species: Lactococcus phage bIL170
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
C;Accession: T03355
R;Crutz-Le Cog, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin
submitted to the EMBL Data Library, June 1997
A;Description: Sequence and organization of the lactococcal isometric bIL170 phage ge
A;Reference number: Z14903
A;Accession: T03355
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-211 <CRU>
A;Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AAC27226.1; PID:g3282307
C;Genetics:
A;Gene: e12
C;Superfamily: Lactococcus phage bIL170 gene e12 protein

Query Match 85.0%; Score 34; DB 2; Length 211;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
Db 29 LSWSWA 34

RESULT 11
E84949
tetrahydrofolyolypolyglutamate synthase (EC 6.3.2.17) [Imported] - Buchnera sp. (strain
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E84949
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84949
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: folic; BU167
C;Superfamily: folypolyglutamate synthase
C;Keywords: ligase

Query Match 85.0%; Score 34; DB 2; Length 411;

Best Local Similarity 80.0%; Pred. NO. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
:||||
Db 219 IDWSW 223

RESULT 12

T31511

hypothetical protein Y116A8C.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000

C:Accession: T31511

R:McMurray, A.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21041

A:Accession: T31511

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-433 <WIL>

A:Cross-references: EMBL:AL117204; PIDN:CAB55145.1; CESP:Y116A8C.9

A:Experimental source: clone Y116A8C

C:Genetics:

A:Gene: CESP:Y116A8C.9

A:Introns: 16/2; 42/2; 75/2; 107/3; 230/3; 262/3; 318/3; 373/1; 398/1

C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.9

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 433;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6

:||||

Db 174 VDWTTWA 179

RESULT 13

T14235

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Synechococcus sp. (strain PCC 70

C:Species: Synechococcus sp.

A:Variety: strain PCC 7002

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002

C:Accession: T14235

R:Klughammer, B.; Sultemeyer, D.; Badger, M.R.; Price, G.D.

submitted to the EMBL Data Library, April 1997

A:Description: Involvement of ndhF3, ndhD3 and ORF427 genes in high affinity CO2 uptake

A:Reference number: Z17936

A:Accession: T14235

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-616 <KLH>

A:Cross-references: EMBL:U97516; NID:G2232044; PID:G2232046; PIDN:AAB62184.1

A:Experimental source: strain PCC 7002

C:Genetics:

A:Note: ndhF3

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 616;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6

:||||

Db 115 MDGWA 120

RESULT 14

A10379

probable potassium efflux system YP03129 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: A10379
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10379

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1139 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:gl5981067; GSPDB:GN00175

C:Genetics:

A:Gene: YP03129

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 1139;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

1 LDWSW 5

:||||

Db 480 MDWSW 484

RESULT 15

B82531

conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C:Accession: B82531

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82531

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-198 <SIM>

A:Cross-references: GB:AB004072; GB:AE003849; NID:g9107884; PIDN:AAF85463.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

J.D.; Junqueira, M.L.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

M.; Tshakoko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2666

C:Superfamily: conserved hypothetical protein MJ1677

Query Match

Best Local Similarity 82.5%; Score 33; DB 2; Length 198;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

2 DWSWA 6

:||||

Db 135 DWNWA 139

Search completed: May 30, 2003, 14:52:40

Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDWSWA 6

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	362	1 DCUP_YEAST	P32347 saccharomyc
2	36	90.0	598	1 MRJ5_APIME	O97432 apis mellif
3	36	90.0	745	1 IKKA_HUMAN	O15111 h inhibitor
4	36	90.0	745	1 IKKA_MOUSE	Q60880 m inhibitor
5	36	90.0	756	1 IKKE_HUMAN	O14920 homo sapien
6	36	90.0	757	1 IKKE_MOUSE	O88351 mus musculu
7	36	90.0	757	1 IKKE_RAT	Q9QV78 rattus norv
8	36	90.0	983	1 EPA3_CHICK	P29318 gallus gall
9	36	90.0	983	1 EPA3_HUMAN	P29320 homo sapien
10	36	90.0	983	1 EPA3_MOUSE	P29319 mus musculu
11	36	90.0	984	1 EPA3_RAT	O08680 rattus norv
12	34	85.0	411	1 FOLC_BUCAI	P57265 buchnera ap
13	33	82.5	376	1 PGLR_PENGR	O93883 penicillium
14	33	82.5	453	1 NRAM_IAMWL	P03470 influenza a
15	33	82.5	454	1 NRAM_IAPUE	P03468 influenza a
16	33	82.5	492	1 AERA_AERTR	P09166 aeromonas t
17	33	82.5	524	1 CP72_CATRO	Q05047 catharanthu
18	33	82.5	656	1 VERE_SALTI	P43112 salmonella
19	33	82.5	840	1 VPH1_YEAST	P32563 saccharomyc
20	33	82.5	1842	1 PAS2_SCHPO	Q10289 s fatty aci
21	32	80.0	86	1 Y2X5_HUMAN	Q9Y530 homo sapien
22	32	80.0	107	1 STEL_RHUVU	P00302 rhus vernic
23	32	80.0	191	1 GDJR_CABEL	Q20496 caenorhabdi
24	32	80.0	210	1 KTHY_SCHPO	P36590 schizosacch
25	32	80.0	272	1 CYL_RHURU	P23135 rhodospiril
26	32	80.0	282	1 3MG2_ECOLI	P04395 escherichia
27	32	80.0	295	1 X769_HUMAN	Q99871 homo sapien
28	32	80.0	296	1 CYOA_BUCAI	P57544 buchnera ap
29	32	80.0	307	1 QOX2_ACEAC	P50653 acetobacter
30	32	80.0	314	1 CYOA_PSEPU	Q99WR1 pseudomonas
31	32	80.0	360	1 WNT2_CAEEL	P34889 caenorhabdi
32	32	80.0	375	1 HIS7_XANCP	P58982 xanthomonas
33	32	80.0	418	1 HLT_VIBPA	Q99289 vibrio para

RESULT 1

ID	DCUP_YEAST	STANDARD;	PRT;	362 AA.
AC	P32347;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).			
GN	HEM12 OR HEM6 OR POP3 OR YD9609.03.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92249304; PubMed=1576986;			
RA	Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,			
RA	Kushner J., Labbe P.;			
RT	"Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12			
RT	gene sequence and evidence for two conserved glycines essential for			
RT	enzymatic activity.";			
RL	Eur. J. Biochem. 205:1011-1016(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93348774; PubMed=8346678;			
RA	Diflumeri C., Larocque R., Keng T.;			
RT	"Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the			
RT	gene for uroporphyrinogen decarboxylase.";			
RL	Yeast 9:613-623(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=S288c / AB972;			
RA	Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;			
RL	Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	MUTANTS.			
RX	MEDLINE=93111946; PubMed=1471989;			
RA	Chelstowska A., Zodek T., Garey J.R., Kushner J., Rytka J.,			
RA	Labbe-Bois R.;			
RT	"Identification of amino acid changes affecting yeast			
RT	uroporphyrinogen decarboxylase activity by sequence analysis of hem12			
RT	mutant alleles.";			
RL	Biochem. J. 288:753-757(1992).			
CC	-1- CATALYTIC ACTIVITY: Uroporphyrinogen-III - coproporphyrinogen + 4			
CC	Co(2).			
CC	-1- PATHWAY: PORPHYRIN AND HEME BIOSYNTHESIS.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.			
CC	-----			
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ALIGNMENTS

34	32	80.0	470	1	NRAM_IADBU	Q07570 influenza a
35	32	80.0	470	1	NRAM_IADCH	Q07571 influenza a
36	32	80.0	470	1	NRAM_IADH2	Q07572 influenza a
37	32	80.0	470	1	NRAM_IADM2	Q07573 influenza a
38	32	80.0	470	1	NRAM_IADU3	Q07599 influenza a
39	32	80.0	470	1	NRAM_IAGFN	Q07574 influenza a
40	32	80.0	470	1	NRAM_IAGHD	Q07577 influenza a
41	32	80.0	470	1	NRAM_IAHJI	Q07578 influenza a
42	32	80.0	470	1	NRAM_IAMAE	Q07583 influenza a
43	32	80.0	470	1	NRAM_IATKL	Q07585 influenza a
44	32	80.0	479	1	BGLA_BACSU	P42973 bacillus su
45	32	80.0	500	1	PROP_ECOLI	P30848 escherichia

```
CC -----
DR EMBL; X63721; CAA45253.1; -
DR EMBL; Z19089; CAA79514.1; -
DR EMBL; Z49209; CAA89078.1; -
DR PIR; S23471; S23471.
DR PIR; S20190; S20190.
DR PIR; S31312; S31312.
DR HSP; P06132; IURO.
DR SGD; S0002454; HEM12.
DR InterPro; IPR000257; Uro_decaboxyls.
DR Pfam; PF01208; URO-D; 1.
DR PROSITE; PS00906; UROD_1; 1.
DR PROSITE; PS00907; UROD_2; 1.
KW Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
FT VARIANT 59 S -> F (IN HEM12-6 AND HEM12-12).
FT VARIANT 62 T -> I (IN HEM12-14).
FT VARIANT 107 L -> S (IN HEM12-3 AND HEM12-13).
FT VARIANT 215 S -> N (IN HEM12-2 AND HEM12-11).
FT MUTAGEN 33 G->D: INACTIVATION.
FT MUTAGEN 300 G->D: INACTIVATION.
SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48E62BC277 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
DB 279 LDWSW 283

RESULT 2
MRJ5_APIME STANDARD; PRT; 598 AA.
AC O97432;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Apoidea; Apidae; Apis.
OX NCBI_TaxID=7460;
RN SEQUENCE FROM N.A.
RP TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;
RT "The family of major royal jelly proteins and its evolution.";
RL J. Mol. Evol. 49:290-297(1999).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
CC -1- DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF
CC THE NURSE HONEY BEE.
CC -1- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; AF004842; AAD01205.1; -
DR InterPro; IPR003534; Royaljelly.
```

```
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PRO1366; ROYALJELLY.
KW Signal; Repeat; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C777ACDF63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
DB 113 DWSWA 117

RESULT 3
IKKA_HUMAN STANDARD; PRT; 745 AA.
ID IKKA_HUMAN
AC O15111; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IkBKA) (IKK-alpha) (Ikkappa kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN IKKA OR CHUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RP TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkappaB kinase.";
RL Cell 90:373-383(1997).
RN [1]
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
RT factor NF-kappaB.";
RL Nature 388:548-554(1997).
RN [3]
RN [4]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RX TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RA "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RA NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RX TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
```

RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain.";
RL Cell. Mol. Biol. Res. 41:537-549(1995).
RN [6]
RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND
RP S-180.
RX MEDLINE-98188283; PubMed-9520446;
RA Ling L., Cao Z., Goeddel D.V.;
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
RT Ser-176.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
RN [7]
RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE-99413720; PubMed-10485710;
RA O'Neil, Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,
RT Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt
RT serine-threonine kinase.";
RL Nature 401:82-85(1999).
RN [8]
RP IKK-IRKB BINDING.
RX MEDLINE-99212141; PubMed-10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
RT IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [9]
RP IKK PHOSPHORYLATION.
RX MEDLINE-99038238; PubMed-9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase Kinase Kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [10]
RP REVIEW.
RX MEDLINE-20178139; PubMed-10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -!- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
CC -!- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
CC WHEN DEPHOSPHORYLATED.
CC -!- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
CC ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
CC MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC
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CC
CC -----
CC EMBL: AF012890; AAC51662.1; --
CC DR EMBL: AF009225; AAC51671.1; --
CC DR EMBL: AF080157; AAD08996.1; --
CC DR EMBL: U22512; AAC50713.1; --
CC DR HSSP: Q63450; 1A06.
CC DR Genew: HGNC:1974; CHUK.
CC MIM: 600664; --

DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_chr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 302 PROTEIN KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 738 743 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
FT MUTAGEN 23 23 DECREASE OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
FT MUTAGEN 176 176 ACTIVITY.
FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
FT CONFLICT 543 543 E -> G (IN REF. 2).
FT CONFLICT 604 604 L -> R (IN REF. 5).
FT CONFLICT 679 680 TS -> AY (IN REF. 5).
FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
FT CONFLICT 686 687 TS -> DL (IN REF. 5).
SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSW 5
Db 738 LDWSW 742
RESULT 4
IKKA_MOUSE STANDARD; PRT; 745 AA.
AC Q60680; Q9D2X3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (BC 2.7.1.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).
GN IKKA OR CHUK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=BALB/c;
RX MEDLINE-96044444; PubMed-7558004;
RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
RT chromosome 10 and mouse chromosome 19.";
RL Genomics 27:348-351(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=BALB/c;
RX MEDLINE-96258427; PubMed-8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase

RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN-C57BL/6J; TISSUE-Colon;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itochi M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RP "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE-20198447; PubMed-10733566;
 RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
 RA Gelezlunas R., Marcu K.B.;
 RP "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT Ikbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE-9818238; PubMed-9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RP "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE-99212141; PubMed-10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RP "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; PubMed-9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RP "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RP "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 CC WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN

CC ALSO BIND TO MAP3K14/NIK, MEKK1, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2/DELTA LH AND
 CC 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS ONLY FOR ISOFORM 1, ISOFORMS 2 AND
 CC 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.
 CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY
 CC E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION
 CC PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.
 CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSE EXTENT BY
 CC MEKK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U12473; AAC52589.1; --
 DR EMBL; AK018671; BAB31335.1; --
 DR HSP; O63450; IA06.
 DR MGD; MGI:99484; Chuk.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR PRODOM; PD000001; Euk_pkinase.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Alternative splicing.
 FT DOMAIN 15 300
 FT PROTEIN KINASE.
 FT DOMAIN 455 476
 FT LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 21 29
 FT NEMO-BINDING.
 FT BINDING 44 44
 FT ATP (BY SIMILARITY).
 FT ACT_SITE 144 144
 FT BY SIMILARITY.
 FT MOD_RES 23 23
 FT PHOSPHORYLATION (BY PKB/AKT1) (BY
 FT SIMILARITY).
 FT MOD_RES 176 176
 FT PHOSPHORYLATION (BY MAP3K14) (BY
 FT SIMILARITY).
 FT VARSPLIC 452 471
 FT MSLRYNANLTKMKNTLIS -> IFRKNVKSMEGRKRGH
 FT SLF (IN ISOFORM 2).
 FT VARSPLIC 472 745
 FT MISSING (IN ISOFORM 2).
 FT VARSPLIC 577 584
 FT DHLYSDST -> GRTLOSQY (IN ISOFORM 3).
 FT VARSPLIC 585 745
 FT MISSING (IN ISOFORM 3).
 FT CONFLICT 236 236
 FT K -> E (IN REF. 3).
 FT CONFLICT 400 400
 FT S -> Y (IN REF. 3).
 SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AFP92233 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 Db 738 LDMSW 742
 RESULT 5
 IKKB_HUMAN
 ID IKKB_HUMAN STANDARD; PRT; 756 AA.
 AC O14920; O75327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase

DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
RT 8p12--p11 by in situ hybridization.";
RL Cytogenet. Cell Genet. 82:32-33(1998).
RN [5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [7]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of
RT mucosal inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
CC COMPLEX.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL
CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND
CC PERIPHERAL BLOOD.
CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
CC WEAKLY AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKKAPAB KINASE SUBFAMILY.

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF029684; AAC51860.1;
CC EMBL: AF080158; AAD08997.1;
CC EMBL: AF031416; AAC64675.1;
CC EMBL: BC006231; AAH06231.1;
CC HSP: Q63450; IAO6.
CC Genew: HGNC:5960; IKKB.
CC MIM: 603258;
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00240; ubiquitin; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Euk_pkinase; 1.
CC ProSite: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC ProSite: PS00108; PROTEIN_KINASE_ST; 1.
CC ProSite: PS00011; PROTEIN_KINASE_DOM; 1.
CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC DOMAIN 15 300 PROTEIN KINASE.
CC DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
CC NP_BIND 737 742 NEMO-BINDING.
CC BINDING 21 29 ATP (BY SIMILARITY).
CC ACT_SITE 44 44 ATP (BY SIMILARITY).
CC MOD_RES 145 145 BY SIMILARITY.
CC MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
CC MOD_RES 177 177 PHOSPHORYLATION.
CC MOD_RES 181 181 PHOSPHORYLATION.
CC MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
CC EFFECT ON BINDING TO NIK.
CC MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
CC MUTAGEN 177 177 S->E: FULL ACTIVATION.
CC MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
CC MUTAGEN 181 181 S->E: FULL ACTIVATION.
CC CONFLICT 231 255 WSKVRKSEVDIVVSEDLNGTVKF -> CYRMPGPGVAHS
CC CONFLICT 425 425 CNFTSLGGRW (IN REF. 5).
CC CONFLICT 425 425 Q -> H (IN REF. 1).
CC SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
CC Query Match 90.0%; Score 36; DB 1; Length 756;
CC Best Local Similarity 100.0%; Pred. No. 88;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 LDWSW 5
CC DB 737 LDWSW 741
CC
CC RESULT 6
CC ID IKKB_MOUSE STANDARD; PRT; 757 AA.
CC AC 088351; Q9RLJ6;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1)
CC DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
CC DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
CC GN IKKB OR IKKB.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]

RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
 RC STRAIN-C57BL/6; TISSUE-Spleen;
 RX MEDLINE-98188238; PubMed-9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE-99455228; PubMed-10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; PubMed-9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RT "The IkappaB/NF-kappaB system: a key determinant of mucosal
 RT inflammation and protection";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-ALPHA BUT
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBQUITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPA-B KINASE SUBFAMILY.
 CC
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 CC
 CC EMBL; AF026524; AAC23557.1;
 CC EMBL; AF088910; AAD52095.1;
 CC HSPB; Q63450; IAO6.
 CC MGI; 1338071; Ikbkb.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT BINDING 21 29 NEMO-BINDING.
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 ATP (BY SIMILARITY).
 FT MOD_RES 23 23 BY SIMILARITY.
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDNSWLMQWDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 DB 737 LDWSW 741
 RESULT 7
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIB).
 OS Rattus norvegicus (Rat).
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; PubMed-9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBQUITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPA-B KINASE SUBFAMILY.

CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P63-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF115282; AAF21978.1;
 CC HSP: Q63450; IAO6.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC Pfam: PF00069; pkinase; 1.
 CC PRINTS: PR00109; TYRKINASE.
 CC ProDom: PD000001; Euk_pkinase; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
 CC phosphorylation.
 CC DOMAIN 15 300 PROTEIN KINASE.
 CC DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC DOMAIN 737 742 NEMO-BINDING.
 CC NP_BIND 21 29 ATP (BY SIMILARITY).
 CC BINDING 44 44 ATP (BY SIMILARITY).
 CC ACT_SITE 145 145 BY SIMILARITY.
 CC MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 CC MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 CC MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 CC SEQUENCE 757 AA; 86866 MW; 3AFFE46A7DF91F9C CRC64;
 CC -----
 CC Query Match 90.08; Score 36; DB 1; Length 757;
 CC Best Local Similarity 100.0%; Pred. No. 88;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 LDWSW 5
 CC DB 737 LDWSW 741
 CC -----
 CC RESULT 8
 CC EPA3_CHICK STANDARD; PRT; 983 AA.
 CC AC P29318;
 CC DT 01-DEC-1992 (Rel. 24, Created)
 CC DT 01-DEC-1992 (Rel. 24, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 CC kinase receptor ETK1) (CEK4).
 CC GN EPA3 OR ETK1 OR CEK4.
 CC OS Gallus gallus (Chicken).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 CC OC Gallus.
 CC NCBI_TaxID=9031;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE-92031278; PubMed-1657122;
 CC RA Sajjadi F.G.; Pasquale E.B.; Subramani S.;
 CC RT Identification of a new eph-related receptor tyrosine kinase gene
 CC from mouse and chicken that is developmentally regulated and encodes
 CC at least two forms of the receptor.";

RL New Biol. 3:769-778(1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M68514; AAA48666.1;
 CC PIR: B45583; B45583.
 CC HSP: P00523; 2PTK.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR001090; Ephrin_receptor.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR003961; FN_III.
 CC InterPro: IPR003962; FNIII_repeat.
 CC InterPro: IPR001660; SAM.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC InterPro: IPR001426; Ykase_receptor.
 CC Pfam: PF00041; fn3; 2.
 CC Pfam: PF00069; pkinase; 1.
 CC Pfam: PF00536; SAM; 1.
 CC Pfam: PF01404; EPH_lbd; 1.
 CC PRINTS: PR00014; FNTYPEIII.
 CC PRINTS: PR00109; TYRKINASE.
 CC ProDom: PD000001; Euk_pkinase; 1.
 CC ProDom: PD001495; Ephrin_receptor; 1.
 CC SMART: SM00001; EGF_like; 1.
 CC SMART: SM00060; FN3; 2.
 CC SMART: SM00454; SAM; 1.
 CC SMART: SM00219; TYRK; 1.
 CC PROSITE: PS01186; EGF_2; UNKNOWN_1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC PROSITE: PS50105; SAM_DOMAIN; 1.
 CC Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC SIGNAL 1 19 BY SIMILARITY.
 CC CHAIN 20 983 EPHRIN TYPE-A RECEPTOR 3.
 CC DOMAIN 20 540 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 541 564 POTENTIAL.
 CC DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 188 321 CIS-RICH.
 CC DOMAIN 322 431 FIBRONECTIN TYPE-III 1.
 CC DOMAIN 432 529 FIBRONECTIN TYPE-III 2.
 CC DOMAIN 621 882 PROTEIN KINASE.
 CC DOMAIN 911 975 SAM.
 CC SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).
 CC NP_BIND 627 635 ATP (BY SIMILARITY).
 CC BINDING 653 653 ATP (BY SIMILARITY).
 CC ACT_SITE 746 746 BY SIMILARITY.
 CC MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 CC MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 CC MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).

FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 983 AA; 109910 MW; E8895F0BDF77651E CRC64;

Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. NO. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSW 5
 Db 342 LMSW 346

RESULT 9
 ID EPA3_HUMAN STANDARD; PRT; 983 AA.
 AC P29320; Q9H2V4; Q9H2V3;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK) (HEK) (HEK4).
 GN EPA3 OR ETK1 OR ETK OR HEK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92179233; PubMed=1311845;
 RA Wicks I.P., Wilkison D., Salvaris E., Boyd A.W.;
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
 RT kinase expressed by human lymphoid tumor cell lines";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Melanoma;
 RA Chari R., Hames G., Stroobant V., Maillere B., Texier C., Mach B.,
 RA Boon T., Coullie P.G.;
 RT "Identification of a tumor specific shared antigen derived from an
 RT Eph-receptor and presented to CD4 T cells on HLA class II
 RT molecules";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
 RX MEDLINE=92147681; PubMed=1737782;
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
 RA Welch K., Loudovaris M., Rockman S., Busmanis I.;
 RT "Isolation and characterization of a novel receptor-type protein
 RT tyrosine kinase (hek) from a human pre-B cell line";
 RL J. Biol. Chem. 267:3262-3267(1992).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
 CC FUNCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
 CC SECRETED (ISOFORM 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC
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 or send an email to license@isb-sib.ch).

 CC EMBL; M83941; AAA58633.1; -
 CC EMBL; AF213459; AAG43576.1; -
 CC EMBL; AF213460; AAG43577.1; -
 CC EMBL; A28003; CAA01906.1; -
 CC PIR; A38224; A38224.
 CC HSP; P00523; 2PTK.
 CC Genew; HGNC:3387; EPHA3.
 CC MIM; 179611; -
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR001090; Ephrin_receptor.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR003961; FN.III.
 CC InterPro; IPR003962; FN.III_repeat.
 CC InterPro; IPR001660; SAM.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC InterPro; IPR001426; YKase_receptorV.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00536; SAM; 1.
 CC Pfam; PF01404; EPH_lbd; 1.
 CC PRINTS; PR00014; FNTYPEII.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC ProDom; PD001495; Ephrin_receptor; 1.
 CC SMART; SM00001; EGF_like; 1.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00454; SAM; 1.
 CC SMART; SM00219; Tyrk; 1.
 CC PROSITE; PS01186; EGF_2; UNKNOWN 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC PROSITE; PS00105; SAM_DOMAIN; 1.
 CC Transfaser; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 CC Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 983
 FT DOMAIN 21 541
 FT TRANSMEM 542 565
 FT DOMAIN 566 983
 FT DOMAIN 189 322
 FT DOMAIN 323 432
 FT DOMAIN 433 530
 FT DOMAIN 621 882
 FT DOMAIN 911 975
 FT SITE 981 983
 FT NP_BIND 627 635
 FT BINDING 553 653
 FT ACT_SITE 746 746
 FT MOD_RES 596 596
 FT MOD_RES 602 602
 FT MOD_RES 779 779
 FT CARBOHYD 232 232
 FT CARBOHYD 337 337
 FT CARBOHYD 391 391
 FT CARBOHYD 404 404
 FT CARBOHYD 493 493
 FT CARBOHYD 532 539
 FT VARSPIC 540 983
 FT CONFLICT 507 507
 FT CONFLICT 724 724
 FT CONFLICT 911 911
 FT CONFLICT 924 924
 SQ SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 983;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSW 5
Db 343 LDWSW 347

RESULT 10

EPA3_MOUSE
ID EPA3_MOUSE STANDARD; PRT; 983 AA.
AC P29319;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
kinase receptor ETK1) (MEK4).
DE EPA3 OR ETK1 OR MEK4 OR TYRO4.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR X Swiss Webster; TISSUE=Embryo;
RX MEDLINE=92031278; PubMed=1657122;
RA Sajjadi F.G., Pasquale E.B., Subramani S.;
RT Identification of a new eph-related receptor tyrosine kinase gene
from mouse and chicken that is developmentally regulated and encodes
at least two forms of the receptor.";
RL New Biol. 3:769-778(1991).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM
IS SECRETED.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
BRAIN, ALSO DETECTED IN TESTIS.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.

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EMBL; M68513; AAA39521.1;
EMBL; M68515; AAA39522.1; ALT_SEQ.
DR PIR; A45583; A45583.
DR HSP; P00523; 2PTK.
DR MGD; MGI:99612; EphA3.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR001426; Ykase_receptorv.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00089; pkinase_1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_lbd; 1.
DR PRINTS; PR00014; FNTYPEII.
DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; phosphorylation;
KW Receptor; transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 983
FT DOMAIN 21 540
FT TRANSMEM 541 564
FT DOMAIN 565 983
FT DOMAIN 188 321
FT DOMAIN 322 431
FT DOMAIN 432 529
FT DOMAIN 621 882
FT DOMAIN 911 975
FT SITE 981 983
FT NP_BIND 627 635
FT BINDING 653 653
FT ACT_SITE 746 746
FT MOD_RES 596 596
FT MOD_RES 602 602
FT MOD_RES 779 779
FT CARBOHYD 231 231
FT CARBOHYD 336 336
FT CARBOHYD 390 390
FT CARBOHYD 403 403
FT CARBOHYD 492 492
FT CARBOHYD 530 530
SQ SEQUENCE 983 AA; 109955 MW; BE44A665D8107A2 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSW 5
Db 342 LDWSW 346

RESULT 11

EPA3_RAT
ID EPA3_RAT STANDARD; PRT; 984 AA.
AC O08680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
kinase receptor REK4) (TYRO-4).
GN EPA3 OR REK4 OR TYRO4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98130505; PubMed=9458884;
RA Li Y.Y., McTierman C.F., Feldman A.M.;
RT "Il-1 beta alters the expression of the receptor tyrosine kinase gene
r-EphA3 in neonatal rat cardiomyocytes.";
RL Am. J. Physiol. 274:H331-H341(1998).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A2, -A3, -A4 AND -A5.

CC CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC CC tyrosine phosphate.
 CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, AND LUNG.
 CC CC -1- INDUCTION: DOWN-REGULATED BY IL1-BETA IN NEONATAL CARDIAC
 CC CC MYOCYTES.
 CC CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC CC RECEPTOR SUBFAMILY.
 CC CC
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 CC CC or send an email to license@isb-sib.ch).
 CC CC
 CC CC EMBL; U69278; AAC06273.1; -
 CC CC HSSP; P00523; 2PTK.
 CC CC InterPro; IPR000561; EGF-like.
 CC CC InterPro; IPR001090; Ephrin_receptor.
 CC CC InterPro; IPR000719; Euk_pkinase.
 CC CC InterPro; IPR003961; FN_III.
 CC CC InterPro; IPR003962; FNIII_repeat.
 CC CC InterPro; IPR001660; SAM.
 CC CC InterPro; IPR001245; Tyr_pkinase.
 CC CC InterPro; IPR001426; Ykase_receptorV.
 CC CC Pfam; PF00041; fn3_2.
 CC CC Pfam; PF00069; pkinase; 1.
 CC CC Pfam; PF00536; SAM; 1.
 CC CC Pfam; PF01404; EPH_lbd; 1.
 CC CC PRINTS; PR00014; FNTYPEIII.
 CC CC PRINTS; PR00109; TYRKINASE.
 CC CC ProDom; PD000001; Euk_pkinase; 1.
 CC CC ProDom; PD001495; Ephrin_receptor; 1.
 CC CC SMART; SM00060; FN3; 2.
 CC CC SMART; SM00454; SAM; 1.
 CC CC SMART; SM00219; Tyrc; 1.
 CC CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
 CC CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC CC PROSITE; PS0105; SAM_DOMAIN; 1.
 CC CC Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC CC SIGNAL 1 20
 CC CC CHAIN 21 984
 CC CC DOMAIN 21 541
 CC CC TRANSMEM 542 565
 CC CC DOMAIN 566 984
 CC CC DOMAIN 189 322
 CC CC DOMAIN 328 431
 CC CC DOMAIN 436 528
 CC CC DOMAIN 622 883
 CC CC DOMAIN 912 976
 CC CC SITE 982 984
 CC CC NP_BIND 628 636
 CC CC BINDING 654 654
 CC CC ACT_SITE 747 747
 CC CC MOD_RES 597 597
 CC CC MOD_RES 603 603
 CC CC MOD_RES 780 780
 CC CC CARBOHYD 232 232
 CC CC CARBOHYD 337 337
 CC CC CARBOHYD 391 391
 CC CC CARBOHYD 404 404
 CC CC CARBOHYD 493 493
 CC CC SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 984;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 DB 343 LDWSW 347
 RESULT 12
 FOLC_BUCAI STANDARD; PRT; 411 AA.
 AC PSY265;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE FOLC bifunctional protein [Includes: Folylpolyglutamate synthase
 DE (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS);
 DE Dihydrofolate synthase (EC 6.3.2.12)].
 GN FOLC OR BU167.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID-118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Tokyo 1998;
 RX MEDLINE-20445173; PubMed-10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.
 CC -1- CATALYTIC ACTIVITY: ATP + (tetrahydrofolyl-[Glu])(N) + L-glutamate
 CC = ADP + phosphate + (tetrahydrofolyl-[Glu])(N+1)
 CC -1- CATALYTIC ACTIVITY: ATP + dihydropterate + L-glutamate = ADP +
 CC phosphate + dihydrofolate.
 CC -1- PATHWAY: BACTERIA REQUIRE FOLATE FOR THE BIOSYNTHESIS OF GLYCINE,
 CC METHIONINE, FORMYL-MET-TRNA, THYMIDYLATES, PURINES, AND
 CC PANTOTHENATE.
 CC -1- SIMILARITY: BELONGS TO THE FOLYLGLUTAMATE SYNTHASE FAMILY.
 CC
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 CC
 CC EMBL; AP001118; BAB12885.1; -
 CC HSSP; P15925; 1FGS.
 CC InterPro; IPR001645; Fpolygl_synthetse.
 CC InterPro; IPR000713; Mur_ligase.
 CC Pfam; PF01225; Mur_ligase; 1.
 CC PROSITE; PS01011; FOLYLGLUTAMATE_SYNTH_1; 1.
 CC PROSITE; PS01012; FOLYLGLUTAMATE_SYNTH_2; FALSE_NEG.
 CC KW Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
 CC Folate biosynthesis; Complete proteome.
 CC FT NP_BIND 50 56
 CC FT BINDING 50 56
 CC SEQUENCE 411 AA; 46970 MW; 5DDC2DC6539935A CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 411;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 DB 219 IDWSW 223
 RESULT 13
 FGLR_PENGR

ID PCLR_PENGR STANDARD; PRT; 376 AA.
 AC 093863;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Polylacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
 GN PGG1
 OS Penicillium griseoroseum.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 OX NCBI_TaxID=84562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CCT 6421;
 RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
 RT "Cloning and characterization of a gene encoding the
 RT endopolylacturonase of Penicillium griseoroseum";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
 CC galactosiduronic linkages in pectate and other galacturonans.
 CC -!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
 CC (POLYLACTURONASES).
 CC -----
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 CC -----
 DR EMBL; AF085238; AAC83692.1; .
 DR InterPro; IPR000743; GH28.
 DR Pfam; PF00295; Glyco_hydro.28; 1.
 DR PROSITE; PS00502; POLYLACTURONASE; 1.
 KW Hydrolase; Glycosidase; Cell wall; Signal.
 FT SIGNAL 1 20 POTENTIAL
 FT CHAIN 21 376 POLYLACTURONASE.
 SQ SEQUENCE 376 AA; 38068 MW; 1EDB1EC56ED56928 CRC64;

 Query Match 82.5%; Score 33; DB 1; Length 376;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 2 DMSWA 6
 DB 350 DMSWS 354

 RESULT 14
 NRAM_IAMWIL STANDARD; PRT; 453 AA.
 ID NRAM_IAMWIL
 AC P03470;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Wilson-Smith/33).
 CC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 CC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82192605; PubMed=7077751;
 RA Hiti A.L., Nayak D.P.;
 RT "Complete nucleotide sequence of the neuraminidase gene of human
 RT influenza virus A/WSN/33";
 RL J. Virol. 41:730-734(1982).
 CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitates
 CC the mobility of the virus to and from the site of infection.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 DR EMBL; J02177; AAA43397.1; ALT_SEQ.
 DR PIR; A00882; NMIV3.
 DR HSSP; P03472; ZQWC.
 DR InterPro; IPR001860; GH_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; GH_34; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 35 ANCHOR.
 FT DOMAIN 36 74 HYPERVARIABLE STALK REGION.
 FT DOMAIN 75 453 HEAD OF NEURAMINIDASE.
 FT ACT_SITE 259 259 PROBABLE.
 FT ACT_SITE 261 261 PROBABLE.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 453 AA; 49623 MW; 7DC56A4416A47BE8 CRC64;

 Query Match 82.5%; Score 33; DB 1; Length 453;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 LDMSW 5
 DB 437 VDMSW 441

 RESULT 15
 NRAM_IAPUE STANDARD; PRT; 454 AA.
 ID NRAM_IAPUE
 AC P03468;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Puerto Rico/8/34).
 CC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 CC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11455;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81148841; PubMed=7010182;
 RA Fields S., Winter G., Brownlee G.G.;
 RT "Structure of the neuraminidase gene in human influenza virus
 RT A/PR/8/34";
 RL Nature 290:213-217(1981).
 CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitates
 CC the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -!- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----

DR EMBL; J02146; AAA43412.1; -
 DR PIR; A00880; NMIV.
 DR HSSP; P03472; 2QWC.
 DR InterPro; IPR001860; GH_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; GH_34; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 35
 FT DOMAIN 36 75
 FT ACT_SITE 76 454
 FT ACT_SITE 260 260
 FT ACT_SITE 262 262
 FT CARBOHYD 44 44
 FT CARBOHYD 58 58
 FT CARBOHYD 73 73
 FT CARBOHYD 131 131
 FT CARBOHYD 220 220
 SQ SEQUENCE 454 AA; 50143 MW; A0DC4C08A2B53705 CRC64;
 HYPERVARIABLE STALK REGION.
 HEAD OF NEURAMINIDASE.
 PROBABLE.
 PROBABLE.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 82.5%; Score 33; DB 1; Length 454;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 :||||
 Db 438 VDWSW 442

Search completed: May 30, 2003, 15:48:50
 Job time : 3.11842 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: US-09-643-260-5
Perfect score: 40
Sequence: 1 LDWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	242	12	Q919K8
2	37	92.5	304	16	Q91719
3	36	90.0	258	5	O45498
4	36	90.0	374	16	Q9HZ10
5	36	90.0	409	10	Q9M3F6
6	36	90.0	597	5	Q9VGP2
7	36	90.0	740	6	Q95KV1
8	36	90.0	756	6	Q95KV0
9	34	85.0	211	9	O80148
10	34	85.0	211	9	O21903
11	34	85.0	309	2	Q9F163
12	34	85.0	323	12	Q9QTE2
13	34	85.0	394	5	Q9U2T2
14	34	85.0	616	2	O33749
15	34	85.0	1139	16	Q8ZC91
16	33	82.5	97	12	Q9QTI1

17	33	82.5	198	16	Q9PA54
18	33	82.5	232	17	Q8ZSR8
19	33	82.5	234	16	Q9X897
20	33	82.5	236	3	Q9P527
21	33	82.5	273	10	Q94JM4
22	33	82.5	273	10	Q94OD6
23	33	82.5	275	10	O65710
24	33	82.5	310	2	Q9XBS7
25	33	82.5	316	16	Q8UBG8
26	33	82.5	322	16	Q8YCK7
27	33	82.5	324	16	Q8YD70
28	33	82.5	330	4	Q96MZ6
29	33	82.5	347	16	Q98KR3
30	33	82.5	359	2	Q9ZFM9
31	33	82.5	360	2	Q50378
32	33	82.5	376	3	Q9UVL4
33	33	82.5	387	2	Q9RG52
34	33	82.5	388	10	Q9LUP8
35	33	82.5	408	16	Q8XWX2
36	33	82.5	415	16	Q8Z002
37	33	82.5	421	5	O16355
38	33	82.5	436	17	O29289
39	33	82.5	437	16	Q92K30
40	33	82.5	444	2	Q9XBD4
41	33	82.5	452	10	Q9SRT7
42	33	82.5	453	12	Q67215
43	33	82.5	453	12	Q67217
44	33	82.5	453	12	Q67216
45	33	82.5	464	12	Q9WMK7

ALIGNMENTS

RESULT 1

Q919K8 ID Q919K8 PRELIMINARY; PRT; 242 AA.
AC Q919K8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FLORIDA1997;
RX MEDLINE=21486685; PubMed=11602755;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
RL J. Virol. 75:11157-11165(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FLORIDA1997;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF403738; AAK94146.1;
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 100.0%; Score 40; DB 12; Length 242;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWA 6
Db 79 LDWSWA 84

RESULT 2

Q91719 PRELIMINARY; PRT; 304 AA.
 AC Q91719; 90.0%; Score 36; DB 5; Length 258;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Probable cytochrome c oxidase assembly factor.
 GN PA0113.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquch S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004449; AAG03503.1; -.
 DR InterPro; IPR000537; UblA.
 DR Pfam; PF01040; UblA; 1.
 DR PROSITE; PS00943; UblA; UNKNOWN_1.
 KW COMPLETE PROTEOME.
 SQ SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 92.5%; Score 37; DB 16; Length 304;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 |||:|
 DB 259 LDWAWA 264

RESULT 3

O45498 PRELIMINARY; PRT; 258 AA.
 AC O45498;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DE F39B2.5 protein.
 GN F39B2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dobson R.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z92834; CAB07386.1; -.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001496; SOCS.
 DR Pfam; PF00017; SH2; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00253; SOCS; 1.

DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 258 AA; 30897 MW; 820D4D73DC5CB060 CRC64;

Query Match 90.0%; Score 36; DB 5; Length 258;
 Best Local Similarity 83.3%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 |||:|
 DB 21 LDWAWA 26

RESULT 4

Q9HZ10 PRELIMINARY; PRT; 374 AA.
 AC Q9HZ10;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Hypothetical protein PA3230.
 GN PA3230.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquch S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004746; AAG06618.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
 |||||
 DB 81 DWSWA 85

RESULT 5

Q9M3F6 PRELIMINARY; PRT; 409 AA.
 AC Q9M3F6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE Putative replication protein.
 GN T1423.110.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
 RA Quetier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL132909; CAB87732.1; -
 DR InterPro; IPR003871; DUF223.
 DR Pfam; PF02721; DUF223; 2.
 SQ SEQUENCE 409 AA; 45738 MW; ADDC4EF597E4EE4 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 Db 190 LDWSW 194

RESULT 6

ID Q9VGP2 PRELIMINARY; PRT; 597 AA.
 AC Q9VGP2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CG6728 protein.
 GN CG6728.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephygroidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-107311132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003691; AAF54634.1; -

DR FlyBase; FBgn0037896; CG6728.
 DR InterPro; IPR000172; GMC_Oxred.
 DR InterPro; IPR000169; SHprot_acsite.
 DR Pfam; PF00732; GMC_Oxred; 1.
 DR PROSITE; PS00624; GMC_Oxred_2; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
 SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFFA902A CRC64;

Query Match 90.0%; Score 36; DB 5; Length 597;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
 Db 159 DWSWA 163

RESULT 7

ID Q95KV1 PRELIMINARY; PRT; 740 AA.
 AC Q95KV1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE IKB kinase-alpha.
 GN BIKKALPHA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
 RT "Identification and characterisation of the bovine IKB kinases (IKKs)
 RT alpha, beta and gamma";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ414555; CAC93866.1; -
 DR InterPro; IPR00719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;

Query Match 90.0%; Score 36; DB 6; Length 740;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 Db 733 LDWSW 737

RESULT 8

ID Q95KV0 PRELIMINARY; PRT; 756 AA.
 AC Q95KV0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE IKB kinase-beta.
 GN BIKKBETA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;

RT SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKKs)
RL alpha, beta and gamma";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ414556; CAC93687.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 90.0%; Score 36; DB 6; Length 756;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
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DB 737 LDWSW 741

RESULT 9
O080148 PRELIMINARY; PRT; 211 AA.
ID O80148
AC O80148;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E12.
GN E12.
OS bacteriophage bil170.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=63118;
RN SEQUENCE FROM N.A.
RA Krutz-Le Coq A.M., Cesselin B., Commissaire J., Anba J.,
RA Kyriakidis S., Chopin M.C.;
RT "Sequence and organization of the lactococcal isometric bil170 phage
RT genome";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF009630; AAC27226.1; -
SQ SEQUENCE 211 AA; 24258 MW; 8C0BF4E1280428FE CRC64;

Query Match 85.0%; Score 34; DB 9; Length 211;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
DB 29 LDWSWA 34

RESULT 10
O21903 PRELIMINARY; PRT; 211 AA.
ID O21903
AC O21903;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 24.3 kDa protein.
OS Bacteriophage sk1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=31532;
RN SEQUENCE FROM N.A.
RP MEDLINE=98043537; PubMed=9383189;
RA Chandry P.S., Moore S.C., Boyce J.D., Davidson B.E., Hillier A.J.;

RT "Analysis of the DNA sequence, gene expression, origin of replication
RT and modular structure of the Lactococcus lactis lytic bacteriophage
RL sk1";
RL Mol. Microbiol. 26:49-64(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chandry P.S., Moore S.C., Boyce J.D., Davidson B.E., Hillier A.J.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF011378; AAB70075.1; -
KW Hypothetical protein.
SQ SEQUENCE 211 AA; 24347 MW; BEC12F6340B3E124 CRC64;

Query Match 85.0%; Score 34; DB 9; Length 211;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
DB 29 LDWSWA 34

RESULT 11
Q9F163 PRELIMINARY; PRT; 309 AA.
ID Q9F163
AC Q9F163;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 33.3 kDa protein.
OS Amycolatopsis mediterranei (Nocardia mediterranei).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=33910;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-U-32;
RX MEDLINE=20272905; PubMed=10813025;
RA Zhang W.W., Yang L.L., Jiang W.H., Zhao G.P., Yang Y., Chiao J.S.;
RT "Molecular analysis and heterologous expression of the gene encoding
RT methylmalonyl-coenzyme A mutase from rifamycin SV-producing strain
RT Amycolatopsis mediterranei U32";
RL Appl. Biochem. Biotechnol. 82:209-225(1999).
DR EMBL; AF117980; AAG47629.1; -
DR InterPro; IPR005129; ArgK.
DR Pfam; PF03308; ArgK; 1.
DR TIGRfams; TIGR00750; laa; 1.
KW Hypothetical protein.
SQ SEQUENCE 309 AA; 33284 MW; E6EF6E71C553E6E3 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 309;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
DB 257 VDMTWA 262

RESULT 12
Q9QTE2 PRELIMINARY; PRT; 323 AA.
ID Q9QTE2
AC Q9QTE2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE UL2 product homolog (UL2 protein).
GN ORF 6 OR UL2.
OS Marek's disease virus serotype 2 MDV2, and
OS Gallid herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=36353, 35250;
RN [1]


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RP SEQUENCE FROM N.A.
RC SPECIES-Gallid herpesvirus 1 (serotype 2); STRAIN-HPRS24;
RA Jang H., Cai J., Izumiya Y., Murakami Y., Mochizuki M., Song C.,
RA Lee Y., Kai C., Takahashi E., Mikami T.;
RT "The complete DNA sequence and transcription map of the unique long
RT genome region of Marek's disease virus type 2.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Gallid herpesvirus 3; STRAIN-HPRS24;
RA Izumiya Y., Jang H., Ono M., Mikami T.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Gallid herpesvirus 3; STRAIN-HPRS24;
RA Izumiya Y., Jang H., Ono M., Mikami T.;
RT "A Complete Genomic DNA Sequence of Marek's Disease Virus Type 2,
RT Strain HPRS24.";
RL Curr. Top. Microbiol. Immunol. 0:0-0(2000).
DR EMBL; AB024414; BAA82895.1; -
DR EMBL; AB049735; BAA16509.1; -
DR HSSP; P10186; IUDH.
DR InterPro; IPR005122; UDNA_glycos.
DR InterPro; IPR002043; U_DNA_glycosylse.
DR InterPro; IPR003249; U_glycosyl.
DR Pfam; PF03167; UDG; 1.
DR ProDom; PD001589; U_glycosyl; 1.
DR TIGRFAMs; TIGR00628; ung; 1.
DR PROSITE; PS00130; U_DNA_GLYCOSYLASE; 1.
SQ SEQUENCE 323 AA; 35771 MW; 4B2E2C8F773C1B7D CRC64;

Query Match 85.0%; Score 34; DB 12; Length 323;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSW 5
Db 103 IDWSW 107

RESULT 13
ID Q9U2T2 PRELIMINARY; PRT; 394 AA.
AC Q9U2T2;
DT 01-MAR-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Y116A8C.9 protein.
GN Y116A8C.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurtry A.A.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL117204; CAB55145.3; -
SQ SEQUENCE 394 AA; 44319 MW; 645FF16CCF7D5E7E CRC64;

Query Match 85.0%; Score 34; DB 5; Length 394;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWA 6
Db 111 IDWSW 107

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Db 174 VDWTA 179

RESULT 14
ID O33749 PRELIMINARY; PRT; 616 AA.
AC O33749;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit 5.
GN NDHF3.
OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RA Klughammer B., Sultemeyer D., Badger M.R., Price G.D.;
RT "Involvement of ndhF3, ndhD3 and ORF427 genes in high affinity CO2
RT uptake in the marine cyanobacterium, Synecococcus sp. strain
RT PCC7002.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
DR EMBL; U97516; AAB62184.1; -
DR InterPro; IPR001750; Oxidored_ql.
DR Pfam; PF00361; oxidored_ql; 1.
DR NAD; Oxidoreductase; Plastocyanone.
SQ SEQUENCE 616 AA; 67201 MW; DCCBB77D30480589 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 616;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSWA 6
Db 115 MDGWA 120

RESULT 15
ID Q8ZC91 PRELIMINARY; PRT; 1139 AA.
AC Q8ZC91;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative potassium efflux system.
GN YPO3129.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Baker S., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414155; CAC92364.1; -
DR InterPro; IPR001880; MSion_channel.
DR Pfam; PF00924; MS_channel; 1.
DR PROSITE; PS01246; UDF0003; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 1139 AA; 128409 MW; 7B54108BFC39A6B1 CRC64;

Query Match 85.0%; Score 34; DB 16; Length 1139;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 :
 Db 480 MDWSW 484

Search completed: May 30, 2003, 14:38:41
 Job time : 16.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDNSWA 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	100	1	US-08-241-853-28
2	36	90.0	100	1	Sequence 28, Appl
3	36	90.0	100	2	Sequence 29, Appl
4	36	90.0	100	2	Sequence 28, Appl
5	36	90.0	745	2	Sequence 29, Appl
6	36	90.0	745	2	Sequence 3, Appl
7	36	90.0	745	2	Sequence 3, Appl
8	36	90.0	745	2	Sequence 4, Appl
9	36	90.0	745	2	Sequence 3, Appl
10	36	90.0	745	2	Sequence 4, Appl
11	36	90.0	745	2	Sequence 4, Appl
12	36	90.0	745	4	Sequence 4, Appl
13	36	90.0	745	4	Sequence 4, Appl
14	36	90.0	745	4	Sequence 4, Appl
15	36	90.0	745	4	Sequence 10, Appl
16	36	90.0	745	4	Sequence 2, Appl
17	36	90.0	756	2	Sequence 2, Appl
18	36	90.0	756	2	Sequence 4, Appl
19	36	90.0	756	2	Sequence 4, Appl
20	36	90.0	756	2	Sequence 4, Appl
21	36	90.0	756	2	Sequence 4, Appl
22	36	90.0	756	2	Sequence 2, Appl
23	36	90.0	756	4	Sequence 2, Appl
24	36	90.0	756	4	Sequence 2, Appl
25	36	90.0	756	4	Sequence 2, Appl
26	36	90.0	756	4	Sequence 15, Appl
27	36	90.0	756	4	Sequence 9, Appl

Sequence 4, Appl
Sequence 16, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 36, Appl
Sequence 2, Appl
Sequence 15, Appl
Patent No. 5217869
Sequence 138, Appl
Sequence 105, Appl
Sequence 35, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 163, Appl

28 36 90.0 982 2 US-08-673-789-4
29 36 90.0 983 1 US-08-162-809-16
30 36 90.0 983 1 US-08-167-919A-10
31 36 90.0 983 2 US-08-449-645A-21
32 36 90.0 983 2 US-08-702-367A-21
33 36 90.0 983 3 US-08-715-106-10
34 36 90.0 983 5 PCT-US95-04581-21
35 35 87.5 117 4 US-09-149-476-360
36 33 82.5 239 4 US-08-379-538-2
37 33 82.5 239 4 US-09-216-295-15
38 32 80.0 5 6 5217869-75
39 32 80.0 69 3 US-08-545-809A-138
40 32 80.0 117 3 US-08-545-809A-105
41 32 80.0 120 1 US-07-942-245-35
42 32 80.0 138 1 US-08-686-878A-33
43 32 80.0 138 4 US-09-175-928-33
44 32 80.0 170 4 US-09-199-637A-339
45 32 80.0 174 4 US-09-325-932A-163

ALIGNMENTS

RESULT 1
US-08-241-853-28
; Sequence 28, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Pang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241.853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-28

Query Match 90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNSW 5

Db 19 LDWSW 23
|||||

RESULT 2

US-08-241-853-29
; Sequence 29, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-241-853-29

Query Match 90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 19 LDWSW 23
|||||

RESULT 3

US-08-850-917-28
; Sequence 28, Application US/08850917
; Patent No. 5854045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey

COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,853
; FILING DATE: 12-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-850-917-28

Query Match 90.0%; Score 36; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 19 LDWSW 23
|||||

RESULT 4

US-08-850-917-29
; Sequence 29, Application US/08850917
; Patent No. 5854045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,853
; FILING DATE: 12-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-29

Query Match 90.0%; Score 36; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 19 LDWSW 23

RESULT 5
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/887,518
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||

Db 738 LDWSW 742

RESULT 6
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 738 LDWSW 742

RESULT 7
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
DB 738 LDWSW 742

RESULT 8
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
DB 738 LDWSW 742

RESULT 9
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
DB 738 LDWSW 742

RESULT 10
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John

;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/099,124A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/890,853
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-099-124A-4
;;
Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSW 5
Db 738 LDWSW 742
RESULT 11
US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/890,854
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-032-476-4
;;
Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSW 5
Db 738 LDWSW 742
RESULT 12
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-854-4
;;
Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 13
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: Ixk-1 Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-023-324-4
Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 14
US-09-168-629-2
; Sequence 2, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: DiDonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ixk Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; CURRENT FILING DATE: 1998-10-08

; EARLIER APPLICATION NUMBER: 60/061,470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 15
US-08-910-820-10
; Sequence 10, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-910-820-10
Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

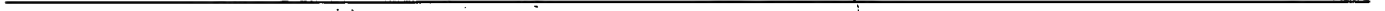
US-08-910-820-10
Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

US-08-910-820-10
Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 30, 2003, 14:41:24

Job time : 7.03947 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2.6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
 - 3: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
 - 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
 - 5: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
 - 6: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
 - 7: /cgn2.6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
 - 8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
 - 9: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
 - 10: /cgn2.6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
 - 11: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
 - 12: /cgn2.6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
 - 13: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
 - 14: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	40	100.0	6	9	US-09-847-940B-4
2	40	100.0	6	9	US-09-847-946A-4
3	40	100.0	6	9	US-09-847-946A-39
4	40	100.0	6	9	US-09-847-946A-51
5	40	100.0	7	9	US-09-847-946A-55
6	40	100.0	8	9	US-09-847-946A-48
7	40	100.0	8	9	US-09-847-946A-56
8	40	100.0	9	9	US-09-847-946A-47
9	40	100.0	9	9	US-09-847-946A-50
10	40	100.0	9	9	US-09-847-946A-53
11	40	100.0	9	9	US-09-847-946A-54
12	40	100.0	10	9	US-09-847-946A-49
13	40	100.0	10	9	US-09-847-946A-52
14	40	100.0	11	9	US-09-847-946A-46
15	40	100.0	501	9	US-10-171-311-234
16	36	90.0	6	9	US-09-847-940B-2
17	36	90.0	6	9	US-09-847-946A-2
18	36	90.0	6	9	US-09-847-946A-33
19	36	90.0	6	9	US-09-847-946A-41

20	36	90.0	6	9	US-09-847-946A-73	Sequence 73, Appl
21	36	90.0	7	9	US-09-847-946A-37	Sequence 37, Appl
22	36	90.0	7	9	US-09-847-946A-77	Sequence 77, Appl
23	36	90.0	8	9	US-09-847-946A-30	Sequence 30, Appl
24	36	90.0	8	9	US-09-847-946A-38	Sequence 38, Appl
25	36	90.0	8	9	US-09-847-946A-70	Sequence 70, Appl
26	36	90.0	8	9	US-09-847-946A-78	Sequence 78, Appl
27	36	90.0	9	9	US-09-847-946A-29	Sequence 29, Appl
28	36	90.0	9	9	US-09-847-946A-32	Sequence 32, Appl
29	36	90.0	9	9	US-09-847-946A-35	Sequence 35, Appl
30	36	90.0	9	9	US-09-847-946A-36	Sequence 36, Appl
31	36	90.0	9	9	US-09-847-946A-69	Sequence 69, Appl
32	36	90.0	9	9	US-09-847-946A-72	Sequence 72, Appl
33	36	90.0	9	9	US-09-847-946A-75	Sequence 75, Appl
34	36	90.0	9	9	US-09-847-946A-76	Sequence 76, Appl
35	36	90.0	10	9	US-09-847-946A-34	Sequence 34, Appl
36	36	90.0	10	9	US-09-847-946A-71	Sequence 71, Appl
37	36	90.0	10	9	US-09-847-946A-74	Sequence 74, Appl
38	36	90.0	11	9	US-09-847-946A-28	Sequence 28, Appl
39	36	90.0	11	9	US-09-847-946A-68	Sequence 68, Appl
40	36	90.0	11	9	US-09-847-946A-132	Sequence 132, App
41	36	90.0	11	9	US-09-847-946A-31	Sequence 140, App
42	36	90.0	11	9	US-09-847-946A-140	Sequence 143, App
43	36	90.0	13	9	US-09-847-946A-143	Sequence 144, App
44	36	90.0	13	9	US-09-847-946A-144	Sequence 145, App
45	36	90.0	13	9	US-09-847-946A-145	

ALIGNMENTS

RESULT 1
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-4

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 1 ADWSWL 6

RESULT 2
US-09-847-946A-4
; Sequence 4, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
| | | | |
Db 1 ADWSWL 6

RESULT 3
US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-39

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
| | | | |
Db 1 ADWSWL 6

RESULT 4
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-51

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
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Db 1 ADWSWL 6

RESULT 5
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-55

Query Match 100.0%; Score 40; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
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Db 1 ADWSWL 6

RESULT 6
US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match 100.0%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||
Db 3 ADWSWL 8

RESULT 7

US-09-847-946A-56
Sequence 56, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-56

Query Match 100.0%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
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Db 1 ADWSWL 6

RESULT 8

US-09-847-946A-47

Sequence 47, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match 100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||
Db 1 ADWSWL 6

RESULT 9

US-09-847-946A-50
Sequence 50, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match 100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
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Db 1 ADWSWL 6

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RESULT 10
US-09-847-946A-53
; Sequence 53, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-53

Query Match      100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
DB 3 ADWSWL 8

RESULT 11
US-09-847-946A-54
; Sequence 54, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-54

Query Match      100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
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DB 2 ADWSWL 7

RESULT 12
US-09-847-946A-49
; Sequence 49, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-49

Query Match      100.0%; Score 40; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
DB 2 ADWSWL 7

RESULT 13
US-09-847-946A-52
; Sequence 52, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-52

Query Match      100.0%; Score 40; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
DB 2 ADWSWL 7
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||

Db 3 ADWSWL 8

RESULT 14

US-09-847-946A-46
; Sequence 46, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-46

Query Match 100.0%; Score 40; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||

Db 3 ADWSWL 8

RESULT 15

US-10-171-311-234
; Sequence 234, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 234

; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-234

Query Match 100.0%; Score 40; DB 9; Length 501;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||

Db 387 ADWSWL 392

Search completed: May 30, 2003, 15:53:15
Job time : 10.4605 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 seconds
(without alignments)
83.741 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADWSWL 6

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	205	16	Q9ACR5 streptomyces
2	40	100.0	452	4	Q96AB7 homo sapien
3	40	100.0	477	11	Q9CVU6 mus musculu
4	40	100.0	484	4	Q9BTU6 homo sapien
5	37	92.5	1083	13	Q90WQ8 oncorhynchu
6	37	92.5	1100	13	Q90WQ9 oncorhynchu
7	37	92.5	1329	16	Q9CD30 mycobacteri
8	36	90.0	48	16	Q8VKB2 mycobacteri
9	36	90.0	261	2	Q9AOG7 caldicellul
10	36	90.0	310	2	Q9XBS7 zymomonas m
11	36	90.0	358	10	O50002 prunus arme
12	36	90.0	703	10	Q9FIS0 arabisdopsis
13	36	90.0	740	6	Q95KVI bos taurus
14	36	90.0	747	16	O69735 mycobacteri
15	36	90.0	756	6	Q95KV0 bos taurus
16	36	90.0	803	17	Q97UH8 sulfolobus

17	36	90.0	889	16	Q9AAZ6
18	36	90.0	996	2	Q9AQH0
19	36	90.0	1005	10	Q9XGZ2
20	36	90.0	1139	16	Q8ZC91
21	36	90.0	1345	16	Q9L060
22	36	90.0	1426	2	Q9X3P6
23	36	90.0	1751	2	Q9AQ84
24	36	90.0	1770	2	Q9X3P5
25	36	90.0	5435	2	Q9L4X2
26	36	87.5	49	6	Q8SPL6
27	35	87.5	161	11	Q9ZLP9
28	35	87.5	323	6	Q9TT79
29	35	87.5	562	16	Q98AG0
30	35	87.5	565	2	Q9KJ20
31	35	87.5	596	5	Q8SSN6
32	35	87.5	616	17	O27025
33	35	87.5	620	6	Q9XT89
34	35	87.5	1205	6	Q9TUX8
35	35	87.5	1206	11	Q9WPK6
36	35	87.5	1409	16	P72939
37	35	87.5	1879	16	P72938
38	35	87.5	3165	16	Q8XYI3
39	34	85.0	214	16	Q9KFX7
40	34	85.0	248	2	O44326
41	34	85.0	276	16	Q9RT43
42	34	85.0	280	16	Q99XK1
43	34	85.0	282	16	Q8X7K0
44	34	85.0	283	16	Q9CDAL
45	34	85.0	287	17	Q97YI1

ALIGNMENTS

RESULT 1

Q9ACR5	PRELIMINARY;	PRT;	205 AA.
ID	Q9ACR5		
AC	Q9ACR5		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Hypothetical protein SCP1.253.		
GN	SCP1.253.		
OS	Streptomyces coelicolor.		
OC	Plasmid SCP1.		
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.		
OX	NCBI_TaxID=1902;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=A3(2);		
RA	Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,		
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,		
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,		
RA	Gronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,		
RA	Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,		
RA	Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,		
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,		
RA	Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,		
RA	Hopwood D.A.;		
RT	"Complete genome sequence of the model actinomycete Streptomyces		
RT	coelicolor A3(2).";		
RL	Nature 417:141-147(2002).		
DR	EMBL; AL590464; CAC36779.1;		
KW	Hypothetical protein; plasmid.		
SQ	SEQUENCE 205 AA; 23051 MW; 6602396CFF93F2D9 CRC64;		

Query Match	100.0%;	Score 40;	DB 16;	Length 205;
Best Local Similarity	100.0%;	Pred. No. 46;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;
QY	1	ADWSWL 6		

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Db      10 ADWSWL 15

RESULT 2
Q96AB7 PRELIMINARY; PRT; 452 AA.
ID Q96AB7;
AC Q96AB7;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 50.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC017335; AAH17335.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25EE38096733 CRC64;

Query Match 100.0%; Score 40; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 338 ADWSWL 343

RESULT 3
Q9CYU6 PRELIMINARY; PRT; 477 AA.
ID Q9CYU6;
AC Q9CYU6;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 2810443J12RIK protein.
GN 2810443J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AK013297; BAB28775.1; -.
DR MGD; MGI:1914478; 2810443J12RIK.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 477 AA; 53201 MW; 2655573524A4BA9C CRC64;

Query Match 100.0%; Score 40; DB 11; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 337 ADWSWL 342

RESULT 4
Q9BTV6 PRELIMINARY; PRT; 484 AA.
ID Q9BTV6;
AC Q9BTV6;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Hypothetical 54.1 kDa protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC003123; AAH03123.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT NON_TER 1
SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7358E CRC64;

Query Match 100.0%; Score 40; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 370 ADWSWL 375

RESULT 5
Q90W08 PRELIMINARY; PRT; 1083 AA.
ID Q90W08;
AC Q90W08;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Inducible nitric oxide synthase (EC 1.14.13.39).
GN INOS.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=GONAD;

RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;

RT "Molecular cloning, gene organization and expression of rainbow trout
 (Oncorhynchus mykiss) inducible nitric oxide synthase (iNOS) gene.";
 RL J. Biochem. 358:747-755(2001).

DR EMBL; AJ300555; CAC83069.1; -

DR InterPro; IPR003097; FAD_binding.

DR InterPro; IPR001226; Flavodoxin.

DR InterPro; IPR004030; NO_synthase.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).

DR Pfam; PF00667; FAD_binding; 1.

DR Pfam; PF00258; flavodoxin; 1.

DR Pfam; PF00175; NAD_binding; 1.

DR Pfam; PF02898; NO_synthase; 1.

DR PROSITE; PS60001; NOS; UNKNOWN_1.

KW Oxidoreductase.

SQ SEQUENCE 1083 AA; 123060 MW; 53E4DFD2FA58B5D CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1083;

Best Local Similarity 83.3%; Pred. No. 7.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6

|||||

Db 402 ADWAWL 407

RESULT 6

Q90WQ9

ID Q90WQ9 PRELIMINARY; PRT; 1100 AA.

AC Q90WQ9;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Inducible nitric oxide synthase (EC 1.14.13.39).

GN iNOS.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;

RT "Molecular cloning, gene organization and expression of rainbow trout
 (Oncorhynchus mykiss) inducible nitric oxide synthase (iNOS) gene.";
 RL J. Biochem. 358:747-755(2001).

DR EMBL; AJ295231; CAC82808.1; -

DR InterPro; IPR003097; FAD_binding.

DR InterPro; IPR001226; Flavodoxin.

DR InterPro; IPR004030; NO_synthase.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).

DR Pfam; PF00667; FAD_binding; 1.

DR Pfam; PF00258; flavodoxin; 1.

DR Pfam; PF00175; NAD_binding; 1.

DR Pfam; PF02898; NO_synthase; 1.

DR PROSITE; PS60001; NOS; UNKNOWN_1.

KW Oxidoreductase.

SQ SEQUENCE 1100 AA; 125079 MW; E476338C97D608F CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1100;

Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6

|||||

Db 419 ADWAWL 424

RESULT 7

Q9CD30

ID Q9CD30 PRELIMINARY; PRT; 1329 AA.

AC Q9CD30;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical protein ML2535.

GN ML2535.

OS Mycobacterium leprae.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1769;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TN;

RE MEDLINE=21128732; PubMed=11234002;

RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,

RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RA Barrell B.G.;

RT "Massive gene decay in the leprosy bacillus.";

RL Nature 409:1007-1011(2001).

DR EMBL; AL583926; CAC32066.1; -

DR Leprosia; ML2535; -

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR002543; FtsK_SpoIIIE.

DR Pfam; PF01580; FtsK_SpoIIIE; 2.

DR SMART; SM00382; AAA; 3.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 1329 AA; 146129 MW; F8A85758D600E7D8 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 1329;

Best Local Similarity 83.3%; Pred. No. 8.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6

|||||

Db 260 SDWSWL 265

RESULT 8

Q8VKB2

ID Q8VKB2 PRELIMINARY; PRT; 48 AA.

AC Q8VKB2;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical protein MF0946.

GN MF0946.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / OSHKOSH;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

RA Kelonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

RA Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and

laboratory strains.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE006980; AAK45193.1; -

DR TIGR: MT0946; --
 KW Hypothetical protein.
 SQ SEQUENCE 48 AA; 5265 MW; C0BFA9D9A2AE8F8DF CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 48;
 Best Local Similarity 83.3%; Pred. No. 41;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWL 6
 Db 13 AEWSWL 18
 RESULT 9
 Q9A0G7 PRELIMINARY; PRT; 261 AA.
 ID Q9A0G7;
 AC Q9A0G7;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Glycosyl hydrolase 6 (Fragment).
 OS Caldicellulosiruptor sp. Tok7B.1.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Syntrophomonadaceae; Caldicellulosiruptor.
 OX NCBI_TaxID=80339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOK7B.1;
 RX MEDLINE=201711169; PubMed=10706665;
 RA Gibbs M.D., Reeves R.A., Farrington G.K., Anderson P., Williams D.P.,
 RA Bergquist P.L.;
 RT "Multidomain and multifunctional glycosyl hydrolases from the extreme
 thermophile Caldicellulosiruptor isolate Tok7B.1.";
 RL Curt. Microbiol. 40:333-340(2000).
 DR EMBL; AF078040; AAK06391.1;
 DR HSSP; Q06851; INBC.
 DR InterPro; IPR001956; CBD_3.
 DR Pfam; PF00942; CBM_3; 1.
 DR ProDom; PD001947; CBD_3; 1.
 KW Hydrolase.
 FT NON_TER 1 261
 FT NON_TER 261 261
 SQ SEQUENCE 261 AA; 28759 MW; 4771744A36A6AE04 CRC64;
 Query Match 90.0%; Score 36; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWL 6
 Db 237 DWSWL 241
 RESULT 10
 Q9XBS7 PRELIMINARY; PRT; 310 AA.
 ID Q9XBS7;
 AC Q9XBS7;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative carboxymethylglutaminylase.
 GN DLH.
 OS Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.
 OX NCBI_TaxID=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZM4;
 RA Um H.W., Kang H.S.;
 RT "The sequence analysis of 42D7 fosmid clone of Zymomonas mobilis
 RT ZM4.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF157493; AAD42398.1;
 DR InterPro; IPR002925; DLH.
 DR InterPro; IPR000379; Ser_estrs_site.
 DR Pfam; PF01738; DLH; 1.
 SQ SEQUENCE 310 AA; 34092 MW; 34AC821E1F91259D CRC64;
 Query Match 90.0%; Score 36; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWL 6
 Db 154 DWSWL 158
 RESULT 11
 O50002 PRELIMINARY; PRT; 358 AA.
 ID O50002;
 AC O50002;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cysteine protease.
 OS Prunus armeniaca (Apricot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=36596;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERGERON; TISSUE-MESOCARP PLUS EXOCARP;
 RA Mbequie-A-Mbequie D., Gomez R.-M., Fills-Lycaon B.;
 RT "Sequence of AFTp1, a Cysteine Proteinase From Apricot Fruit
 RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
 RT 179)."
 RL Plant Physiol. 115:1730-1730(1997).
 DR EMBL; U93166; AAB97142.1;
 DR HSSP; P07711; ICUL.
 DR MEROPS; C01.041;
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprot_acsite.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPAIN.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydrolase; Protease; Thiol protease.
 SQ SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;
 Query Match 90.0%; Score 36; DB 10; Length 358;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 Db 108 ADWSW 112
 RESULT 12
 Q9FIS0 PRELIMINARY; PRT; 703 AA.
 ID Q9FIS0;
 AC Q9FIS0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Genomic DNA, chromosome 5, Pl clone:MTG10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
RL DNA Res. 5:297-308(1998).
DR ENBL; AB016880; BAB10180.1;
SQ SEQUENCE 703 AA; 79216 MW; DEE247BC38868F7B CRC64;

Query Match          90.0%; Score 36; DB 10; Length 703;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
Db 4 DWSWL 8

RESULT 13
Q95KV1 PRELIMINARY; PRT; 740 AA.
AC Q95KV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ikb kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKKs)
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AJ414555; CAC93686.1;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00219; TykKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;

Query Match          90.0%; Score 36; DB 6; Length 740;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
Db 734 DWSWL 738

RESULT 14
O69735 PRELIMINARY; PRT; 747 AA.
AC O69735;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 80.9 kDa protein (FtsK/spoIIIE family protein).

```

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GN RV3870 OR MTV027.05 OR MT3983.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCB1_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence.";
RN Nature 393:537-544(1998).
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL022120; CAAL7962.1;
DR DR ENBL; AE007190; AAK48351.1;
DR TIGR; MT3983;
DR TubercuList; RV3870;
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 747 AA; 80912 MW; CF6AA9153BE6F41E CRC64;

Query Match          90.0%; Score 36; DB 16; Length 747;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
Db 267 DWSWL 271

RESULT 15
Q95KV0 PRELIMINARY; PRT; 756 AA.
AC Q95KV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ikb kinase-beta.
GN BIKKBETA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKKs)
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AJ414556; CAC93687.1;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.

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DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;
 Query Match 90.0%; Score 36; DB 6; Length 756;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DWSWL 6
 Db 738 DWSWL 742

Search completed: May 30, 2003, 14:38:39
 Job time : 15.7632 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADWSW 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	174	4	US-09-325-932A-163
2	36	90.0	225	4	Sequence 163, App
3	36	90.0	378	4	Sequence 162, App
4	36	90.0	616	4	Sequence 158, App
5	36	90.0	745	2	US-09-136-574A-47
6	36	90.0	745	2	Sequence 47, Appl
7	36	90.0	745	2	Sequence 3, Appl
8	36	90.0	745	2	Sequence 4, Appl
9	36	90.0	745	2	Sequence 3, Appl
10	36	90.0	745	2	Sequence 4, Appl
11	36	90.0	745	4	US-09-032-476-4
12	36	90.0	745	4	US-08-890-854-4
13	36	90.0	745	4	US-09-023-324-4
14	36	90.0	745	4	US-09-168-629-2
15	36	90.0	745	4	US-08-810-820-10
16	36	90.0	745	4	US-08-810-131A-2
17	36	90.0	756	2	US-08-887-518-4
18	36	90.0	756	2	US-09-023-321-4
19	36	90.0	756	2	US-08-890-853-2
20	36	90.0	756	2	US-09-032-475-4
21	36	90.0	756	2	US-09-099-125A-2
22	36	90.0	756	2	US-09-099-124A-2
23	36	90.0	756	4	US-09-032-476-2
24	36	90.0	756	4	US-08-890-854-2
25	36	90.0	756	4	US-09-023-324-2
26	36	90.0	756	4	US-09-168-629-15
27	36	90.0	756	4	US-08-910-820-9

28 36 90.0 1426 4 US-09-136-574A-43 Sequence 43, Appl
29 36 90.0 1751 4 US-09-136-574A-44 Sequence 44, Appl
30 35 87.5 1205 1 US-07-908-245-2 Sequence 2, Appl
31 35 87.5 1205 2 US-08-319-866-10 Sequence 10, Appl
32 35 87.5 1205 4 US-09-123-708-6 Sequence 6, Appl
33 35 87.5 1205 4 US-09-123-624-6 Sequence 6, Appl
34 34 85.0 170 4 US-09-139-637A-339 Sequence 339, App
35 34 85.0 518 4 US-09-085-383-27 Sequence 27, Appl
36 34 85.0 537 4 US-09-655-270A-11 Sequence 11, Appl
37 34 85.0 537 4 US-09-651-941-11 Sequence 11, Appl
38 34 85.0 537 4 US-09-955-597-11 Sequence 5, Appl
39 34 85.0 1144 1 US-08-147-812-5 Sequence 12, Appl
40 34 85.0 1144 2 US-08-319-866-12 Sequence 2, Appl
41 34 85.0 1144 4 US-09-123-708-2 Sequence 2, Appl
42 34 85.0 1144 4 US-09-123-624-2 Sequence 12, Appl
43 34 85.0 1146 4 US-09-126-109-12 Sequence 2, Appl
44 34 85.0 1153 1 US-08-314-917-2 Sequence 2, Appl
45 34 85.0 1153 1 US-08-265-046-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant dev
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 109 ADWSW 113

RESULT 2
US-09-325-932A-162
; Sequence 162, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant dev
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;

Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
11111
Db 100 ADWSW 104

RESULT 3

US-09-325-932A-158
; Sequence 158, Application US/09325932A
; Patent No. 6451604

; GENERAL INFORMATION:

; APPLICANT: Flinn, Barry

; TITLE OF INVENTION: Compositions affecting programmed cell

; FILE OF INVENTION: death and their use in the modification of forestry plant develo

; FILE REFERENCE: 1022

; CURRENT APPLICATION NUMBER: US/09/325,932A

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 206

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 158

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
11111
Db 128 ADWSW 132

RESULT 4

US-09-136-574A-47

; Sequence 47, Application US/09136574A

; Patent No. 6294366

; GENERAL INFORMATION:

; APPLICANT: Farrington, Graham K.

; Anderson, Paige

; Gibbs, Moreland

; Bergquist, Peter

; Daniels, Roy

; Morgan, Hugh W.

; Williams, Diane P.

; TITLE OF INVENTION: Compositions and Methods for

; Treating Cellulose Containing Fabrics Using Truncated

; Cellulase Enzyme Compositions

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Center, P.O. Box 457

; CITY: Spring House

; STATE: PA

; COUNTRY: USA

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/136,574A

; FILING DATE: 19-Aug-1998

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/932,571

; FILING DATE: September 19, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 616 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-136-574A-47

Query Match 90.0%; Score 36; DB 4; Length 616;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
11111
Db 123 DWSWL 127

RESULT 5

US-08-887-518-3

; Sequence 3, Application US/08887518

; Patent No. 5843721

; GENERAL INFORMATION:

; APPLICANT: Rothe, Mike

; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,518

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
11111
Db 739 DWSWL 743

RESULT 6
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 739 DWSWL 743

RESULT 7
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 739 DWSWL 743

RESULT 8
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWSWL 6
|||||
Db 739 DWSWL 743

RESULT 9

US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760

GENERAL INFORMATION:

; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 745 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWSWL 6
|||||
Db 739 DWSWL 743

RESULT 10

US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302

GENERAL INFORMATION:

; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWSWL 6
|||||
Db 739 DWSWL 743

RESULT 11

US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492

GENERAL INFORMATION:

; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaoan
; APPLICANT: R grier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

RESULT 12
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6

Db 739 DMSWL 743

RESULT 13
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

RESULT 14
US-09-168-629-2
; Sequence 2, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470

; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
Db 739 DWSWL 743

RESULT 15
US-08-910-820-10
; Sequence 10, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-910-820-10

Query Match 90.0%; Score 36; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
Db 739 DWSWL 743

Search completed: May 30, 2003, 14:41:23
Job time : 6.03947 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	132	2 S65785	mel-13a protein -
2	37	92.5	1329	2 D87226	conserved hypothetical
3	36	90.0	122	2 S69909	Ig V-D-J region (M
4	36	90.0	745	1 I49101	conserved helix-lo
5	36	90.0	747	2 D70802	hypothetical prote
6	36	90.0	803	2 E90485	hypothetical prote
7	36	90.0	889	2 E87304	tonB-dependent rec
8	36	90.0	915	2 A43802	cellulase (EC 3.2.
9	36	90.0	1039	2 S02711	cellulase (EC 3.2.
10	36	90.0	1139	2 A10379	O-antigen biosynth
11	36	90.0	1275	2 T18556	type I restriction
12	35	87.5	616	2 C69226	conserved hypothetical
13	35	87.5	1202	2 S71424	nitric-oxide synth
14	35	87.5	1203	1 A47501	nitric-oxide synth
15	35	87.5	1205	1 A38943	nitric-oxide synth
16	35	87.5	1409	2 S74916	alkaline phosphata
17	35	87.5	1879	2 S74915	extracellular nucl
18	34	85.0	214	2 G83692	hypothetical prote
19	34	85.0	220	2 D64316	restriction modifi
20	34	85.0	248	2 T44932	3-oxoacyl-[acyl-ca
21	34	85.0	276	2 B75337	hypothetical prote
22	34	85.0	282	1 DGECEM	DNA-3-methyladenin
23	34	85.0	282	2 E90988	3-methyl-adenine D
24	34	85.0	282	2 G85833	3-methyl-adenine D
25	34	85.0	283	2 A86923	probable glycosyl
26	34	85.0	287	2 C90290	hypothetical prote
27	34	85.0	289	2 A10770	DNA-3-methyladenin
28	34	85.0	304	1 B70696	probable rfbE prot
29	34	85.0	368	2 AF1434	AA3-600 quinol oxi

30	34	85.0	368	2 AF1806	AA3-600 quinol oxi
31	34	85.0	410	2 D75475	lycopene cyclase -
32	34	85.0	529	2 C86958	probable GMP synth
33	34	85.0	549	2 A87347	hypothetical prote
34	34	85.0	578	2 C64452	restriction modifi
35	34	85.0	590	2 S72813	GMP synthase (glut
36	34	85.0	623	2 E75221	type I restriction
37	34	85.0	1144	1 A43271	nitric-oxide synth
38	34	85.0	1147	1 S47647	nitric-oxide synth
39	34	85.0	1147	1 S65755	nitric-oxide synth
40	34	85.0	1147	1 S38253	nitric-oxide synth
41	34	85.0	1147	1 T53165	nitric-oxide synth
42	34	85.0	1147	2 JC5027	nitric-oxide synth
43	34	85.0	1147	2 JC5028	nitric-oxide synth
44	34	85.0	1147	2 JC5029	nitric-oxide synth
45	34	85.0	1147	2 S65440	nitric-oxide synth

ALIGNMENTS

RESULT 1

S65785
mel-13a protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S65785
R:Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A:Title: Cloning and characterization of two transcripts generated from the mel-13 ge
A:Reference number: S65785; MUID:96180310; PMID:8597592
A:Accession: S65785
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TET>
A:Cross-references: EMBL:U35309
C:Genetics:
A:Gene: mel-13
C:Superfamily: mouse mel-13a protein
C:Keywords: alternative splicing

Query Match 92.5%; Score 37; DB 2; Length 132;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWL 6
:|||||
Db 57 SDWSWL 62

RESULT 2

D87226
conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87226
R:Cole, S.T.; Eiglmeter, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.N.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D87226
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1329 <STO>
A:Cross-references: GB:AL450380; NID:gl3093796; PIDN:CAC32066.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML2535

Query Match 92.5%; Score 37; DB 2; Length 1329;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
:|||||
Db 260 SDMSWL 265

RESULT 3

Ig V-D-J region (MS) - human
A:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69909
R:Sanota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multiple myeloma
A:Reference number: S69909; MUID:94335315; PMID:8057663
A:Accession: S69909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SAH>
A:Cross-references: EMBL:Z33399; NID:g871348; PIDN:CAA83850.1; PID:g871349
A:Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are identical
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IM>

Query Match 90.0%; Score 36; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 33 DMSWL 37

RESULT 4

I49101
Conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I49101
Genomics 27, 348-351, 1995
A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 12p11.2
A:Reference number: I49101; MUID:96044444; PMID:7558004
A:Accession: I49101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <RES>
A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C:Genetics:

A:Gene: CHUK
C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 739 DMSWL 743

RESULT 5

D70802
hypothetical protein RV3870 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: D70802
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70802
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-747 <COL>
A:Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAA17962.1; PID:g296
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV3870

Query Match 90.0%; Score 36; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 267 DMSWL 271

RESULT 6

F90485
Hypothetical protein SSO3039 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: F90485
R:She, Q.; Singh, K.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chong, J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90485
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-803 <KUR>
A:Cross-references: GB:AE006641; NID:gl3816440; PIDN:AAK43141.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO3039

Query Match 90.0%; Score 36; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 540 DMSWL 544

RESULT 7

E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87304
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, N.; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapero, L.; Venter, J.C.; Fraser, C.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87304
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-889 <STO>
A:Cross-references: GB:AE005673; NID:gl3421615; PIDN:AAK22433.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 618 ADWSW 622
|||||

RESULT 8
A43802
cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Caldocellum
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Caldocellum saccharolyticum
C;Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
C;Accession: A43802
R;Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L.
Appl. Environ. Microbiol. 56, 3117-3124, 1990
A;Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile
C;Reference number: A43802; MUID:91136262; PMID:2126700
A;Accession: A43802
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-915 <SAU>
A;Cross-references: EMBL:X13602
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A;Pathway: cellulose degradation
C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;20-320/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 915;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 469 DWSWL 473
|||||

RESULT 9
S02711
cellulase (EC 3.2.1.4) precursor - Caldocellum saccharolyticum
N;Alternate names: endo-1,4-beta-glucanase
N;Contains: cellulase (EC 3.2.1.4); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91)
C;Species: Caldocellum saccharolyticum
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S02711
R;Saul, D.J.; Williams, L.C.; Love, D.R.; Chamley, L.W.; Bergquist, P.L.
Nucleic Acids Res. 17, 439, 1989
A;Title: Nucleotide sequence of a gene from Caldocellum saccharolyticum encoding for ex
A;Reference number: S02711; MUID:89098398; PMID:2789517
A;Accession: S02711
A;Molecule type: DNA
A;Residues: 1-1039 <SAU>
A;Cross-references: EMBL:X13602; NID:g40645; PIDN:CAA31936.1; PID:g40646
C;Genetics:
A;Gene: celB
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A;Pathway: cellulose degradation
C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1039/Product: cellulase #status predicted <MAT>
F;72-373/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 1039;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 469 DWSWL 473
|||||

Db 540 DWSWL 544
|||||

RESULT 10
A10379
probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: A10379
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: A10379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1139 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:gl5981067; GSPDB:GN00175
C;Genetics:
A;Gene: YPO3129

Query Match 90.0%; Score 36; DB 2; Length 1139;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 481 DWSWL 485
|||||

RESULT 11
T18556
O-antigen biosynthesis protein homolog rfbC - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18556
R;Guo, D.; Bowden, M.G.; Pershad, R.; Kaplan, H.B.
J. Bacteriol. 178, 1631-1639, 1996
A;Title: The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette transpo
A;Reference number: Z18970; MUID:96198166; PMID:8626291
A;Accession: T18556
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1275 <GUO>
A;Cross-references: EMBL:U36795; NID:gl235659; PID:gl235662; PIDN:AAB05019.1
C;Genetics:
A;Note: rfbC

Query Match 90.0%; Score 36; DB 2; Length 1275;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 348 ADWSWL 353
|||||

RESULT 12
C69226
type I restriction modification enzyme, subunit M - Methanobacterium thermoautotroph
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: C69226
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69226
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-616 <MTH>
A:Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85440.1; PID:g262204
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH942
A:Start codon: GTG
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 87.5%; Score 35; DB 2; Length 616;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||:|:
DB 425 ADWAWI 430

RESULT 13
S71424
nitric-oxide synthase (EC 1.14.13.39), endothelial - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 04-Mar-2000
C:Accession: S71424
R:Gnanapandithen, K.; Chen, Z.; Kau, C.L.; Gorczynski, R.M.; Marsden, P.A.
Biochim. Biophys. Acta 1308, 103-106, 1996
A:Title: Cloning and characterization of murine endothelial constitutive nitric oxide synthase
A:Reference number: S71424; MUID:96350460; PMID:8764825
A:Accession: S71424
A:Molecule type: mRNA
A:Residues: 1-1202 <GNA>
A:Cross-references: EMBL:U53142; NID:gl518955; PIDN:AAC52766.1; PID:gl518956
A:Experimental source: fetal cardiac
C:Genetics:
A:Gene: NOS
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase
C:Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN
F:490-509/Region: calmodulin binding #status predicted
F:519-1158/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:521-702/Domain: flavodoxin homology <FLX>
F:647-679/Region: FMN binding #status predicted
F:790-803/Region: FAD-pyrophosphate binding #status predicted
F:934-945/Region: FAD-isalloxazine binding #status predicted
F:1009-1027/Region: NADP-ribose binding #status predicted
F:1107-1123/Region: NADP-adenine binding #status predicted
F:2/Modified site: NADP-adenine binding #status predicted
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:183/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 2; Length 1202;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||:|:
DB 442 ADWAWI 447

RESULT 14
A47501
nitric-oxide synthase (EC 1.14.13.39), endothelial - human
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 03-Mar-2000
C:Accession: A47501; S24052; A38948; A49813; A42867; S45691; I37361
R:Marsden, P.A.; Heng, H.H.Q.; Scherer, S.W.; Stewart, R.J.; Hall, A.V.; Shi, X.M.; Tsui, J. Biol. Chem. 268, 17478-17488, 1993
A:Title: Structure and chromosomal localization of the human constitutive endothelial nitric oxide synthase
A:Reference number: A47501; MUID:93352539; PMID:7688726
A:Accession: A47501
A:Molecule type: DNA
A:Residues: 1-1203 <MARI>
A:Cross-references: GB:L10709; NID:g348235; PIDN:AAA36365.1; PID:g348237; GB:L10693; NID:0698; NID:g348224; GB:L10699; NID:g348225; GB:L10700; NID:g348226; GB:L10701; NID:g348223

ID:g348232; GB:L10707; NID:g348233; GB:L10708; NID:g348234
R:Marsden, P.A.; Schappert, K.T.; Chen, H.S.; Flowers, M.; Sundell, C.L.; Wilcox, J.N
FEBS Lett. 307, 287-293, 1992
A:Title: Molecular cloning and characterization of human endothelial nitric oxide synthase
A:Reference number: S24052; MUID:92354731; PMID:1379542
A:Accession: S24052
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <MAR2>
A:Cross-references: GB:M95296; NID:gl89259; PIDN:AAA36372.1; PID:gl89260
R:Janssens, S.P.; Shimouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D.
submitted to GenBank, September 1992
A:Reference number: A38948
A:Accession: A38948
A:Molecule type: mRNA
A:Residues: 1-1203 <JAN1>
A:Cross-references: GB:M93718; NID:gl89211; PIDN:AAA36364.1; PID:gl89212
A:Note: the sequence in GenBank entry HUMNIOXSYN, release 111.0, has been corrected
R:Janssens, S.P.; Shimouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D.
J. Biol. Chem. 267, 22694b, 1992
A:Reference number: A49813; MUID:93054573; PMID:1383404
A:Accession: A49813
A:Molecule type: mRNA
A:Residues: 1191-1203 <JAN2>
A:Cross-references: PIDN:AAB23920.1; PID:g258793
A:Note: sequence extracted from NCBI backbone (NCBI:117314)
R:Janssens, S.P.; Shimouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D.
J. Biol. Chem. 267, 14519-14522, 1992
A:Title: Cloning and expression of a cDNA encoding human endothelium-derived relaxing factor
A:Reference number: A42867; MUID:92340475; PMID:1378832
A:Accession: A42867
A:Molecule type: mRNA
A:Residues: 1-82, 'S', '84-179, 'F', '181-566, 'W', '568-647, 'Q', '649-854, 'V', '856-1008, 'G', '1010-1018, 'Q', '1019-1023, 'S', '1024-1028, 'Q', '1029-1033, 'S', '1034-1038, 'Q', '1039-1043, 'S', '1044-1048, 'Q', '1049-1053, 'S', '1054-1058, 'Q', '1059-1063, 'S', '1064-1068, 'Q', '1069-1073, 'S', '1074-1078, 'Q', '1079-1083, 'S', '1084-1088, 'Q', '1089-1093, 'S', '1094-1098, 'Q', '1099-1103, 'S', '1104-1108, 'Q', '1109-1113, 'S', '1114-1118, 'Q', '1119-1123, 'S', '1124-1128, 'Q', '1129-1133, 'S', '1134-1138, 'Q', '1139-1143, 'S', '1144-1148, 'Q', '1149-1153, 'S', '1154-1158, 'Q', '1159-1163, 'S', '1164-1168, 'Q', '1169-1173, 'S', '1174-1178, 'Q', '1179-1183, 'S', '1184-1188, 'Q', '1189-1193, 'S', '1194-1198, 'Q', '1199-1203, 'S', '1204-1208, 'Q', '1209-1213, 'S', '1214-1218, 'Q', '1219-1223, 'S', '1224-1228, 'Q', '1229-1233, 'S', '1234-1238, 'Q', '1239-1243, 'S', '1244-1248, 'Q', '1249-1253, 'S', '1254-1258, 'Q', '1259-1263, 'S', '1264-1268, 'Q', '1269-1273, 'S', '1274-1278, 'Q', 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F;184/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1203;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
DB 443 ADMAWI 448

RESULT 15

A38943

Nitric-oxide synthase (EC 1.14.13.39), endothelial - bovine

N;Alternate names: ECNOS; nitric-oxide synthase type III

C;Species: Bos primigenius taurus (cattle)

C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 03-Mar-2000

C;Accession: A38943; A46033; A45946; A42841; I45946; A38944

R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.

submitted to GenBank, July 1992

A;Reference number: A38943

A;Accession: A38943

A;Molecule type: mRNA

A;Residues: 1-1205 <LAMI>

A;Cross-references: GB:M89952; NID:g162976; PIDN:AAA30494.1; PID:g162977

A;Experimental source: aortic endothelial cells

R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.

Proc. Natl. Acad. Sci. U.S.A. 89, 6348-6352, 1992

A;Title: Endothelial nitric oxide synthase: molecular cloning and characterization of a

A;Reference number: A46033; MUID:92335295; PMID:1378626

A;Accession: A46033

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-860, 'I', 862-1205 <LAM2>

A;Cross-references: GB:M89952; NID:g162976

A;Experimental source: endothelial

A;Note: sequence extracted from NCBI backbone (NCBIP:108720)

R;Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; Al

J. Clin. Invest. 90, 2092-2096, 1992

A;Title: Molecular Cloning and Characterization of the constitutive bovine aortic Endoth

A;Reference number: I45945; MUID:93055452; PMID:1385480

A;Accession: I45945

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1205 <NIS>

A;Cross-references: GB:M99057; NID:g163421; PIDN:AAA30667.1; PID:g163422

R;Sessa, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly

J. Biol. Chem. 267, 15274-15276, 1992

A;Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric ox

A;Reference number: A42841; MUID:92348367; PMID:1379225

A;Accession: A42841

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-51, 'N', 53-99, 'R', 101-147, 'M', 149-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-3

'K', 517-692, 'G', 694-740, 'A', 742-753, 'N', 755-799, 'N', 801-803, 'SA', 806-856, 'V', 858-906, 'LV

A;Experimental source: aortic endothelial cells

A;Note: sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typog

A;Accession: I45946

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-99, 'R', 101-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-454, 'Y', 456-458, 'P', 460

A;Cross-references: GB:M95874; NID:g163426; PIDN:AAA30669.1; PID:g163427

A;Experimental source: aortic endothelial cells

A;Note: submitted to GenBank, August 1992

A;Accession: I45946

A;Status: GenBank entry BOVNOS, release 103.0, has a typographical error in the reference

C;Function:

A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH

C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferritinoprotein reduct

C;Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN

F;493-512/Region: calmodulin binding #status predicted

F;522-1161/Domain: NADPH-ferritinoprotein reductase homology <FEH>

F;524-705/Domain: flavodoxin homology <FLX>

F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F;3/Modified site: aspartic acid (Asn) #status predicted
F;186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1205;

Best Local Similarity 66.7%; Pred. No. 5.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
DB 445 ADMAWI 450

Search completed: May 30, 2003, 14:52:38

Job time : 6.5921 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	470	1 NOS2_ONCMY	Q92091 oncorhynch
2	36	90.0	470	1 NRAM_IADBU	Q07570 influenza a
3	36	90.0	470	1 NRAM_IADCH	Q07571 influenza a
4	36	90.0	470	1 NRAM_IADH2	Q07572 influenza a
5	36	90.0	470	1 NRAM_IADM2	Q07573 influenza a
6	36	90.0	470	1 NRAM_IADU3	Q07599 influenza a
7	36	90.0	470	1 NRAM_IAGD	Q07574 influenza a
8	36	90.0	470	1 NRAM_IAGH	Q07577 influenza a
9	36	90.0	470	1 NRAM_IADJI	Q07578 influenza a
10	36	90.0	470	1 NRAM_IADAE	Q07585 influenza a
11	36	90.0	470	1 NRAM_IADKL	Q07585 influenza a
12	36	90.0	745	1 IKKA_HUMAN	O15111 h inhibitor
13	36	90.0	745	1 IKKA_MOUSE	O60680 m inhibitor
14	36	90.0	756	1 IKKB_HUMAN	O14920 homo sapien
15	36	90.0	757	1 IKKB_MOUSE	O88351 mus musculus
16	36	90.0	757	1 IKKB_RAT	Q9qy78 rattus norv
17	36	90.0	1039	1 GUNA_CALSA	P10474 c endogluc
18	36	90.0	1275	1 RFBC_MYXXA	Q50864 myxococcus
19	35	87.5	99	1 NOS3_SHEEP	P79209 ovis aries
20	35	87.5	914	1 GUX2_CLOSR	P50900 clostridium
21	35	87.5	1201	1 NOS3_MOUSE	P70313 mus musculus
22	35	87.5	1202	1 NOS3_HUMAN	P29474 homo sapien
23	35	87.5	1204	1 NOS3_BOVIN	P29473 bos taurus
24	35	87.5	1204	1 NOS3_PIG	Q28969 sus scrofa
25	34	85.0	220	1 Y132_METJA	Q57596 methanococc
26	34	85.0	282	1 3MG2_ECOLI	P04395 escherichia
27	34	85.0	410	1 Y801_DEIRA	Q9r468 deinooccus
28	34	85.0	529	1 GURA_MYLE	P46810 mycobacteri
29	34	85.0	578	1 YC20_METJA	Q58617 methanococc
30	34	85.0	579	1 YC12_KLEPN	Q48458 klebsiella
31	34	85.0	591	1 NOS2_CANFA	O62699 canis fami
32	34	85.0	1144	1 NOS2_MOUSE	P29477 mus musculus
33	34	85.0	1147	1 NOS2_RAT	Q06518 rattus norv

RESULT 1

ID	NOS2_ONCMY	STANDARD;	PRT;	470 AA.
AC	Q92091;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)			
DE	(Inducible NOS) (NOS) (Fragment).			
GN	NOS2.			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Grabowski P.S., Laing K.J., Hardie L., Macquigan F., Ralston S.,			
RA	Secombes C.J.;			
RT	"Detection of mRNA for a nitric oxide synthase in macrophages and			
RT	gill of rainbow trout challenged with an attenuated bacterial			
RT	pathogen.";			
RL	(in) Moncada S., Stamler J., Gross S., Higgs E.A. (eds.);			
RL	4th International meeting on the biology of nitric oxide, Amelia			
RL	Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,			
RL	Brookfield (1996).			
CC	-1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE			
CC	WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO			
CC	MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.			
CC	-1- CATALYTIC ACTIVITY: L-arginine + NADPH + M O(2) = citrulline +			
CC	nitric oxide + N NADP(+)			
CC	-1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES			
CC	TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF			
CC	THE ENZYME (BY SIMILARITY).			
CC	-1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY			
CC	SIMILARITY).			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE NOS FAMILY.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; X97013; CAA65736.1; -.			
DR	HSSP; P29477; INOS.			
DR	InterPro; IPR003097; FAD_binding.			
DR	InterPro; IPR001094; Flavodoxin-like.			
DR	InterPro; IPR001226; Flavodoxin.			
DR	InterPro; IPR004030; NO_synthase.			
DR	Pfam; PF00258; flavodoxin; 1.			
DR	Pfam; PF00667; FAD_binding; 1.			
DR	Pfam; PF02898; NO_synthase; 1.			

ALIGNMENTS

34	34	85.0	1147	1	NS2D_HUMAN	O60591 homo sapien
34	34	85.0	1149	1	NOS2_CAVPO	O54705 cavia porce
35	36	85.0	1153	1	NS2A_HUMAN	P35228 homo sapien
36	34	85.0	1331	1	MANB_CALSA	P22533 caldocellum
37	34	85.0	1742	1	GUNA_CALSA	P22534 caldocellum
38	34	85.0	1742	1	GUNA_CALSA	P22534 caldocellum
39	33	82.5	232	1	CLB3_SHEEP	P80943 ovis aries
40	33	82.5	333	1	CLB2_SHEEP	Q29422 ovis aries
41	33	82.5	336	1	NOSO_BACSU	Q34453 bacillus su
42	33	82.5	339	1	YJGB_ECOLI	O93883 escherichia
43	33	82.5	376	1	PGLR_PENGR	O93883 penicillium
44	33	82.5	421	1	YDW4_SCHPO	O13911 schizosacch
45	33	82.5	470	1	NRAM_IQIT	Q07584 influenza a

FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	398	398	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	470 AA;	51989 MW;	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	470 AA;	DLA6F07460F6F8AD CRC64;	
Query Match				
Best Local Similarity 100.0%; Score 36; DB 1; Length 470;				
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	ADWSW 5		
DB	453	ADWSW 457		
RESULT 3				
NRAM	NRAM_IADCH	STANDARD;	PRT;	470 AA.
ID	NRAM_IADCH	STANDARD;	PRT;	470 AA.
AC	007571;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neuraminidase (EC 3.2.1.18).			
DE	Neuraminidase			
GN	NA.			
OS	Influenza A virus (strain A/Duck/Chabarovsk/1610/72).			
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC	Influenza A viruses; Influenzavirus A.			
OC	NCBI_TaxID=38957;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=93212520; PubMed=8460490;			
RA	Saito T., Kawakita Y., Webster R.G.;			
RT	"Phylogenetic analysis of the N8 neuraminidase gene of influenza A			
RT	viruses.";			
RL	Virology 193:868-876(1993).			
CC	-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side			
CC	chains of the host cell surface proteins and from the viral			
CC	envelope. Such a reaction prevents self-aggregation and facilitate			
CC	the mobility of the virus to and from the site of infection.			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,			
CC	alpha-(2-8)-glycosidic linkages of terminal sialic residues in			
CC	oligosaccharides, glycoproteins, glycolipids, colominic acid and			
CC	synthetic substrates.			
CC	-1- SUBUNIT: HOMOTETRAMER.			
CC	-1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED			
CC	SPIKE ON THE SURFACE OF THE VIRION			
CC	-1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; L06573; AAA43367.1; -			
DR	HSP; P06820; 2BAT.			
DR	InterPro; IPR001860; GH_34.			
DR	Pfam; PF00064; neur; 1.			
DR	ProDom; PD000431; GH_34; 1.			
DR	Hydrolase; Glycosidase; Glycoprotein; Transmembrane.			
FT	TRANSMEM	7	38	ANCHOR (BY SIMILARITY).
FT	DOMAIN	39	68	HYPERVARIABLE STALK REGION.
FT	DOMAIN	89	470	HEAD OF NEURAMINIDASE.
FT	ACT_SITE	273	275	BY SIMILARITY.
FT	ACT_SITE	275	275	BY SIMILARITY.
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	84	84	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	398	398	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	470 AA;	52070 MW;	163AB89FBE8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 453 ADWSW 457

RESULT 4

NRAM_IADH2 STANDARD; PRT; 470 AA.
AC Q07572; 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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EMBL; L06574; AAA43372.1; -
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; GH_34; 1.
DR Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
KW TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52015 MW; E1CD3E2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 453 ADWSW 457

RESULT 5

NRAM_IADM2 STANDARD; PRT; 470 AA.
AC Q07573; 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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EMBL; L06575; AAA43404.1; -
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; GH_34; 1.
DR Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
KW TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F59FE364C1F49 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 453 ADWSW 457

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RESULT 6
NRAM_IADU3          STANDARD;          PRT;    470 AA.
AC Q07599;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Ukraine/1/63).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
  viruses."
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
  chains of the host cell surface proteins and from the viral
  envelope. Such a reaction prevents self-aggregation and facilitate
  the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
  alpha-(2->8)-glycosidic linkages of terminal sialic residues in
  oligosaccharides, glycoproteins, glycolipids, colominic acid and
  synthetic substrates.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
  SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; L06576; AAA16234.1; -
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; GH_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 38 88
FT TRANSMEM 7 37
FT ACT_SITE 273 273
FT ACT_SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
FT SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;
SQ
Query Match          90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 7
NRAM_IAGFN          STANDARD;          PRT;    470 AA.
AC Q07577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
  viruses."
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
  chains of the host cell surface proteins and from the viral
  envelope. Such a reaction prevents self-aggregation and facilitate
  the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
  alpha-(2->8)-glycosidic linkages of terminal sialic residues in
  oligosaccharides, glycoproteins, glycolipids, colominic acid and
  synthetic substrates.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
  SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; L06584; AAA43428.1; -
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; GH_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 38 88
FT TRANSMEM 7 38
FT ACT_SITE 273 273
FT ACT_SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
FT SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;
SQ
Query Match          90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 8
NRAM_IARGD          STANDARD;          PRT;    470 AA.
AC Q07577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE  Neuraminidase (EC 3.2.1.18).
GN  NA.
OS
ON  Influenza A virus (strain A/Herring gull/DE/677/88).
OC  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC  Influenza A viruses; Influenzavirus A.
OX  NCBI_TaxID=38964;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93212520; PubMed=8460490;
RA  Saito T., Kawaoka Y., Webster R.G.;
RT  "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
    viruses."
RL  Virology 193:868-876(1993).
CC  -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
    chains of the host cell surface proteins and from the viral
    envelope. Such a reaction prevents self-aggregation and facilitate
    the mobility of the virus to and from the site of infection.
CC  -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
    alpha-(2-8)-glycosidic linkages of terminal sialic residues in
    oligosaccharides, glycoproteins, glycolipids, colominic acid and
    synthetic substrates.
CC  -1- SUBUNIT: HOMOTETRAMER.
CC  -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
    SPIKE ON THE SURFACE OF THE VIRION.
CC  -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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    or send an email to license@isb-sib.ch).
CC
CC  EMBL; L06585; AAA43368.1; -.
DR  HSP; P06820; 2BAT.
DR  InterPro: IPR001860; GH_34.
DR  Pfam; PF00064; neur; 1.
DR  ProDom; PD000431; GH_34; 1.
KW  Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT  TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT  DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT  ACT_SITE 273 273 BY SIMILARITY.
FT  ACT_SITE 275 275 BY SIMILARITY.
FT  CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 9
NRAM_IAHJI STANDARD; PRT; 470 AA.
AC Q07578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Equine/Jilin/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

```

```

OC  Influenza A viruses; Influenzavirus A.
OX  NCBI_TaxID=11401;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93212520; PubMed=8460490;
RA  Saito T., Kawaoka Y., Webster R.G.;
RT  "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
    viruses."
RL  Virology 193:868-876(1993).
CC  -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
    chains of the host cell surface proteins and from the viral
    envelope. Such a reaction prevents self-aggregation and facilitate
    the mobility of the virus to and from the site of infection.
CC  -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
    alpha-(2-8)-glycosidic linkages of terminal sialic residues in
    oligosaccharides, glycoproteins, glycolipids, colominic acid and
    synthetic substrates.
CC  -1- SUBUNIT: HOMOTETRAMER.
CC  -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
    SPIKE ON THE SURFACE OF THE VIRION.
CC  -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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    or send an email to license@isb-sib.ch).
CC
CC  EMBL; L06579; AAA43374.1; -.
DR  HSP; P06820; 2BAT.
DR  InterPro: IPR001860; GH_34.
DR  Pfam; PF00064; neur; 1.
DR  ProDom; PD000431; GH_34; 1.
KW  Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT  TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT  DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT  ACT_SITE 273 273 BY SIMILARITY.
FT  ACT_SITE 275 275 BY SIMILARITY.
FT  CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 10
NRAM_IAMAE STANDARD; PRT; 470 AA.
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC  Influenza A viruses; Influenzavirus A.
OX  NCBI_TaxID=38965;
RN  [1]
RP  SEQUENCE FROM N.A.

```

```

RX MEDLINE-93212520; PubMed-8460490;
RA Saito T., Kawaoaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RL viruses."
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06586; AAA43369.1; -
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; GH_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 7 38
FT DOMAIN 39 88
FT ACT_SITE 273 273
FT ACT_SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
FT SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
DB 453 ADWSW 457
RESULT 11
NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93212520; PubMed-8460490;
RA Saito T., Kawaoaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."

```

```

RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06588; AAA43410.1; -
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; GH_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; GH_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 7 38
FT DOMAIN 39 88
FT ACT_SITE 273 273
FT ACT_SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
FT SEQUENCE 470 AA; 52352 MW; DE573742ABFF1E6B CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
DB 453 ADWSW 457
RESULT 12
IKKA_HUMAN STANDARD; PRT; 745 AA.
AC 015111; 014666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkkappaB kinase)
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN IKK1 OR CHUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE-97386461; PubMed-9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkkappaB kinase."
RT Cell 90:373-383(1997).

```


RN [2] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-9739466; PubMed-9252186;
 RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RT "A cytokine-responsive IkappaB kinase that activates the transcription
 RL factor NF-kappaB.";
 RN Nature 388:548-554(1997).
 [3]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE-Cervical carcinoma;
 RX MEDLINE-98008813; PubMed-9346484;
 RA Mercuro F., Zhu H., Murray B.W., Shervenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa W., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RL NF-kappaB activation.";
 RL Science 278:860-866(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE-99032998; PubMed-9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RL embryonic tissues but localized to different human chromosomes.";
 RN Gene 222:31-40(1998).
 [5]
 RP SEQUENCE OF 32-745 FROM N.A.
 RC TISSUE-Cervical carcinoma;
 RX MEDLINE-96258427; PubMed-8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RL families of interacting proteins, contains a serine-threonine kinase
 RL catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 [6]
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND
 RP S-180.
 RX MEDLINE-98188283; PubMed-9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RL Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE-99413720; PubMed-10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RL serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 [8]
 RP IKKA-IKKB BINDING.
 RX MEDLINE-99212141; PubMed-10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RL IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 [9]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; PubMed-9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RL kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 [10]
 RP REVIEW.
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RL inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND

CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 CC WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 CC ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
 CC MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF012890; AAC51662.1;
 CC EMBL; AF009225; AAC51671.1;
 CC EMBL; AF080157; AAC08996.1;
 CC EMBL; U22512; AAC50713.1;
 CC HSSP; Q63450; IA06.
 CC Genew; HGNC:1974; CHUK.
 CC MTM; 600664;
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 KW Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
 FT ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS -> DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DWSWL 6
 Db 739 DWSWL 743
 RESULT 13

IKKA_MOUSE STANDARD; PRT; 745 AA.

AC 060680; Q9D2X3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1-)

DE (I-kappa-B kinase alpha) (IKK- α) (IKK- α) (Ikkapab kinase)

DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous

DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1A).

GN IKKA OR CHUK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN-BALB/C;

RX MEDLINE-96044444; PubMed-7558004;

RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;

RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human

RT chromosome 10 and mouse chromosome 19.";

RL Genomics 27:348-351(1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN-BALB/C;

RX MEDLINE-96258427; PubMed-8777433;

RA Connolly M.A., Marcu K.B.;

RT "CHUK, a new member of the helix-loop-helix and leucine zipper

RT families of interacting proteins, contains a serine-threonine kinase

RT catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC STRAIN-C57BL/6J; Tissue-Colon;

RX MEDLINE-21085660; PubMed-11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aikawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [4]

RP ALTERNATIVE SPLICING.

RX MEDLINE-20198447; PubMed-10733566;

RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,

RA Gelezunas R., Marcu K.B.;

RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking

RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and

RT IKKbeta have different activation requirements.";

RL Mol. Cell. Biol. 20:2635-2649(2000).

RN [5]

RP PHOSPHORYLATION BY MAP3K14/NIK.

RX MEDLINE-9818238; PubMed-9520401;

RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,

RA Okumura K.;

RT "Differential regulation of IkappaB kinase alpha and beta by two

RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated

RT protein kinase/ERK kinase-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).

RN [6]

RP IKKA- α BINDING.

RX MEDLINE-99212141; PubMed-10195894;

RA Delhase M., Hayakawa M., Chen Y., Karin M.;

RT "Positive and negative regulation of IkappaB kinase activity through

RT IKKbeta subunit phosphorylation.";

RL Science 284:309-313(1999).

RN [7]

RP IKK PHOSPHORYLATION.

RX MEDLINE-99038238; PubMed-9819420;

RA Nemoto S., DiDonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein

RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343(1998).

RN [8]

RP REVIEW.

RX MEDLINE-20178139; PubMed-10712233;

RA Jobin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of

RT mucosal inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462(2000).

CC [1-] FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO

CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND

CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.

CC [2-] ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED

CC WHEN DEPHOSPHORYLATED.

CC [3-] SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT

CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.

CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN

CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50

CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.

CC [4-] SUBCELLULAR LOCATION: Cytoplasmic.

CC [5-] ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2/DELTA LH AND

CC 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.

CC [6-] DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY

CC E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION

CC PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.

CC [7-] PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY

CC MEK1. AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.

CC [8-] SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC IKAPPAB KINASE SUBFAMILY.

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CC -----

DR EMBL; U12473; AAC52589.1; --

DR EMBL; AK018671; BAB31335.1; --

DR HSSP; O63450; 1A06.

DR MGD; MG1:99484; Chuk.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; pkinase.1.

DR ProDom; PD000001; Euk_pkinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR Transferrase; Serine/threonine-protein kinase; ATP-binding;

KW phosphorylation; Alternative splicing.

KW DOMAIN 15 300 PROTEIN KINASE.

FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).

FT NEMO-BINDING.

FT NP_BIND 21 29 ATP (BY SIMILARITY).

FT BINDING 44 44 ATP (BY SIMILARITY).

FT ACT_SITE 144 144 BY SIMILARITY.

FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1) (BY

FT MOD_RES 176 176 SIMILARITY).
 FT VARSPLIC 452 471 SIMILARITY).
 FT MSLIRYNANLTKMNTLIS -> IFRKNVKSMEGRKRGH
 FT SLF (IN ISOFORM 2).
 FT MISSING (IN ISOFORM 2).
 FT DLYSDST -> GKTLQSQY (IN ISOFORM 3).
 FT MISSING (IN ISOFORM 3).
 FT K -> E (IN REF. 3).
 FT S -> Y (IN REF. 3).
 FT CONFLICT 236 236
 FT CONFLICT 400 400
 SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AFF92233 CRC64;

Query Match 90.08; Score 36; DB 1; Length 745;
 Best Local Similarity 100.08; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWSWL 6
 Db 739 DWSWL 743
 I I I I I

RESULT 14
 ID IKKB_HUMAN STANDARD; PRT; 756 AA.
 AC O14920; 075327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.;
 RL Science 278:860-866(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RX MEDLINE=98008814; PubMed=9346485;
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 RA "IkappaB kinase-beta: NF-kappaB activation and complex formation with
 RT IkappaB kinase-alpha and NIK.";
 RL Science 278:866-869(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 RT 8p12--p11 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [7]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -I- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -I- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND
 CC PERIPHERAL BLOOD.
 CC -I- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF029684; AAC51860.1; -
 CC EMBL; AF080158; AAD08997.1; -
 CC EMBL; AF031416; AAC64675.1; -
 CC EMBL; BC006231; AAO06231.1; -
 CC HSPF; Q63450; IAO6.
 CC Genes; HGNC:5960; IKKB.
 CC MIN; 603258; -
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00240; ubiquitin; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC PRODOM; PD000001; Euk_pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 KW DOMAIN 15 300 PROTEIN KINASE.
 FT FT 15 300 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 458 479 NEMO-BINDING.
 FT FT 737 742
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION.
 FT MOD_RES 181 181 K->A: LOSS OF KINASE ACTIVITY AND NO
 FT MUTAGEN 44 44 EFFECT ON BINDING TO NIK.
 FT FT 177 177 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.

FT CONFLICT 231 255 WISKVROKSEVDIVVSDNGTVKF -> CVRWMPGTVAHS
 FT CONFLICT 425 425 CMPTLGGGRWI (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 756;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSWL 6
 Db 738 DMSWL 742
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 ID IKKB_MOUSE STANDARD; PRT; 757 AA.
 AC 088351: 09RLJ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1)-
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Oiu W.R.;
 RT "Murine IKK kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of IKK.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Oiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The IkappaB/NF-kappaB system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN

CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBQUITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.

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DR EMBL; AF026524; AAC23557.1;
 DR EMBL; AF088910; AAD32095.1;
 DR HSSP; Q63450; 1A06.
 DR MGD; MGI:1338071; Ikkb.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; P0000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDNSWLQMEDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;

Query Match 90.0%; Score 36; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 Db 738 DMSWL 742

Search completed: May 30, 2003, 15:48:50
 Job time : 4.11842 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 10123694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	6	9	US-09-847-940B-3
2	26	100.0	6	9	US-09-847-946A-3
3	26	100.0	28	9	US-09-847-940B-19
4	26	100.0	240	9	US-09-847-946A-19
5	26	100.0	600	9	US-09-738-626-4338
6	26	100.0	600	9	US-09-746-660A-106
7	26	100.0	638	9	US-09-983-204-18
8	26	100.0	638	9	US-10-133-157-8
9	26	100.0	659	9	US-09-738-626-6815
10	26	100.0	745	9	US-09-738-626-4761
11	26	100.0	745	9	US-09-746-660A-104
12	26	100.0	745	10	US-09-919-835-2
13	24	92.3	14	9	US-10-038-612-107
14	24	92.3	20	9	US-10-038-612-35
15	24	92.3	21	9	US-10-038-612-106
16	24	92.3	40	9	US-10-044-967-18
17	24	92.3	298	10	US-09-771-161A-187
18	24	92.3	304	9	US-09-976-059-3
19	24	92.3	359	10	US-09-923-109-2

20	24	92.3	405	9	US-10-078-107-6	Sequence 6, Appli
21	24	92.3	405	9	US-10-077-751-6	Sequence 6, Appli
22	24	92.3	405	10	US-09-815-242-10096	Sequence 10096, A
23	24	92.3	506	10	US-09-815-242-13990	Sequence 13990, A
24	24	92.3	544	9	US-10-072-036-113	Sequence 113, App
25	24	92.3	544	9	US-10-072-036-115	Sequence 115, App
26	24	92.3	622	9	US-09-738-626-4817	Sequence 4817, Ap
27	23	88.5	88	10	US-10-016-157A-213	Sequence 213, App
28	23	88.5	95	10	US-09-956-425-23	Sequence 23, Appl
29	23	88.5	159	10	US-09-731-872-419	Sequence 419, App
30	23	88.5	201	9	US-10-107-931-8	Sequence 8, Appli
31	23	88.5	201	9	US-10-212-793-4	Sequence 4, Appli
32	23	88.5	201	10	US-09-901-540-3	Sequence 3, Appli
33	23	88.5	201	10	US-09-896-856-8	Sequence 8, Appli
34	23	88.5	201	10	US-09-901-257-3	Sequence 3, Appli
35	23	88.5	220	9	US-10-071-338-18	Sequence 18, Appl
36	23	88.5	255	9	US-10-125-540-427	Sequence 427, App
37	23	88.5	255	10	US-09-764-870-427	Sequence 427, App
38	23	88.5	277	9	US-10-108-605-109	Sequence 109, App
39	23	88.5	368	9	US-09-925-299-849	Sequence 849, App
40	23	88.5	368	10	US-09-925-299-849	Sequence 849, App
41	23	88.5	464	9	US-09-839-446-35	Sequence 35, Appl
42	23	88.5	464	9	US-09-839-446-36	Sequence 36, Appl
43	23	88.5	464	9	US-09-839-446-37	Sequence 37, Appl
44	23	88.5	464	9	US-09-839-446-38	Sequence 38, Appl
45	23	88.5	464	10	US-09-742-311-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-847-940B-3
; Sequence 3, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPT-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-3

Query Match 100.0%; Score 26; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
| | | | |
Db 1 LDASAL 6

RESULT 2

US-09-847-946A-3
; Sequence 3, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkelstein, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; PRIOR FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-3

Query Match 100.0%; Score 26; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 1 LDASAL 6

RESULT 3
US-09-847-940B-19
;; Sequence 19, Application US/09847940B
;; Patent No. US20020156000A1
;; GENERAL INFORMATION:
;; APPLICANT: May, Michael J.
;; APPLICANT: Ghosh, Sankar
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-117CP
;; CURRENT APPLICATION NUMBER: US/09/847,940B
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 19
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19

Query Match 100.0%; Score 26; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 20 LDASAL 25

RESULT 4
US-09-847-946A-19
;; Sequence 19, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:
;; APPLICANT: May, Michael J
;; APPLICANT: Ghosh, Sankar
;; APPLICANT: Findels, Mark A
;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Hannig, Gerhard
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 19
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

Query Match 100.0%; Score 26; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 20 LDASAL 25

RESULT 5
US-09-738-626-4338
;; Sequence 4338, Application US/09738626
;; Publication No. US20020197605A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAGAWA, SATOSHI
;; APPLICANT: MIZOGUCHI, HIROSHI
;; APPLICANT: ANDO, SEIKO
;; APPLICANT: HAYASHI, MIKIRO
;; APPLICANT: OCHIAI, KEIKO
;; APPLICANT: YOKOI, HARUHIKO
;; APPLICANT: TATEISHI, NAKO
;; APPLICANT: SENOH, AKIHIRO
;; APPLICANT: IKEDA, MASATO
;; APPLICANT: OZAKI, AKIO
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-125
;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 4338
;; LENGTH: 240
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4338

Query Match 100.0%; Score 26; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 70 LDASAL 75

RESULT 6
US-09-746-660A-106
;; Sequence 106, Application US/09746660A
;; Publication No. US20030049804A1
;; GENERAL INFORMATION:
;; APPLICANT: Pompejus, Markus
;; APPLICANT: Kroger, Burkhard
;; APPLICANT: Schroder, Hartwig

APPLICANT: Zelder, Oskar
APPLICANT: Habernauer, Gregor
APPLICANT: Kim, Jun-won
APPLICANT: Lee, Heung-Schick
APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/603124
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 106
LENGTH: 600
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-746-660A-106

Query Match 100.0%; Score 26; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 140 LDASAL 145

RESULT 7
US-09-983-204-18
Sequence 18, Application US/09983204
Patent No. US20020173000A1
GENERAL INFORMATION:
APPLICANT: RENARD, STEPHANE
APPLICANT: BESNARD, FRANCOIS
APPLICANT: GRAHAM, DAVID
TITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
FILE REFERENCE: 07586.0010
CURRENT APPLICATION NUMBER: US/09/983,204
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/424,666
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/02884
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 97401196.7
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 638
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: HNACHD
US-09-983-204-18

Query Match 100.0%; Score 26; DB 9; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 551 LDASAL 556

RESULT 8
US-10-133-157-8
Sequence 8, Application US/10133157
Publication No. US20020184054A1
GENERAL INFORMATION:
APPLICANT: CALLAMARAS, NICHOLAS
APPLICANT: CHANG, HONG
TITLE OF INVENTION: HIGH THROUGHPUT CELL-BASED ASSAY FOR MONITORING SODIUM
CHANNEL ACTIVITY AND DISCOVERY OF SALTY TASTE
MODULATING COMPOUNDS
FILE REFERENCE: 078003-0280790
CURRENT APPLICATION NUMBER: US/10/133,157
CURRENT FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: 60/287,413
PRIOR FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 638
TYPE: PRT
ORGANISM: Homo sapiens
US-10-133-157-8

Query Match 100.0%; Score 26; DB 9; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 551 LDASAL 556

RESULT 9
US-09-738-626-6815
Sequence 6815, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIALI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENO, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6815
LENGTH: 659
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6815

Query Match 100.0%; Score 26; DB 9; Length 659;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 132 LDASAL 137

RESULT 10
US-09-738-626-4761
; Sequence 4761, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 4761
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4761

Query Match 100.0%; Score 26; DB 9; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 140 LDASAL 145

RESULT 11
US-09-746-660A-104
; Sequence 104, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Kim, Jun-Won
; APPLICANT: Lee, Heung-Schick
; APPLICANT: Hwang, Byung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CP2
; CURRENT APPLICATION NUMBER: US/09/746,660A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/606740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142101

QY 1 LDASAL 6
Db 140 LDASAL 145

RESULT 12
US-09-919-835-2
; Sequence 2, Application US/09919835
; Patent No. US20020110877A1
; GENERAL INFORMATION:
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: MOECKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: HUTHMACHER, KLAUS
; APPLICANT: RUECKERT, CHRISTIAN
; APPLICANT: KALINOWSKI, JOERN
; APPLICANT: PUEHLER, ALFRED
; APPLICANT: BINDER, MICHAEL
; APPLICANT: GREISSINGER, DIETER
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METE GENE
; FILE REFERENCE: 211710US0X
; CURRENT APPLICATION NUMBER: US/09/919,835
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: DE 10038023.9
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: DE 10109689.5
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/294,250
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-919-835-2

Query Match 100.0%; Score 26; DB 10; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 140 LDASAL 145

RESULT 13
US-10-038-612-107
; Sequence 107, Application US/10038612
; Patent No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively

;; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
;; FILE REFERENCE: 1242.1029-000 (CMCC-679)
;; CURRENT APPLICATION NUMBER: US/10/038,612
;; CURRENT FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 09/161,094
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 172
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 107
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: ACETYLATION
;; LOCATION: (1)...(0)
;; OTHER INFORMATION: benzyl ester at position 1
;; NAME/KEY: AMIDATION
;; LOCATION: (0)...(14)
;; OTHER INFORMATION:
;; OTHER INFORMATION: CDK2
US-10-038-612-107

Query Match 92.3%; Score 24; DB 9; Length 14;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
Db 6 MDASAL 11

RESULT 14

US-10-038-612-35
;; Sequence 35, Application US/10038612
;; Patent No. US20020160478A1
;; GENERAL INFORMATION:
;; APPLICANT: Ben-Sasson, Shmuel A.

;; TITLE OF INVENTION: Short Peptides Which Selectively
;; FILE REFERENCE: 1242.1029-000 (CMCC-679)
;; CURRENT APPLICATION NUMBER: US/10/038,612
;; CURRENT FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 09/161,094
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 172
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 35
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: unknown
;; FEATURE:
;; OTHER INFORMATION: CDK2
US-10-038-612-35

Query Match 92.3%; Score 24; DB 9; Length 20;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
Db 12 MDASAL 17

RESULT 15

US-10-038-612-106
;; Sequence 106, Application US/10038612
;; Patent No. US20020160478A1
;; GENERAL INFORMATION:
;; APPLICANT: Ben-Sasson, Shmuel A.

;; TITLE OF INVENTION: Short Peptides Which Selectively
;; FILE REFERENCE: 1242.1029-000 (CMCC-679)

;; CURRENT APPLICATION NUMBER: US/10/038,612
;; CURRENT FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 09/161,094
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 172
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 106
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: MYRISTATE
;; LOCATION: (1)...(0)
;; NAME/KEY: AMIDATION
;; LOCATION: (0)...(21)
;; OTHER INFORMATION:
;; OTHER INFORMATION: CDK2
US-10-038-612-106

Query Match 92.3%; Score 24; DB 9; Length 21;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
Db 13 MDASAL 18

Search completed: May 30, 2003, 15:53:15
Job time : 11.4605 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	100.0	84	2 D70672	hypothetical prote
2	26	100.0	129	2 T31200	hypothetical prote
3	26	100.0	130	2 F90278	conserved hypothet
4	26	100.0	171	2 F87628	hypothetical prote
5	26	100.0	230	2 E95326	Atra transcription
6	26	100.0	259	2 F69311	conserved hypothet
7	26	100.0	281	2 C83635	hypothetical prote
8	26	100.0	334	2 T37024	probable DNA-bindi
9	26	100.0	383	2 H98287	hypothetical prote
10	26	100.0	394	2 H81807	conserved hypothet
11	26	100.0	394	2 H81062	conserved hypothet
12	26	100.0	437	2 A70587	hypothetical prote
13	26	100.0	483	2 AH3265	aspartate ammonia-
14	26	100.0	512	2 H81847	hypothetical prote
15	26	100.0	513	2 A96265	hypothetical prote
16	26	100.0	513	2 AH3019	sigma 54 dependent
17	26	100.0	516	2 E81092	hypothetical prote
18	26	100.0	550	2 H70772	probable args prot
19	26	100.0	586	2 T49210	hypothetical prote
20	26	100.0	638	2 T39196	amiloride sensitiv
21	26	100.0	855	2 T41336	probable nitrog
22	26	100.0	894	2 G82260	leucyl-tRNA synthe
23	26	100.0	920	2 I40614	surface array prot
24	26	100.0	1006	2 T41439	putative sulfite r
25	26	100.0	1313	1 JC2038	peptidyl-dipeptida
26	24	92.3	58	2 S55558	allophycocyanin be
27	24	92.3	157	2 C70882	hypothetical prote
28	24	92.3	166	2 AC1940	purine-binding che
29	24	92.3	179	2 B96989	probable membrane

30	24	92.3	197	2 A64484	conserved hypothet
31	24	92.3	279	2 A83986	hypothetical prote
32	24	92.3	292	2 A95163	hypothetical prote
33	24	92.3	292	2 H98028	hypothetical prote
34	24	92.3	294	2 T26946	hypothetical prote
35	24	92.3	298	2 A41227	protein kinase (EC
36	24	92.3	304	2 T42939	hypothetical prote
37	24	92.3	326	2 T09995	phosphoprotein pho
38	24	92.3	346	1 I78840	protein kinase (EC
39	24	92.3	359	1 ADEC2A	fructose-bisphosph
40	24	92.3	359	2 D91103	fructose-bisphosph
41	24	92.3	359	2 AC0875	fructose-1,6-bisph
42	24	92.3	384	2 G85948	fructose-bisphosph
43	24	92.3	393	2 S69191	adenosylmethionine
44	24	92.3	401	2 AC2113	alanine racemase (
45	24	92.3	405	1 XUECSD	dihydrolipoamide S

ALIGNMENTS

RESULT 1

D70672

hypothetical protein Rv2975c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: D70672

R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A: Reference number: A70500; MUID:98295987; PMID:9634230

A: Accession: D70672

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-84 <COL>

A: Cross-references: GB:283018; GB:AL123456; NID:g3261671; PIDN:CAB05437.1; PID:g28336

A: Experimental source: strain H37RV

C: Geneticks:

A: Gene: Rv2975c

Query Match 100.0%; Score 26; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 8 LDASAL 13

RESULT 2

T31200

hypothetical protein 633 - Sphingomonas aromaticivorans plasmid pNL1

C:Species: Sphingomonas aromaticivorans

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T31200

R: Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.
submitted to the EMBL Data Library, July 1998

A: Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas arom

A: Reference number: Z20992

A: Accession: T31200

A: Status: preliminary; translated from GB/EMBL/DDBJ

A: Molecule type: DNA

A: Residues: 1-129 <ROM>

A: Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378341; PIDN:AAD03924.1

C: Geneticks:

A: Genome: plasmid pNL1

A: Note: orf633

Query Match 100.0%; Score 26; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
Db 6 LDASAL 11

RESULT 3

F90278

conserved hypothetical protein [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: F90278

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: F90278

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <KUR>

A:Cross-references: GB:AE006641; NID:gl13814439; PIDN:AAK41485.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO1243

Query Match 100.0%; Score 26; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
Db 8 LDASAL 13

RESULT 4

F87628

hypothetical protein CC3064 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: F87628

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon-
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: F87628

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <STO>

A:Cross-references: GB:AE005673; NID:gl3424712; PIDN:AAK25026.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3064

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 171;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
Db 118 LDASAL 123

RESULT 5

E95326

AtrA transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplas

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: E95326

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows-
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli-
A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: E95326

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-230 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK65175.1; PID:gl4523620; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl-

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau-

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: atrA

A:Genome: plasmid

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 230;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
Db 83 LDASAL 88

RESULT 6

F69311

conserved hypothetical protein AF0494 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000

C:Accession: F69311

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod-

g, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: F69311

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-259 <KLE>

A:Cross-references: GB:AE001070; GB:AE000782; NID:2689393; PIDN:AA890743.1; PID:9265

C:Superfamily: conserved hypothetical protein MTH682

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 259;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
Db 149 LDASAL 154

RESULT 7

C83635

hypothetical protein PA0086 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83635

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: C83635
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <STO>
A:Cross-references: GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AA03476.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0086

Query Match 100.0%; Score 26; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
|||||
Db 79 LDASAL 84

RESULT 8

T37024

Probable DNA-binding regulator - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37024
R:Murphy, L.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21619
A:Accession: T37024
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-334 <MUR>
A:Cross-references: EMBL:AL109989; PIDN:CAB53417.1; GSPDB:GN00070; SCOEDB:SCJ12.05c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCJ12.05c

Query Match 100.0%; Score 26; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
|||||
Db 139 LDASAL 144

RESULT 9

H98287

hypothetical protein AGR_L_2514 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: H98287
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194

A:Accession: H98287
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>

A:Cross-references: GB:AE007870; PIDN:AAK89826.1; PID:g15159760; GSPDB:GN00170
C:Genetics:

A:Gene: AGR_L_2514

A:Map position: linear chromosome

Query Match 100.0%; Score 26; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
|||||
Db 270 LDASAL 275

RESULT 10

H81807

conserved hypothetical protein NMA1819 [imported] - Neisseria meningitidis (strain Z2

C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: H81807
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: H81807

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <PAR>

A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85044.1; PID:g738

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1819

Query Match 100.0%; Score 26; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
|||||
Db 365 LDASAL 370

RESULT 11

B81062

conserved hypothetical protein NMB1620 [imported] - Neisseria meningitidis (strain MC

C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: B81062

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, B.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: B81062

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <TBT>

A:Cross-references: GB:AE002512; GB:AE002098; NID:g7226866; PIDN:AAFA1972.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1620

Query Match 100.0%; Score 26; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
|||||
Db 365 LDASAL 370

RESULT 12

A70587

hypothetical protein RV2370c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: A70587

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70587

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-437 <COL>

A:Cross-references: GB:295208; GB:AL123456; NID:g3261747; PIDN:CAB08469.1; PID:e315159;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2370c

Query Match 100.0%; Score 26; DB 2; Length 437;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

|||||

DB 96 LDASAL 101

RESULT 13

AH3265

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AH3265

R:Belvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

; Mazur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AH3265

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <KUR>

A:Cross-references: GB:AE008917; PIDN:AAL51291.1; PID:g17981985; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10109

A:Map position: 1

C:Superfamily: fumarate hydratase

C:Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 100.0%; Score 26; DB 2; Length 483;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

|||||

DB 452 LDASAL 457

RESULT 14

H81847

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: H81847

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: AB1775; MUID:2022556; PMID:10761919

A:Accession: H81847

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-512 <PAR>

A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84784.1; PID:g738019

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1557

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 512;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

|||||

DB 318 LDASAL 323

RESULT 15

A96265

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002

C:Accession: A96265

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: A96265

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-513 <KUR>

A:Cross-references: GB:AE007870; PIDN:AAK89643.1; PID:g15159542; GSPDB:GN00170

C:Genetics:

A:Gene: AGR_L_2141

A:Map position: linear chromosome

C:Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 513;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

|||||

DB 346 LDASAL 351

Search completed: May 30, 2003, 14:52:38

Job time : 8.5921 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	214	1 RADC_RHOCA	P72255 rhodobacter
2	26	100.0	550	1 SYR_MYCTU	Q10609 mycobacteri
3	26	100.0	638	1 SCAD_HUMAN	P51172 homo sapien
4	26	100.0	638	1 SCAD_PANTR	O46347 pan troglod
5	26	100.0	855	1 GYL_SCHPO	Q10280 schizosacch
6	26	100.0	858	1 SYL_VIBCH	Q9kte6 vibrio chol
7	26	100.0	1006	1 MT10_SCHPO	Q09878 schizosacch
8	26	100.0	1313	1 ACE_RAT	P47820 rattus norv
9	24	92.3	197	1 YE74_METJA	O58869 methanococ
10	24	92.3	298	1 CDK2_HUMAN	P24941 homo sapien
11	24	92.3	298	1 CDK2_RAT	O63699 rattus norv
12	24	92.3	346	1 CDK2_MOUSE	P97377 mus musculu
13	24	92.3	358	1 ALF_ECOLI	P11604 escherichia
14	24	92.3	358	1 ALR_ANASP	Q8vu96 anabaena sp
15	24	92.3	393	1 DCM_HORCH	O42829 hordeum chi
16	24	92.3	404	1 OD02_ECOLI	P07016 escherichia
17	24	92.3	446	1 DTA2_RALSO	Q8xub6 raistonia s
18	24	92.3	518	1 FLAA_AQUAE	O67803 aquifex aeo
19	24	92.3	933	1 SLAP_CAMFE	P35827 campylobact
20	24	92.3	964	1 MSH2_YEAST	P25847 saccharomyc
21	24	92.3	970	1 SECA_CHLPN	Q9z765 chlamydia p
22	24	92.3	3255	1 POLG_LMV0	P31999 l genome po
23	24	92.3	3255	1 POLG_LMVE	P89876 l genome po
24	23	88.5	145	1 MA29_DERFA	P39674 dermatophag
25	23	88.5	161	1 PHAB_SYNTP6	P06113 synchococc
26	23	88.5	193	1 ACD1_XANAC	P58902 xanthomonas
27	23	88.5	201	1 CTF1_HUMAN	Q16619 homo sapien
28	23	88.5	242	1 6PGL_PSEPU	Q9ev79 pseudomonas
29	23	88.5	247	1 6PGL_MYCTU	O06814 mycobacteri
30	23	88.5	249	1 CYSH_SYN3	P72794 synchocyst
31	23	88.5	249	1 STXA_HUMAN	O60499 homo sapien
32	23	88.5	351	1 PTA_RICPR	Q9ze39 rickettsia
33	23	88.5	355	1 LEU3_SPIPL	Q00412 spirulina p

34 23 88.5 366 1 REQ2_XENLA
35 23 88.5 372 1 MTOX_SALTI
36 23 88.5 372 1 MTOX_SALTY
37 23 88.5 380 1 SCHA_STRHA
38 23 88.5 388 1 REQ1_XENLA
39 23 88.5 400 1 DCM_MAIZE
40 23 88.5 411 1 BHB2_MOUSE
41 23 88.5 411 1 BHB2_RAT
42 23 88.5 429 1 FLIK_BACSU
43 23 88.5 442 1 IFR2_HUMAN
44 23 88.5 464 1 GAR3_RAT
45 23 88.5 529 1 4F2_HUMAN

Q9w636 xenopus lae
P58524 salmonella
P58525 salmonella
Q05361 streptomyc
Q9w638 xenopus lae
Q24575 zea mays (m
Q35185 mus musculu
O35780 rattus norv
P23451 bacillus su
Q12894 homo sapien
P50573 rattus norv
P08195 homo sapien

ALIGNMENTS

RESULT 1

RADC_RHOCA STANDARD; PRT; 214 AA.

AC P72255;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE DNA repair protein radc homolog.

GN RADC.

OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).

OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;

OC Rhodobacter.

OX NCBI_TaxID=1061;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33303 / B10;

RX PubMed=10652786;

RA Katsiou E., Nickel C.M., Garcia A.F., Tadros M.H.;

RT "Molecular analysis and identification of the radc gene from the

phototrophic bacterium Rhodobacter capsulatus B10.";

RL Microbiol. Res. 154:233-239(1999).

CC -!- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).

CC -!- INDUCTION: Induced about five-fold after UV-irradiation.

CC -!- SIMILARITY: BELONGS TO THE RADC FAMILY.

CC -----
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CC EMBL; U74017; AAB18255.1; -

DR InterPro; IPR001405; RADC.

DR ProDom; PD007415; RADC; 1.

DR TIGRFAIMS; TIGR00608; radc; 1.

DR PROSITE; PS01302; RADC; 1.

KW DNA repair.

SQ SEQUENCE 214 AA; 23792 MW; D008997B20C6743D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 214;

Best Local Similarity 100.0%; Pred No. 16;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

Db 154 LDASAL 159

|||||

RESULT 2

SYR_MYCTU

ID SYR_MYCTU STANDARD; PRT; 550 AA.

AC Q10609;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
 DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ARGRS).
 GN ARG5 OR RV1292 OR MT1331 OR MFCY373.12.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
 CC di-phosphate + L-arginyl-tRNA(Arg).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
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 CC EMBL; Z73419; CAA97757.1; -;
 CC DR EMBL; AE007007; AAK45593.1; -;
 CC TIGR; MT1331; -;
 CC TubercuList; RV1292; -;
 CC DR InterPro; IPR001278; Arg_tRNA-synt_1c.
 CC DR InterPro; IPR005148; N.
 CC DR InterPro; IPR001412; tRNA-synt_1.
 CC DR Pfam; PF00750; tRNA-synt_1d; 1.
 CC DR Pfam; PF03485; N-Arg; 1.
 CC DR PRINTS; PR01038; TRNASNTUARG.
 CC DR TIGRFAMS; TIGR00456; args; 1.
 CC DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 CC DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 CC Complete proteome.
 KW SITE 130 140 "HIGH" REGION.
 KW SITE 374 378 "RMSKS" REGION.
 FT BINDING 377 377 ATP (BY SIMILARITY).
 SQ SEQUENCE 550 AA; 59709 MW; 4F11239A6238124D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 550;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 |||||
 Db 23 LDASAL 28

RESULT 3
 ID SCAD_HUMAN STANDARD; PRT; 638 AA.
 AC P51172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Amiloride-sensitive sodium channel delta-subunit (Epithelial Na+
 DE channel delta subunit) (Delta ENaC) (Nonvoltage-gated sodium channel.
 DE 1 delta subunit) (SCNED) (Delta NaCh).
 GN SCNED OR DNACH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96070858; PubMed=7499195;
 RA Waldmann R., Champigny G., Bassilana F., Voilley N., Lazdunski M.;
 RT "Molecular cloning and functional expression of a novel amiloride-
 RT sensitive Na+ channel.";
 RL J. Biol. Chem. 270:27411-27414(1995).
 CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
 CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION
 CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
 CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
 CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
 CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
 CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
 CC FAMILY.
 CC
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 CC
 CC EMBL; U38254; AAC50283.1; -;
 CC DR EMBL; HGNC:10601; SCNND.
 CC DR MIM; 601328; -;
 CC DR InterPro; IPR004724; EnaC.
 CC DR InterPro; IPR001873; Na+channel_ASC.
 CC DR Pfam; PF00858; ASC; 1.
 CC DR PRINTS; PR01078; AMINACHANNEL.
 CC DR TIGRFAMS; TIGR00859; ENaC; 1.
 CC DR PROSITE; PS01206; ASC; 1.
 CC DR Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 KW DOMAIN 1 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT DOMAIN 108 530 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 531 551 POTENTIAL.
 FT DOMAIN 552 638 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 638 AA; 70274 MW; 7CD5181F8497F5CF CRC64;

Query Match 100.0%; Score 26; DB 1; Length 638;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 |||||
 Db 551 LDASAL 556

RESULT 4

ID	SCAD_PANTR	STANDARD	PRT	638 AA
AC	046547			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DE	Amiloride-sensitive sodium channel delta-subunit (Epithelial Na+ channel delta subunit) (Delta ENAC) (Nonvoltage-gated sodium channel 1 delta subunit) (SCNED) (Delta Nach).			
GN	SCNN1D OR DNACH.			
OS	Pan troglodytes (Chimpanzee).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.			
OX	NCBI_TaxID=9598;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Testis;			
RA	Al-Khalili O.K., Eaton D.C.;			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY) THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS. ALSO PLAYS A ROLE IN TASTE PERCEPTION (BY SIMILARITY).			
CC	-1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; AF038165; AAB92659.1; -			
DR	InterPro; IPR004724; Enac.			
DR	InterPro; IPR001873; Na+channel_ASC.			
DR	Pfam; PF00858; ASC; 1.			
DR	PRINTS; PR01078; AMINACHANNEL.			
DR	TIGRFAMs; TIGR00859; ENAC; 1.			
DR	PROSITE; PS01206; ASC; 1.			
KW	ionic channel; Transmembrane; Ion transport; Glycoprotein.			
FT	DOMAIN 1 86			
FT	TRANSMEM 87 107			
FT	DOMAIN 108 530			
FT	TRANSMEM 531 551			
FT	DOMAIN 552 638			
FT	CARBOHYD 166 166			
FT	CARBOHYD 211 211			
FT	CARBOHYD 384 384			
SO	SEQUENCE 638 AA; 70187 MW; 321E9597D6A78D38 CRC64;			
Query Match	100.0%; Score 26; DB 1; Length 638;			
Best Local Similarity	100.0%; Pred. No. 52;			
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 LDASAL 6			
Db	551 LDASAL 556			
RESULT 5				
GAFL1_SCHPO	STANDARD;			
ID	Q10280; Q9482; Q9USK9;			
AC	Q10280; Q9482; Q9USK9;			
DT	01-NOV-1997 (Rel. 35, Created)			

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Transcription factor gaf1 (Gaf-1).

GN GAF1 OR SPCC417.01C OR SPCC1902.01.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC SPRAIN-972;

RA MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgueros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grymonprez B., Weidjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borgez K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

RN [2]

RP SEQUENCE OF 566-855 FROM N.A.

RX MEDLINE=98382525; PubMed=9714831;

RA Hoe K.-L., Won M.S., Chung K.-S., Park S.-K., Kim D.-U., Jang Y.-J., Yoo O.-J., Yoo H.-S.;

RT "Molecular cloning of gaf1, a Schizosaccharomyces pombe GATA factor, which can function as a transcriptional activator.";

RL Gene 215:319-328(1998).

CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.

CC -----

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CC -----

DR EMBL; AL035076; CAA22647.1; -

DR EMBL; AL049521; CAB40003.1; -

DR EMBL; L31601; AAC35593.1; -

DR HSSP; P17429; 4GAT.

DR TRANSFAC; T02831; -

DR InterPro; IPR000679; Znf_GATA.

DR Pfam; PF00320; GATA; 1.

DR PRINTS; PR00619; GATAZNFINGER.

DR SMART; SM00401; Znf_GATA; 1.

DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.

DR PROSITE; PS0114; GATA_ZN_FINGER_2; 1.

KW Transcription regulation; Activator; DNA-binding; Zinc-finger; Nuclear protein.

FT ZN_FING 635 659 GATA-TYPE.

SQ SEQUENCE 855 AA; 91776 MW; 3D932F83D2DE6774 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
| | | | |
DB 211 LDASAL 216

RESULT 6

SYL_VIBCH STANDARD; PRT; 858 AA.
ID Q9KTE6;
AC O9KTE6;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Leucyl-tRNA synthetase (EC 6.1.1.4) (leucine-tRNA ligase) (LeuRS).
GN LEUS OR VC0956.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae";
RL Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL; AF004177; AAF94118.1; ALT_INIT.
CC TIGR; VC0956;
CC InterPro; IPR002302; Leu-trnaSynthetase.
CC InterPro; IPR002300; trna-synt_1a.
CC InterPro; IPR001412; trna-synt_1.
CC Pfam; PF00133; trna-synt_1.1.
CC PRINTS; PR00395; TRNASYNTHLEU.
CC TIGRfams; TIGR00396; leus_dact; 1.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 42 52 "HIGH" REGION.
FT SITE 618 622 "KMSKS" REGION.
FT BINDING 621 621 ATP (BY SIMILARITY).
SQ SEQUENCE 858 AA; 96621 MW; A4D59A2E1C9F1292 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 858;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
| | | | |
DB 688 LDASAL 693

RESULT 7

MT10_SCHPO STANDARD; PRT; 1006 AA.
ID Q09878;
AC Q09878;
DT 01-FEB-1996 (Rel. 33, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable sulfite reductase [NADPH] flavoprotein component.
DE (EC 1.8.1.2).
GN SPC584.OIC.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe".
RL Nature 415:871-880(2002).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF
SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED
FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O = sulfite + 3
NADPH.
CC -1- COFACTOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
ONE FAD PER CHAIN (BY SIMILARITY).
CC
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CC
CC EMBL; AL032824; CAA21818.2;
CC HSSP; P00388; IAMO.
CC InterPro; IPR003097; FAD_binding.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00175; NAD_binding; 1.
CC Pfam; PF00667; FAD_binding; 1.
CC PRINTS; PR00371; FPNCR.
KW Oxidoreductase; Flavoprotein; NADP; FAD; FMN; Electron transport;
KW Cysteine biosynthesis.

FT NP_BIND 658 669 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 788 798 FAD (FLAVIN PART) (BY SIMILARITY).
 SQ SEQUENCE 1006 AA; 111352 MW; 2EA2086D69561D33 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 26; DB 1; Length 1006;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 DB 554 LDASAL 559

RESULT 8
 ACE_RAT STANDARD; PRT; 1313 AA.

AC P47820;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
 DE (ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).
 GN DCPI OR ACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lung;
 RX MEDLINE-94121658; PubMed-8292044;
 RA Koike G., Krieger J.E., Jacob H.J., Mukoyama M., Pratt R.E.,
 RA Dzau V.J.;
 RA "Angiotensin converting enzyme and genetic hypertension: cloning of
 rat cDNAs and characterization of the enzyme.";
 RL Biochem. Biophys. Res. Commun. 198:380-386(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SUPRAIN-LEW/N; TISSUE-Lung;
 RA Jafarian-Fehrani M., Listwak S., Barrientos R.M., Michaud A.,
 RA Corvol P., Sternberg E.M.;
 RT "Characterization of a missense mutation in the angiotensin
 I-converting enzyme cDNA in exudative inflammation resistant F344/N
 rats.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
 THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
 VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
 CC -1- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
 oligopeptide-l-xaa-xbb, when xaa is not Pro, and xbb is neither
 Asp nor Glu. Converts angiotensin I to angiotensin II.
 CC -1- COFACTOR: BINDS 2 ZINC IONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; somatic (shown here) and testis-
 specific; are produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U03708; AAA82110.1;
 CC EMBL; U03734; AAA82111.1;
 CC EMBL; AF201332; AAG355597.1;
 CC MEROPS; M02.001;
 CC MEROPS; M02.004;
 CC InterPro; IPR001548; Peptidase_M2.
 CC InterPro; IPR000130; Zn_Mtpeptidse.
 CC Pfam; PF01401; Peptidase_M2; 2.

DR PRINTS; PR00791; PEPTIDASEA.
 DR PROSITE; PD004184; Peptidase_M2; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 2.
 KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
 KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.
 FT SIGNAL 1 35
 FT CHAIN 36 1313
 FT ANGIOTENSIN-CONVERTING ENZYME, SOMATIC
 FT ISOFORM.
 FT DOMAIN 36 1265
 FT TRANSMEM 1266 1282
 FT DOMAIN 1283 1313
 FT REPEAT 233 589
 FT REPEAT 831 1187
 FT METAL 396 396
 FT ACT_SITE 397 397
 FT METAL 994 994
 FT ACT_SITE 995 995
 FT METAL 998 998
 FT CARBOHYD 44 44
 FT CARBOHYD 60 60
 FT CARBOHYD 80 80
 FT CARBOHYD 117 117
 FT CARBOHYD 152 152
 FT CARBOHYD 166 166
 FT CARBOHYD 324 324
 FT CARBOHYD 515 515
 FT CARBOHYD 683 683
 FT CARBOHYD 701 701
 FT CARBOHYD 720 720
 FT CARBOHYD 766 766
 FT CARBOHYD 948 948
 FT CARBOHYD 1197 1197
 FT VARIANT 207 207
 FT R -> K.
 SQ SEQUENCE 1313 AA; 150907 MW; 8CB5D0015F129591 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 1313;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 DB 600 LDASAL 605

RESULT 9
 YE74_METJA STANDARD; PRT; 197 AA.
 AC Q58869;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ1474.
 GN MJ1474.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID-2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE-96337999; PubMed-6880807;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RT Science 273:1058-1073(1996).
 RL

CC -1- SIMILARITY: BELONGS TO THE UPF0129 FAMILY.
 CC -----
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 CC -----
 DR EMBL; U67588; AAB99480.1; -
 DR TIGR; MJ1474; -
 DR InterPro: IPR002851; DUF133.
 DR Pfam: PF02000; DUF133; 1.
 DR ProDom: PD013236; DUF133; 1.
 KW Hypothetical protein; Complete proteome.
 FT DOMAIN 181 197 LYS-RICH.
 SQ SEQUENCE 197 AA; 22781 MW; 70075BB626934F58 CRC64;
 Query Match 92.3%; Score 24; DB 1; Length 197;
 Best Local Similarity 83.3%; Pred. No. 50;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 DB 36 LDASAI 41
 RESULT 10
 ID CDK2_HUMAN STANDARD; PRT; 298 AA.
 AC P24941;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cell division protein kinase 2 (EC 2.7.1.-) (p33 protein kinase).
 GN CDK2
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91330891; PubMed-1714386;
 RA Elledge S.J., Spottswood M.N.;
 RT "A new human p34 protein kinase, CDK2, identified by complementation
 RT of a cdc28 mutation in *Saccharomyces cerevisiae*, is a homolog of
 RT Xenopus Egl.";
 RL EMBO J. 10:2653-2659(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91367262; PubMed-1653904;
 RA Tsai L.-H., Harlow E., Meyerson M.;
 RT "Isolation of the human cdk2 gene that encodes the cyclin A- and
 RT adenovirus E1A-associated p33 kinase.";
 RL Nature 353:174-177(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92020980; PubMed-1717994;
 RA Nimiyi-Tsuji J., Nomoto S., Yasuda H., Reed S.I., Matsumoto K.;
 RT "Cloning of a human cDNA encoding a CDC2-related kinase by
 RT complementation of a budding yeast cdc28 mutation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9006-9010(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE-93010995; PubMed-1396589;
 RA Gu Y., Rosenblatt J., O'Morgan D.O.;
 RT "Cell cycle regulation of CDK2 activity by phosphorylation of Thr160

RT and Tyr15.";
 RL EMBO J. 11:3995-4005(1992).
 RN [6]
 RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RA MEDLINE-93288132; PubMed-8510751;
 RA de Bondt H.L., Rosenblatt J., Jancarik J., Jones H.D.,
 RA Morgan D.O., Kim S.-H.;
 RT "Crystal structure of cyclin-dependent kinase 2.";
 RL Nature 363:595-602(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CYCLIN A.
 RX MEDLINE-95356811; PubMed-7630397;
 RA Jeffrey P.D., Russo A.A., Polyak K., Gibbs E., Hurwitz J.,
 RA Massague J., Pavletich N.P.;
 RT "Mechanism of CDK activation revealed by the structure of a
 RT cyclinA-CDK2 complex.";
 RL Nature 376:313-320(1995).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.33 ANGSTROMS) OF COMPLEX WITH L868276.
 RX MEDLINE-96181476; PubMed-8610110;
 RA de Azevedo W.F. Jr., Muleer-Dieckmann H.-J., Schulze-Gahmen U.,
 RA Worland P.J., Sausville E., Kim S.-H.;
 RT "Structural basis for specificity and potency of a flavonoid
 RT inhibitor of human CDK2, a cell cycle kinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:2735-2740(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CG2A AND KIP1.
 RX MEDLINE-96300318; PubMed-8684460;
 RA Russo A.A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.;
 RT "Crystal structure of the p27Kip1 cyclin-dependent-kinase inhibitor
 RT bound to the cyclin A-CDK2 complex.";
 RL Nature 382:325-331(1996).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CG2A.
 RX MEDLINE-96313126; PubMed-8756328;
 RA Russo A.A., Jeffrey P.D., Pavletich N.P.;
 RT "Structural basis of cyclin-dependent kinase activation by
 RT phosphorylation.";
 RL Nat. Struct. Biol. 3:696-700(1996).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-97075215; PubMed-8917641;
 RA Schulze-Gahmen U., de Bondt H.L., Kim S.-H.;
 RT "High-resolution crystal structures of human cyclin-dependent kinase
 RT 2 with and without ATP: bound waters and natural ligand as guides for
 RT inhibitor design.";
 RL J. Med. Chem. 39:4540-4546(1996).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE-97475219; PubMed-9334743;
 RA Lawrie A.M., Noble M.E.M., Tunnah P., Brown N.R., Johnson L.N.,
 RA Endicott J.A.;
 RT "Protein kinase inhibition by staurosporine revealed in details of
 RT the molecular interaction with CDK2.";
 RL Nat. Struct. Biol. 4:796-801(1997).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CKS1.
 RX MEDLINE-96182647; PubMed-8601310;
 RA Bourne Y., Watson M.H., Hickey M.J., Holmes W., Rocque W., Reed S.I.,
 RA Tainer J.A.;
 RT "Crystal structure and mutational analysis of the human CDK2 kinase
 RT complex with cell cycle-regulatory protein CksHsl.";
 RL Cell 84:863-874(1996).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
 RX MEDLINE-98342369; PubMed-9677190;
 RA Gray N.S., Wodicka L., Thunnissen A.-M.W.H., Norman T.C., Kwon S.,
 RA Espinoza F.H., Morgan D.O., Barnes G., Leclerc S., Meijer L.,
 RA Kim S.H., Lockhart D.J., Schultz P.G.;
 RT "Exploiting chemical libraries, structure, and genomics in the search
 RT for kinase inhibitors.";
 RL Science 281:533-538(1998).
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.

```

CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
CC DURING S PHASE AND G2.
CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CDKX SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X61622; CAA43807.1; -
DR EMBL; X62071; CAA43985.1; -
DR EMBL; M68520; AAA35667.1; -
DR EMBL; BC003065; AAH03065.1; -
DR PIR; A41227; A41227.
DR PIR; S16520; S16520.
DR PIR; S17873; S17873.
DR PDB; 1FIN; 27-JAN-97.
DR PDB; 1HCK; 07-DEC-96.
DR PDB; 1HCL; 07-DEC-96.
DR PDB; 1A01; 12-NOV-97.
DR PDB; 1JST; 11-JAN-97.
DR PDB; 1JSU; 29-JUL-97.
DR PDB; 1BUH; 09-SEP-98.
DR PDB; 1B38; 23-DEC-98.
DR PDB; 1B39; 23-DEC-98.
DR PDB; 1CKP; 13-JAN-99.
DR Genew; HGNC:1771; CDK2.
DR MIM; 116953; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase: ATP-binding;
KW Cell cycle; Cell division; Mitosis; Phosphorylation; 3D-structure.
KW Cell cycle; Cell division; Mitosis; Phosphorylation; 3D-structure.
FT DOMAIN 4 286 PROTEIN KINASE.
FT NP_BIND 10 18 ATP (BY SIMILARITY).
FT BINDING 33 33 ATP (BY SIMILARITY).
FT ACT_SITE 127 127 BY SIMILARITY.
FT MOD_RES 14 14 PHOSPHORYLATION.
FT MOD_RES 15 15 PHOSPHORYLATION.
FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK).
FT MUTAGEN 14 14 T->A: INCREASE ACTIVITY 2 FOLD.
FT MUTAGEN 15 15 Y->F: INCREASE ACTIVITY 2 FOLD.
FT MUTAGEN 160 160 T->A: ABOLISHES ACTIVITY.
SQ SEQUENCE 298 AA; F90A0F4E70910B51 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 298;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 91 MDASAL 96

RESULT 11
CDK2_RAT
ID CDK2_RAT STANDARD; PRT; 298 AA.
AC Q63699; Q09136;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cell division protein kinase 2 (EC 2.7.1.-).

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GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=95166553; PubMed=7862443;
RA Kotani S., Endo T., Kitagawa M., Higashi H., Onaya T.;
RT "A variant form of cyclin-dependent kinase 2 (Cdk2) in a malignant
RL transformed rat thyroid (FRTL-Tc) cell line.";
RN Oncogene 10:663-669(1995).
RP [2]
RP SEQUENCE OF 19-124 FROM N.A.
RX MEDLINE=96113578; PubMed=8673024;
RA Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;
RT "Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F-1
RT during the prolactin-induced G1/S transition in rat Nb2 pre-T
RT lymphoma cells.";
RL Biochem. Mol. Biol. Int. 37:393-399(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
CC DURING S PHASE AND G2.
CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CDK2-ALPHA (SHOWN HERE) AND
CC CDK2-BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CDKX SUBFAMILY.
CC -----
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CC -----
DR EMBL; D28753; BAA05947.1; -
DR EMBL; D63162; BAA09638.1; -
DR HSP; P24941; IAO1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase: ATP-binding; Cell cycle;
KW Cell division; Mitosis; Phosphorylation; Alternative splicing.
FT DOMAIN 4 286 PROTEIN KINASE.
FT NP_BIND 10 18 ATP (BY SIMILARITY).
FT BINDING 33 33 ATP (BY SIMILARITY).
FT ACT_SITE 127 127 BY SIMILARITY.
FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
FT CONFLICT 79 79 V -> C (IN REF. 2).
FT CONFLICT 99 99 L -> I (IN REF. 2).
FT CONFLICT 124 124 L -> C (IN REF. 2).
SQ SEQUENCE 298 AA; C8CB3ADCE9B97F88 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 298;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 91 MDASAL 96

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RESULT 12
CDK2_MOUSE
ID CDK2_MOUSE STANDARD; PRT; 346 AA.
AC P97377; O55105;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell division protein kinase 2 (EC 2.7.1.-).
GN CDK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORM CDK2-ALPHA).
RC STRAIN=C57BL/6;
RA Jun D., Lee Y.H., Park H.K., Kim Y.H.;
RT "Exon-intron organization of the murine cyclin-dependent kinase-2
RT genes Cdk2-alpha and Cdk2-beta.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Ellenrieder C., Bartosch B., Lee G.Y., Murphy M., Sweeney C.,
RA Hergersberg M., Hunt T., Carrington M., Jaussi R.;
RT "The 39 kDa form of CDK2 arises through alternative splicing, is
RT expressed in many but not all mammals, and is an active kinase.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
CC DURING S PHASE AND G2.
CC -!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
CC SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CDK2-ALPHA AND CDK2-BETA (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDK2/CDKX SUBFAMILY.
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CC -----
DR EMBL; U63337; AAB37128.1;
DR EMBL; AJ223732; CAAL1533.1;
DR EMBL; AJ223733; CAAL1534.1;
DR EMBL; AJ223733; CAAL1535.1;
DR HSP; P24941; IAO1.
DR MGP; MGI:104772; Cdk2.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
KW Cell division; Mitosis; Phosphorylation; Alternative splicing.
FT DOMAIN 4 334 PROTEIN KINASE.
FT NP_BIND 10 18 ATP (BY SIMILARITY).
FT BINDING 33 33 ATP (BY SIMILARITY).
FT ACT_SITE 127 127 BY SIMILARITY.
FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 160 160 PHOSPHORYLATION (BY Cdk2) (BY SIMILARITY).
FT VARSPPLIC 197 244 MISSING (IN CDK2-ALPHA).
SQ SEQUENCE 346 AA; 38978 MW; D806BC2F150AEDFC CRC64;

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Query Match 92.3%; Score 24; DB 1; Length 346;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 91 MDASAL 96
:|||||
:|||||

RESULT 13
ALF_ECOLI
ID ALF_ECOLI STANDARD; PRT; 358 AA.
AC P11604;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fructose-bisphosphate aldolase class II (EC 4.1.2.13) (FBP aldolase).
GN FBA OR FBA OR FBA OR B2925 OR Z4263 OR ECS3796.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=K12 / CS520;
RX MEDLINE=89313302; PubMed=2546007;
RA A founder P.R., Baldwin S.A., Perham S.A., Short N.J.;
RT "Identification, molecular cloning and sequence analysis of a gene
RT cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
RT phosphoglycerate kinase and a putative second glyceraldehyde 3-
RT phosphate dehydrogenase of Escherichia coli.";
RL Mol. Microbiol. 3:723-732(1989).
RN [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RX MEDLINE=89193446; PubMed=2649077;
RA A founder P.R., Baldwin S.A., Perham R.N., Short N.J.;
RT "Cloning, sequence analysis and over-expression of the gene for the
RT class II fructose 1,6-bisphosphate aldolase of Escherichia coli.";
RL Biochem. J. 257:529-534(1989).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11205551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 050952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).

```

[6]
 RN SEQUENCE OF 1-12.
 RC STRAIN=K12 / EMG2;
 RA MEDLINE=97443975; PubMed=9298646;
 RX Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of *Escherichia coli* K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 [7]
 RN ZINC-LIGANDS, AND MUTAGENESIS.
 RP MEDLINE=93170474; PubMed=8436219;
 RA Berry A., Marshall K.E.;
 RT "Identification of zinc-binding ligands in the class II fructose-1,6-
 biphosphate aldolase of *Escherichia coli*.";
 RL FEBS Lett. 318:11-16(1993).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS).
 RP MEDLINE=96433074; PubMed=8836102;
 RA Blom N.S., Tetreault S., Coulombe R., Sygusch J.;
 RT "Novel active site in *Escherichia coli* fructose 1,6-bisphosphate
 aldolase.";
 RL Nat. Struct. Biol. 3:856-862(1996).
 [9]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RP MEDLINE=97094986; PubMed=8939754;
 RA Cooper S.J., Leonard G.A., McSweeney S.M., Thompson A.W.,
 RA Naismith J.H., Qamar S., Plater A., Berry A., Hunter W.N.;
 RT "The crystal structure of a class II fructose-1,6-bisphosphate
 aldolase shows a novel binuclear metal-binding active site embedded
 in a familial fold.";
 RL Structure 4:1303-1315(1996).
 [10]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP MEDLINE=99182425; PubMed=10080900;
 RA Hall D.R., Leonard G.A., Reed C.D., Watt C.I., Berry A., Hunter W.N.;
 RT "The crystal structure of *Escherichia coli* class II fructose-1,
 6-bisphosphate aldolase in complex with phosphoglycolohydroxamate
 reveals details of mechanism and specificity.";
 RL J. Mol. Biol. 287:383-394(1999).
 CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 phosphate + D-glyceraldehyde 3-phosphate.
 CC -1- COFACTOR: ZINC.
 CC -1- PATHWAY: Glycolysis; sixth step.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE
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 EMBL; X14436; CAA32605.1;
 EMBL; U28377; AAA9092.1;
 EMBL; A6000376; AAC75962.1;
 EMBL; A6005522; AAG58051.1; ALT_INIT.
 EMBL; AP002563; BAB37219.1;
 PIR; S02177; ADEC2A.
 PDB; 1D0S; 07-JUL-97.
 PDB; 1ZEN; 07-JUL-97.
 PDB; 1B57; 07-JAN-00.
 SWISS-2DPAGE; P11604; COLI.
 EcoGene; EG10282; fbaA.
 InterPro; IPR000771; F_bp_aldolase.
 Pfam; PF01116; F_bp_aldolase; 1.
 ProDom; PD002376; F_bp_aldolase; 1.
 TIGRFAMS; TIGR00167; cbbA; 1.
 PROSITE; PS00602; ALDOLASE_CLASS_II_1; 1.
 PROSITE; PS00806; ALDOLASE_CLASS_II_2; 1.
 Lyase; Glycolysis; Zinc; 3D-structure; Complete proteome.

FT INIT_MET 0 0
 FT METAL 107 107 ZINC.
 FT METAL 110 110 ZINC.
 FT MUTAGEN 107 107 H->A: LOSS OF ACTIVITY.
 FT MUTAGEN 110 110 H->A: LOSS OF ACTIVITY.
 FT MUTAGEN 111 111 C->A: PARTIAL LOSS OF ACTIVITY.
 SQ SEQUENCE 358 AA; 39016 MW; ED5A0FDC66246031 CRC64;
 Query Match 92.3%; Score 24; DB 1; Length 358;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 Db 190 MDASAL 195
 RESULT 14
 ALR_ANASP STANDARD; PRT; 386 AA.
 ID ALR_ANASP
 AC QBYU96;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alanine racemase (EC 5.1.1.1).
 GN ALR OR ALR2458.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium *Anabaena* sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 CC -1- FUNCTION: Provides the D-alanine required for cell wall
 biosynthesis (By similarity).
 CC -1- CATALYTIC ACTIVITY: L-alanine -> D-alanine.
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- PATHWAY: Along with D-alanine-D-alanine ligase, it makes up the
 D-alanine branch of the peptidoglycan biosynthetic route.
 CC -1- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 EMBL; AP003589; BAB74157.1; ALT_INIT.
 DR InterPro; IPR000821; Ala_racemase.
 DR Pfam; PF00842; Ala_racemase; 1.
 DR PRINTS; PR00992; ALARACEMASE.
 DR TIGRFAMS; TIGR00492; alr; 1.
 DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
 KW isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
 Complete proteome.
 FT ACT_SITE 48 48 CATALYTIC BASE SPECIFIC TO D-ALANINE
 (BY SIMILARITY).
 FT ACT_SITE 278 278 CATALYTIC BASE SPECIFIC TO L-ALANINE
 (BY SIMILARITY).
 FT BINDING 48 48 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 386 AA; 42159 MW; 56F88B75D655BED CRC64;
 Query Match 92.3%; Score 24; DB 1; Length 386;
 Best Local Similarity 83.3%; Pred. No. 1e-02;

	Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	Mismatches	1;	Conservative	5;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	LDASAL 6												1	LDASAL 6					
Db	331	IDASAL 336												266	MDASAL 271					

Search completed: May 30, 2003, 15:48:49
Job time : 5.11842 secs

RESULT 15
DCAM_HORCH STANDARD; PRT; 393 AA.
AC Q42829;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SambC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
GN SAMDC.
OS Hordeum chilense (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=15565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=96270379; PubMed=8639739;
RA Drexelhaus T., Barcelo P., Hagel C., Loerz H., Humbeck K.;
RT "Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine decarboxylase that is circadian-clock-regulated.";
RL Plant Mol. Biol. 30:1021-1033(1996).
CC 1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
CC 1- COFACTOR: PYRUVOYL GROUP.
CC 1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE BIOSYNTHESIS FROM PUTRESCINE.
CC 1- SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETDC FAMILY.

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DR EMBL; X83881; CAA58762.1; -
DR HSSP; P17707; LJEN.
DR InterPro; IPR001985; SAM_decarbox.
DR Pfam; PF01536; SAM_decarbox; 1.
DR ProDom; PD002379; SAM_decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCcase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Spermidine biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.
FT CHAIN 1 70 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA CHAIN (BY SIMILARITY).
FT CHAIN 71 393 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA CHAIN (BY SIMILARITY).
FT SITE 70 71 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
FT MOD_RES 71 71 CONVERTED TO A PYRUVOYL GROUP (BY SIMILARITY).
FT ACT_SITE 11 11 IMPORTANT FOR CATALYTIC ACTIVITY (BY SIMILARITY).
FT ACT_SITE 14 14 IMPORTANT FOR CATALYTIC ACTIVITY (BY SIMILARITY).
FT ACT_SITE 85 85 IMPORTANT FOR CATALYTIC ACTIVITY (BY SIMILARITY).
SQ SEQUENCE 393 AA; 42895 MW; 6CDIAA94792AF6CB CRC64;
Query Match 92.3%; Score 24; DB 1; Length 393;
Best Local Similarity 83.3%; Pred. No. 1e+02;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	92	10 Q9AS65	Q9as65 oryza sativ
2	26	100.0	92	16 P95120	P95120 mycobacteri
3	26	100.0	129	2 O85909	O85909 sphingomona
4	26	100.0	130	17 Q97YS3	Q97ys3 sulfolobus
5	26	100.0	130	17 Q96ZNI	Q96zn1 sulfolobus
6	26	100.0	171	16 Q9A3Y6	Q9a3y6 caulobacter
7	26	100.0	191	16 Q9KY23	Q9ky23 streptomyce
8	26	100.0	191	16 Q9KY22	Q9ky22 streptomyce
9	26	100.0	230	16 Q922G8	Q922g8 rhizobium m
10	26	100.0	237	10 Q94IZ7	Q94iz7 oryza sativ
11	26	100.0	245	3 Q9HFU7	Q9hfu7 pneumocysti
12	26	100.0	247	2 Q9XCY6	Q9xcy6 vibrio para
13	26	100.0	259	17 Q29756	Q29756 archaeoglob
14	26	100.0	281	16 Q91746	Q91746 pseudomonas
15	26	100.0	304	10 Q9ASJ7	Q9asj7 oryza sativ
16	26	100.0	334	16 Q9RI53	Q9ri53 streptomyce

17	26	100.0	349	5 Q9VR43	Q9vr43 drosophila
18	26	100.0	383	16 Q8U4W2	Q8u4w2 agrobacteri
19	26	100.0	394	16 Q9JYE3	Q9jye3 neisseria m
20	26	100.0	394	16 Q9JR41	Q9jr41 neisseria m
21	26	100.0	420	2 Q9L9M3	Q9l9m3 escherichia
22	26	100.0	437	16 Q05828	Q05828 mycobacteri
23	26	100.0	455	4 Q96S13	Q96s13 homo sapien
24	26	100.0	483	16 Q8XJH4	Q8xjh4 bruceella m
25	26	100.0	512	16 Q8JU05	Q8ju05 neisseria m
26	26	100.0	513	16 Q8U9G4	Q8u9g4 agrobacteri
27	26	100.0	516	16 Q9JZ08	Q9jz08 neisseria m
28	26	100.0	580	10 Q93ZS9	Q93zs9 arabidopsis
29	26	100.0	586	10 Q9LX47	Q9lx47 arabidopsis
30	26	100.0	673	10 Q9FVG4	Q9fv94 zea mays (m
31	26	100.0	813	5 Q9V9C6	Q9v9c6 drosophila
32	26	100.0	903	2 Q9KI05	Q9kiq5 bacillus st
33	26	100.0	903	2 Q8VTF1	Q8vtf1 bacillus st
34	26	100.0	920	2 Q07366	Q07366 campylobact
35	26	100.0	941	10 Q9L9T9	Q9l9t9 arabidopsis
36	26	100.0	1313	11 Q9EQM9	Q9eqm9 rattus norv
37	24	92.3	157	16 Q33314	Q33314 mycobacteri
38	24	92.3	158	10 Q9LXJ9	Q9lkj9 oryza sativ
39	24	92.3	166	16 Q8XXY6	Q8xyx6 anabaena sp
40	24	92.3	179	16 Q97L41	Q97l41 clostridium
41	24	92.3	185	2 Q9XCD9	Q9xcd9 mycobacteri
42	24	92.3	191	16 Q9KXW4	Q9kxw4 streptomyce
43	24	92.3	264	4 Q75100	Q75100 homo sapien
44	24	92.3	279	16 Q9K9F8	Q9k9f8 bacillus ha
45	24	92.3	292	16 Q97Q31	Q97q31 streptococc

ALIGNMENTS

RESULT 1

Q9AS65 PRELIMINARY; PRT; 92 AA.
AC Q9AS65;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE P0028E10.27 protein.
GN P0028E10.27.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0028E10.27";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002912; BAB39923.1;
SQ SEQUENCE 92 AA; 9407 MW; 6DE8E32F046CD92 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDASAL 6
Db 31 LDASAL 36

RESULT: 2

P95120 PRELIMINARY; PRT; 92 AA.
ID P95120;
AC P95120;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein RV2975c.
 GN RV2975C OR MT3052.1 OR MTCY349.12.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badoock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Stulton J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z83018; CAB05437.1; ALT_INIT.
 DR EMBL; AE007126; AAK47379.1; -;
 DR TIGR; MT3052.1; -;
 DR TubercuList; RV2975c; -;
 DR InterPro; IP001969; Aspartate_site.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN.1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 92 AA; 9850 MW; 50BD1AFCFCDFD253 CRC64;

 Query Match 100.0%; Score 26; DB 16; Length 92;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LDASAL 6
 Db 16 LDASAL 21

 RESULT 3
 O85909
 ID O85909 PRELIMINARY; PRT; 129 AA.
 AC O85909;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 13.3 kDa protein precursor.
 GN ORF633.
 OS Sphingomonas aromaticivorans.
 OC Plasmid pWLI.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Novosphingobium.
 OX NCBI_TaxID=48935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FI99;
 RA Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C.,
 RA Sensen C.W., Gaasterland T., Saffer J.D., Fredrickson J.K.;
 RT "Complete sequence of a 184 kb catabolic plasmid from Sphingomonas
 RT aromaticivorans strain FI99.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF079317; AAD03924.1; -;
 DR InterPro; IPR005342; PF03655.
 DR Pfam; PF03655; UPF0110; 1.
 KW Hypothetical protein; Plasmid; Signal.
 FT SIGNAL 1 39 POTENTIAL.
 SQ SEQUENCE 129 AA; 13287 MW; 9B6F200F1767A297 CRC64;

 Query Match 100.0%; Score 26; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LDASAL 6
 Db 6 LDASAL 11

 RESULT 4
 Q97YS3
 ID Q97YS3 PRELIMINARY; PRT; 130 AA.
 AC Q97YS3;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Hypothetical protein SSO1243.
 GN SSO1243.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726;
 RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006739; AAK41485.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 130 AA; 15118 MW; 15F684AA970B9115 CRC64;

 Query Match 100.0%; Score 26; DB 17; Length 130;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LDASAL 6
 Db 8 LDASAL 13

 RESULT 5
 Q96ZNI
 ID Q96ZNI PRELIMINARY; PRT; 130 AA.
 AC Q96ZNI;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical protein Str1801.
 GN Str1801.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

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RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yanagishi A.,
RA Oshima T., Kikuchi H.,
RT "Complete genome sequence of an aerobic thermophilic
RL Crenarchaeon, Sulfolobus tokodaii strain7.",
RL DNA Res. 8:123-140(2001).
DR EMBL: AF000987; BAB66893.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 130 AA; 14958 MW; 4C4A5C20D664E991 CRC64;

Query Match 100.0%; Score 26; DB 17; Length 130;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 7 LDASAL 12

RESULT 6
Q9A3Y6 PRELIMINARY; PRT; 171 AA.
AC Q9A3Y6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CC3064.
GN CC3064.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uitterback T., Tran K., Wolf A., Vanathavan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AF005969; AAK25026.1; -.
DR HSSP: P32173; 1E5K.
DR TIGR: CC3064; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 171 AA; 17046 MW; 7252F45EC2E1CEAC CRC64;

Query Match 100.0%; Score 26; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 118 LDASAL 123

RESULT 7
Q9KY23 PRELIMINARY; PRT; 191 AA.
AC Q9KY23;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SC02367.
GN SC02367 OR SCC8A.25C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

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OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutterford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL356892; CAB92843.1; -.
DR InterPro: IPR003325; TcrD.
DR Pfam: PF02342; TcrD; 1.
KW Hypothetical protein.
SQ SEQUENCE 191 AA; 20414 MW; C280293C548F3988 CRC64;

Query Match 100.0%; Score 26; DB 16; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 41 LDASAL 46

RESULT 8
Q9KY22 PRELIMINARY; PRT; 191 AA.
AC Q9KY22;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SC02368.
GN SC02368 OR SCC8A.26C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;

```

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [3]
 RC SEQUENCE FROM N.A.
 RX MEDLINE-97000351; PubMed-8843436;
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James D.E., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL356892; CAB2844.1; --
 DR InterPro; IPR003325; TerD.
 DR Pfam; PF02342; TerD; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 191 AA; 20387 MW; 39E9C1EC8C47AA7E CRC64;

Query Match 100.0%; Score 26; DB 16; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
 DB 41 LDASAL 46

RESULT. 9

ID Q92ZG8 PRELIMINARY; PRT; 230 AA.
 AC Q92ZG8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE ATRA transcriptional regulator.
 GN ATRA OR RA0517 OR SMA0955.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymA (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE-21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federpiet N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSymA megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL; AE007243; AAK65175.1; --
 DR InterPro; IPR000524; HTH_GntR.
 DR Pfam; PF00392; gntR; 1.
 DR PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 230 AA; 25843 MW; 82DECAC87E91B94E CRC64;

Query Match 100.0%; Score 26; DB 16; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
 DB 83 LDASAL 88

RESULT 10

ID Q94I27 PRELIMINARY; PRT; 237 AA.
 AC Q94I27;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE OSJNB003817.13 protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Eukaryotophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Erihartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 clone:OSJNB003817.1";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AP003104; BAB55721.1; --
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 KW Zinc-finger.
 SQ SEQUENCE 237 AA; 23871 MW; EA9F0F14F9B625DC CRC64;

Query Match 100.0%; Score 26; DB 10; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
 DB 91 LDASAL 96

RESULT 11

ID Q9HFU7 PRELIMINARY; PRT; 245 AA.
 AC Q9HFU7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Ornithine decarboxylase antizyme.
 GN ANTIZYME.
 OS Pneumocystis carinii.
 CC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 CC Pneumocystis.
 OX NCBI_TaxID=4754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ivanov I.P., Gesteland R.F., Atkins J.F.;
 RT "Antizyme expression: a subversion of triplet decoding, which is
 RT remarkably conserved by evolution, is a sensor for an autoregulatory
 RT circuit.";
 RL Nucleic Acids Res. 28:0-0(2000).
 DR EMBL; AF291574; AAG16234.1; --
 DR SEQUENCE 245 AA; 27677 MW; 2ED98BA35CDE5EBD CRC64;

Query Match 100.0%; Score 26; DB 3; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6

```

Db          93 LDASAL 98
|||||
Q9XCX6      PRELIMINARY;      PRT;      247 AA.
AC Q9XCX6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TonB-like protein.
GN TONB1.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=474801;
RX MEDLINE=9287846; PubMed=10348876;
RA O'Malley S.W., Mouton S.L., Occhino D.A., Deanda M.T., Rashidi J.R.,
RA Fuson K.L., Rashidi C.E., Mora M.Y., Payne S.M., Henderson D.P.;
RT *Comparison of the heme iron utilization systems of pathogenic
RT vibrios.*;
RL J. Bacteriol. 181:3594-3598(1999).
DR EMBL; AF119047; AAD39909.1; -.
DR InterPro; IPR003538; TonB.
DR PRINTS; PR01374; TONBPROTEIN.
SQ SEQUENCE 247 AA; 27121 MW; D9497117BA4D400E CRC64;

Query Match 100.0%; Score 26; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
DB 210 LDASAL 215

RESULT 13
O29756
ID O29756 PRELIMINARY; PRT; 259 AA.
AC O29756;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein AF0494.
GN AF0494.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickley E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT *The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.*;
RL Nature 390:364-370(1997).
DR EMBL; AE001070; AAB90743.1; -.
DR TIGR; AF0494; -.
DR InterPro; IPR001247; 3_Exonase.

Db          93 LDASAL 98
|||||
Q9XCX6      PRELIMINARY;      PRT;      247 AA.
AC Q9XCX6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TonB-like protein.
GN TONB1.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=474801;
RX MEDLINE=9287846; PubMed=10348876;
RA O'Malley S.W., Mouton S.L., Occhino D.A., Deanda M.T., Rashidi J.R.,
RA Fuson K.L., Rashidi C.E., Mora M.Y., Payne S.M., Henderson D.P.;
RT *Comparison of the heme iron utilization systems of pathogenic
RT vibrios.*;
RL J. Bacteriol. 181:3594-3598(1999).
DR EMBL; AF119047; AAD39909.1; -.
DR InterPro; IPR003538; TonB.
DR PRINTS; PR01374; TONBPROTEIN.
SQ SEQUENCE 247 AA; 27121 MW; D9497117BA4D400E CRC64;

Query Match 100.0%; Score 26; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
DB 210 LDASAL 215

RESULT 14
Q9I746      PRELIMINARY;      PRT;      281 AA.
ID Q9I746;
AC Q9I746;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA0086.
GN PA0086.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT *Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.*;
RL Nature 406:959-964(2000).
DR EMBL; AE004447; AAG03476.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 281 AA; 30361 MW; C799ECFACA03F4A8 CRC64;

Query Match 100.0%; Score 26; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
DB 79 LDASAL 84

RESULT 15
Q9ASJ7
ID Q9ASJ7 PRELIMINARY; PRT; 304 AA.
AC Q9ASJ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P0439B06.15 protein.
GN P0439B06.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT *Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0439B06.*;

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RL Submitted (Oct-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF002882; BAB39880.1; -.
DR HSP; F05092; 2RMC.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMASE.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
SQ SEQUENCE 304 AA; 31411 MW; BAEF1183D78F2D9 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||||
DB 230 LDASAL 235

Search completed: May 30, 2003, 14:38:38
Job time : 16.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73.*

1: Piri.*

2: Piri.*

3: Piri.*

4: Piri.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	40	100.0	745	1 I49101	conserved helix-lo
2	38	95.0	1139	2 A10379	probable potassium
3	37	92.5	322	2 A13395	NADH2 dehydrogenas
4	36	90.0	122	2 S69909	Ig V-D-J region (M
5	36	90.0	132	2 S65785	mel-13a protein -
6	36	90.0	277	1 JC5900	bo-type ubiquinol
7	36	90.0	296	2 A84985	cytochrome o ubiq
8	36	90.0	307	1 A36885	bo-type ubiquinol
9	36	90.0	318	2 AD0384	cytochrome o ubiq
10	36	90.0	331	2 D83480	cytochrome o ubiq
11	36	90.0	344	2 AG3489	cytochrome o ubiq
12	36	90.0	353	2 A87469	ubiquinol oxidase
13	36	90.0	362	2 S23471	uroporphyrinogen d
14	36	90.0	386	2 C96006	probable cytochrom
15	36	90.0	409	2 T47298	probable replicati
16	36	90.0	747	2 D70802	hypothetical prote
17	36	90.0	803	2 F90485	hypothetical prote
18	36	90.0	915	2 A43802	cellulase (EC 3.2.
19	36	90.0	983	2 B45883	receptor tyrosine
20	36	90.0	983	2 A38224	protein-tyrosine k
21	36	90.0	983	2 A45883	receptor tyrosine
22	36	90.0	1039	2 S02711	cellulase (EC 3.2.
23	36	90.0	1329	2 D87226	conserved hypothet
24	35	87.5	182	2 C70829	hypothetical-prote
25	35	87.5	348	2 G97514	NADH dehydrogenase
26	35	87.5	348	2 AE2733	NADH ubiquinone ox
27	35	87.5	443	2 AE0309	probable sugar tra
28	34	85.0	82	2 C69013	hypothetical prote
29	34	85.0	116	2 T03472	conserved hypothet

30	34	85.0	214	2	G83692	hypothetical prote
31	34	85.0	282	1	DGEOMA	DNA-3-methyladenin
32	34	85.0	282	2	E90988	3-methyl-adenine D
33	34	85.0	282	2	G85833	3-methyl-adenine D
34	34	85.0	289	2	A10770	DNA-3-methyladenin
35	34	85.0	299	2	B83243	hypothetical prote
36	34	85.0	332	2	AH2593	cytochrome o ubiq
37	34	85.0	377	2	E97376	cytochrome ba(3) (
38	34	85.0	394	2	C85064	hypothetical prote
39	34	85.0	411	2	E84949	tetrahydrofolylpol
40	34	85.0	414	2	B82408	hypothetical prote
41	34	85.0	418	2	D85064	hypothetical prote
42	34	85.0	420	2	A54759	cytochrome ba(3) c
43	34	85.0	501	2	S45914	probable glucan 1,
44	34	85.0	764	2	H98143	cbbBc protein (U60
45	34	85.0	764	2	AD3144	formate dehydrogen

ALIGNMENTS

RESULT 1

I49101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse

C:Species: Mus musculus (house mouse)

✓C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: I49101

R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

Genomics 27, 348-351, 1995

A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 2

A:Reference number: I49101; MUID:96044444; PMID:7558004

A:Accession: I49101

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-745 <RES>

A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493

C:Genetics:

A:Gene: CHUK

C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase hom

C:Keywords: ATP; phosphotransferase

F:13-283/Domain: protein kinase homology <KIN>

Query Match 100.0%; Score 40; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. NO. 54;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6

|||||

Db 738 LDWSWL 743

RESULT 2

A10379

probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: A10379

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10379

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1139 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:gl5981067; GSPDB:GN00175

C:Genetics:

A:Gene: YPO3129

Query Match 95.0%; Score 38; DB 2; Length 1139;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
:|||||
DB 480 MDWSWL 485

RESULT 3

A:Accession: A13395
A:Title: NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) [Imported] - Brucella melitensis (strain 1
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C:Accession: A13395
R:DelVecchio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
; Mazur, M.; Goltman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Leteser
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: A03252; PMID:11756688
A:Accession: A13395
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-322 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52332.1; PID:g17983126; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BWE1151
A:Map position: 1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C:Keywords: oxidoreductase

Query Match 92.5%; Score 37; DB 2; Length 322;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
:|||||
DB 174 LDWSWL 179

RESULT 4

A:Accession: S69909
A:Title: Ig V-D-J region (MS) - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69909
R:Sahota, S.; Hamblin, T.; Oslcer, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A:Reference number: S69909; MUID:94335315; PMID:8057663
A:Accession: S69909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SAH>
A:Cross-references: EMBL:Z33399; NID:g871348; PIDN:CAA83850.1; PID:g871349
A:Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 36; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
:|||||
DB 33 DWSWL 37

RESULT 5

A:Accession: S65785
A:Title: mel-13a protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S65785

R:Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A:Title: Cloning and characterization of two transcripts generated from the mel-13 ge
A:Reference number: S65785; MUID:96180310; PMID:8597592
A:Accession: S65785
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TET>
A:Cross-references: EMBL:U35309
C:Genetics:
A:Gene: mel-13
C:Superfamily: mouse mel-13a protein
C:Keywords: alternative splicing

Query Match 90.0%; Score 36; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
:|||||
DB 58 DWSWL 62

RESULT 6

A:Accession: JC5900
A:Title: bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum
C:Species: Bradyrhizobium japonicum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JC5900
R:Surpin, M.A.; Luebben, M.; Maier, R.J.
Gene 183, 201-206, 1996
A:Title: The Bradyrhizobium japonicum coxWYZ gene cluster encodes a bb3-type ubiquin
A:Reference number: JC5900; MUID:97149299; PMID:8996107
A:Accession: JC5900
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-277 <SUR>
C:Genetics:
A:Gene: coxW
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; r

Query Match 90.0%; Score 36; DB 1; Length 277;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
:|||||
DB 108 LDWSWL 113

RESULT 7

A:Accession: A84985
A:Title: cytochrome o ubiquinol oxidase subunit II [Imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
C:Accession: A84985
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A:Reference number: A84985; MUID:20445173; PMID:10993077
A:Accession: A84985
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: cyoA; BU472
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 296;

Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
111 11
Db 125 LDWKWL 130

RESULT 8

A36885
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter acetii
N:Alternate names: cytochrome a1 chain II
C:Species: Acetobacter acetii
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A36885
R:Fukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, Y.; Horinouchi, J. Bacteriol. 175, 4307-4314, 1993
A:Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in *Acetobacter acetii*
A:Reference number: A36885; MUID:93322308; PMID:8392509
A:Accession: A36885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <FUK>
A:Cross-references: GB:D13185; NID:g409064; PIDN:BAA02480.1; PID:g433186
A:Experimental source: isolate 1023
C:Genetics:
A:Gene: *cyoA*
C:Complex: heterotetramer; chains I, II, III and IV
C:Function:
A:Description: terminal oxidase for ethanol oxidation
A:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain II precursor; electron transfer; heterotetramer; membrane-associated complex; oxidoreductase; copper; cytochrome-c oxidase chain II precursor
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>
F:48-64/Domain: transmembrane #status predicted <TM1>
F:89-105/Domain: transmembrane #status predicted <TM2>

Query Match 90.0%; Score 36; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
111 11
Db 135 LDWKWL 140

RESULT 9

AD0384
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - *Yersinia pestis* (strain 26480) [imported]
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD0384
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N. Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92399.1; PID:gl5981102; GSPDB:GN00175
C:Genetics:
A:Gene: *cyoA*
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain II precursor; electron transfer; membrane-associated complex; oxidoreductase; respiration; copper; cytochrome-c oxidase chain II precursor

Query Match 90.0%; Score 36; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSWL 6

Db 135 LDWKWL 140
111 11

RESULT 10

D83480
cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - *Pseudomonas aeruginosa*
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83480
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <STO>
A:Cross-references: GB:AF004561; GB:AF004091; NID:g9947253; PIDN:AAG04706.1; GSPDB:GN00190
A:Experimental source: strain PA01
C:Genetics:
A:Gene: *cyoA*; PA1317
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain II precursor; electron transfer; membrane-associated complex; respiratory chain; copper; cytochrome-c oxidase chain II precursor

Query Match 90.0%; Score 36; DB 2; Length 331;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
111 11
Db 133 LDWKWL 138

RESULT 11

AG3489
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - *Brucella melitensis*
C:Species: *Brucella melitensis*
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002
C:Accession: AG3489
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Lett, P. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A:Reference number: AD3252; PMID:11756688
A:Accession: AG3489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <KUR>
A:Cross-references: GB:AB008917; PIDN:AAL53082.1; PID:gl7983945; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: *BME1901*
A:Map position: 1
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain II precursor; electron transfer; membrane-associated complex; oxidoreductase; respiration; copper; cytochrome-c oxidase chain II precursor

Query Match 90.0%; Score 36; DB 2; Length 344;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
111 11
Db 141 LDWKWL 146

RESULT 12

A87469
ubiquinol oxidase subunit II [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001

C:Accession: A87469
 R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Emlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87469
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-353 <STO>
 A:Cross-references: GB:AE005673; NID:g13423199; PIDN:AAK23749.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC1773
 A:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 353;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 |||||
 Db 146 LDWKWL 151

RESULT 13
 S23471
 uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein YP9609.03; protein YDR047w
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 R:Accession: S23471; S33965; S54033; S20190; S27348; S31312
 R:Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytka, J.; Harrison, L.; Kushner, J.; La
 eur, J. Biochem. 205, 1011-1016, 1992
 A:Title: Uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence
 A:Reference number: S23471; MUID:92249304; PMID:1576986
 A:Accession: S23471
 A:Molecule type: DNA
 A:Residues: 1-362 <GAR>
 A:Cross-references: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
 R:Diflumeri, C.; Laroque, R.; Keng, T.
 Yeast 9, 613-623, 1993
 A:Title: Molecular analysis of HEM6 (HEM12) in *Saccharomyces cerevisiae*, the gene for u
 A:Reference number: S33965; MUID:93348774; PMID:8346678
 A:Accession: S33965
 A:Molecule type: DNA
 A:Residues: 1-362 <DIF>
 A:Cross-references: EMBL:L19089; NID:g4775; PIDN:CAA79514.1; PID:g4776
 R:Hunt, S.; Bowman, S.; Harris, D.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54031
 A:Accession: S54033
 A:Molecule type: DNA
 A:Residues: 1-362 <HUN>
 A:Cross-references: EMBL:L49209; NID:g798897; PIDN:CAA89078.1; PID:g798900; MIPS:YDR047w
 C:Genetics:
 A:Gene: HEM12; HEM6; POP3
 A:Cross-references: MIPS:YDR047w; SGD:S0002454
 A:Map position: 4R
 A:Superfamily: uroporphyrinogen decarboxylase
 C:Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 |||||
 Db 279 LDWSW 283

RESULT 14

C96006

probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [Imported] - S
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C96006
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her
 proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing e
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C96006
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-386 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:g15141202; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Anpe, F.; Barloy-Hubl
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hymann, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leiau
 hebault, P.; Vandenhof, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: cyoA; SMD21487
 A:Genome: plasmid
 C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
 C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; r

Query Match 90.0%; Score 36; DB 2; Length 386;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 |||||
 Db 141 LDWKWL 146

RESULT 15

T47298
 probable replication protein - *Arabidopsis thaliana*
 N:Alternate names: protein T14K23.110
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T47298
 R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M
 Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24458
 A:Accession: T47298
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-409 <NYA>
 A:Cross-references: EMBL:AL132909
 A:Experimental source: cultivar Columbia; BAC clone T14K23
 C:Genetics:
 A:Map position: 3
 A:Introns: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3
 A:Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 |||||
 Db 190 LDWSW 194

Search completed: May 30, 2003, 14:52:36
 Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	745	1 IKKA_HUMAN	O15111 h inhibitor
2	40	100.0	745	1 IKKA_MOUSE	O60680 m inhibitor
3	40	100.0	756	1 IKKB_HUMAN	O14920 homo sapien
4	40	100.0	757	1 IKKB_MOUSE	O88351 mus musculus
5	40	100.0	757	1 IKKB_RAT	Q9qy78 rattus norv
6	36	90.0	296	1 CYOA_BUCAI	P57544 buchnera ap
7	36	90.0	307	1 QOX2_ACEAC	P50653 acetobacter
8	36	90.0	314	1 CYOA_PSEPU	Q9wvr1 pseudomonas
9	36	90.0	362	1 DCUP_YEAST	P32347 saccharomyc
10	36	90.0	983	1 EPA3_CHICK	P29318 gallus gall
11	36	90.0	983	1 EPA3_HUMAN	P29320 homo sapien
12	36	90.0	983	1 EPA3_MOUSE	P29319 mus musculus
13	36	90.0	984	1 EPA3_RAT	O08680 rattus norv
14	36	90.0	1039	1 GUNB_CALSA	P10474 c endoglucan
15	34	85.0	282	1 3MG2_ECOLI	P04395 escherichia
16	34	85.0	411	1 FOIC_BUCAI	P57265 buchnera ap
17	34	85.0	501	1 YBQ6_YEAST	P38081 saccharomyc
18	34	85.0	1331	1 MANE_CALSA	P22533 caldocellum
19	34	85.0	1742	1 GUNA_CALSA	P22534 caldocellum
20	33	82.5	336	1 NOSO_BACSU	O34453 bacillus su
21	33	82.5	411	1 CYB_CHRVI	O31215 chromatium
22	33	82.5	453	1 NRAM_IAMJL	P03470 influenza a
23	33	82.5	454	1 NRAM_IAPUE	P03468 influenza a
24	33	82.5	524	1 CP72_CATRO	Q92047 catharanthu
25	33	82.5	552	1 NU5M_RHISA	Q95047 rhipicephal
26	33	82.5	579	1 VC12_KLEPN	O48458 klebsiella
27	33	82.5	656	1 VEXE_SALTI	P43112 salmonella
28	33	82.5	840	1 VPHI_YEAST	P32563 saccharomyc
29	32	80.0	191	1 GDIR_CAEEL	Q20496 caenorhabdi
30	32	80.0	210	1 KTHY_SCHPO	P36590 schizosacch
31	32	80.0	272	1 CYL_RHORU	P23135 rhodospiril
32	32	80.0	281	1 Y373_MYCPN	P75227 mycoplasma
33	32	80.0	360	1 WNT2_CAEEL	P34889 caenorhabdi

RESULT 1

IKKA_HUMAN

ID IKKA_HUMAN STANDARD; PRT; 745 AA.
AC O15111; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)
DE (I kappa-B kinase alpha) (IKK-A) (IKK-alpha) (IKK-A) (IkappaB kinase)
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase)
DE Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN IKKA OR CHUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkappaB kinase";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
factor NF-kappaB";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
families of interacting proteins, contains a serine-threonine kinase
catalytic domain.";

ALIGNMENTS

34 32 80.0 376 1 PGLR_PENGR
35 32 80.0 387 1 INTD_ECOLI
36 32 80.0 400 1 HOFD_ECOLI
37 32 80.0 470 1 NOS2_ONCMY
38 32 80.0 470 1 NRAM_IADBU
39 32 80.0 470 1 NRAM_IADCH
40 32 80.0 470 1 NRAM_IADH2
41 32 80.0 470 1 NRAM_IADH2
42 32 80.0 470 1 NRAM_IADU3
43 32 80.0 470 1 NRAM_IAGFN
44 32 80.0 470 1 NRAM_IAGHD
45 32 80.0 470 1 NRAM_IANJ1
O93883 penicillium
P24218 escherichia
P36646 escherichia
Q92091 oncorhynchu
Q07570 influenza a
Q07571 influenza a
Q07572 influenza a
Q07573 influenza a
Q07599 influenza a
Q07574 influenza a
Q07577 influenza a
Q07578 influenza a

Cell. Mol. Biol. Res. 41:537-549(1995).

[6] PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND S-180.

RA MEDLINE=98188283; PubMed=9520446;

RX Ling L., Cao Z., Goeddel D.V.;

RA "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";

RT Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

RL [7]

RN PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.

RN MEDLINE=99413720; PubMed=10495710;

RX Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,

RA Donner D.B.;

RA "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";

RT Nature 401:82-85(1999).

RL [8]

RN IKK- α BINDING.

RN MEDLINE=99212141; PubMed=10195894;

RX Delhase M., Hayakawa M., Chen Y., Karin M.;

RA "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";

RT Science 284:309-313(1999).

RL [9]

RN IKK PHOSPHORYLATION.

RN MEDLINE=99038238; PubMed=9819420;

RX Nemoto S., DiDonato J.A., Lin A.;

RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase-1 and NF-kappaB-inducing kinase.";

RT Mol. Cell. Biol. 18:7336-7343(1998).

RL [10]

RN REVIEW.

RN MEDLINE=20178139; PubMed=10712233;

RX Jobin C., Sartor R.B.;

RA "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";

RT Am. J. Physiol. 278:C451-C462(2000).

RL -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND ULTIMATELY THE DEGRADATION OF THE INHIBITOR.

CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED WHEN DEPHOSPHORYLATED.

CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO. HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.

CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.

CC -----

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CC -----

CC EMBL: AF012890; AAC51662.1;

CC EMBL: AF002225; AAC51671.1;

CC EMBL: AF080157; AAC08996.1;

CC EMBL: U22512; AAC50713.1;

CC HSP: G63450; 1A06.

CC Genew: HGNC:1974; CHUK.

CC MIM: 600664;

CC InterPro: IPR000719; Euk_pkinase.

CC InterPro: IPR002290; Ser_thr_pkinase.

CC Pfam: PF00069; pkinase; 1.

SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN-C57BL/6J; TISSUE-Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
 RA Gelezianus R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKK-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
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 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 CC WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MAP3K14/NIK, MEKK1, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2/DELTA LH AND
 CC 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS ONLY FOR ISOFORM 1, ISOFORMS 2 AND
 CC 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.
 CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY
 CC E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION
 CC PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.
 CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
 CC MEKK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC -----
 CC EMBL; U12473; AAC52589.1; -;
 DR EMBL; AK018671; BAB31335.1; -;
 DR HSSP; Q63450; 1A06.
 DR MGD; MGI-99484; Chuk.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Alternative splicing.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 PHOSPHORYLATION (BY PKB/AKT1) (BY
 FT MOD_RES 23 23 SIMILARITY).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14) (BY
 FT VARSPLIC 452 471 SIMILARITY).
 FT VARSPLIC 472 471 MSLRYNNANITMKWNILIS -> IFRKNVKSMEGRKKGH
 FT VARSPLIC 472 745 SLF (IN ISOFORM 2).
 FT VARSPLIC 577 584 MISSING (IN ISOFORM 2).
 FT VARSPLIC 585 745 DHLYSDST -> GKTLOSQY (IN ISOFORM 3).
 FT CONFLICT 236 236 MISSING (IN ISOFORM 3).
 FT CONFLICT 400 400 K -> E (IN REF. 3).
 FT CONFLICT 400 400 S -> Y (IN REF. 3).
 SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AFF92233 CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWL 6
 Db 738 LDMSWL 743
 RESULT 3
 IKKB_HUMAN
 ID IKKB_HUMAN STANDARD; PRT; 756 AA.
 AC O14920; 075327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKIKB).
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RX MEDLINE=98008814; PubMed=9346485;
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
 RT IkappaB kinase-alpha and NIK.";
 RL Science 278:866-869(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 RT 8p12-->p11 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [7]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
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 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND
 CC PERIPHERAL BLOOD.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----

DR EMBL; AF029684; AAC51860.1; -
 DR EMBL; AF080158; AAD08997.1; -
 DR EMBL; AF031416; AAC64675.1; -
 DR EMBL; BC006231; AAH06231.1; -
 DR HSSP; O63450; 1A06
 DR Genew; HGNC:5960; IKKB.
 DR MIM; 603258; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00240; ubiquitin; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 21 29 NEMO-BINDING.
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 ATP (BY SIMILARITY).
 FT MOD_RES 23 23 BY SIMILARITY.
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
 FT MUTAGEN 177 177 EFFECT ON BINDING TO NIK.
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 231 255 S->E: FULL ACTIVATION.
 FT CONFLICT 231 255 WHSKYRKSEVDIVVSEDLNGTVKF -> CYRMWFGTVNHS
 FT CONFLICT 425 425 CNPSTLGGGRGRI (IN REF. 5).
 FT CONFLICT 756 756 Q -> H (IN REF. 1).
 SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;

Query Match 100.0%; Score 40; DB 1; Length 756;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSWL 6
 Db 737 LDWSWL 742

RESULT 4

IKKB_MOUSE
 ID IKKB_MOUSE STANDARD; PRT; 757 AA.
 AC O88351; O9R136;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 GN IKKB OR IKKBK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=98188238; PubMed=9520401;

RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RN IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase-1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
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 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The IkappaB/NF-kappaB system: a key determinant of mucosal
 RT inflammation and protection.";
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 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
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 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
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 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKB-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKB-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBQUITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GLANDS, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPA B KINASE SUBFAMILY.
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 CC -----
 CC EMBL: AF026524; AAC23557.1;
 DR EMBL: AF088910; AAD52095.1;
 DR HSPG: Q63450; IAO6.
 DR MGD: MGI:1338071; Ikbkb.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
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 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 N -> D (IN REF. 2).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 K -> E (IN REF. 2).
 FT CONFLICT 356 356 L -> F (IN REF. 2).
 FT CONFLICT 390 390 P -> Q (IN REF. 2).
 FT CONFLICT 406 406 K -> R (IN REF. 2).
 FT CONFLICT 573 573 TLDNSWLMDEERCSLEQACD -> VTA (IN REF. 2).
 FT CONFLICT 736 757
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWSWL 6
 Db 737 LDWSWL 742
 RESULT 5
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (1-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKBK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase-1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RN REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKB-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKB-ALPHA IS FURTHER RELEASED FROM THE

CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC
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 CC
 CC EMBL: AF115282; AAF21978.1; -
 CC HSSP: Q63450; 1A06.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC Pfam: PF00069; pkinase; 1.
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Euk_pkinase; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 CC FT DOMAIN 15 300 PROTEIN KINASE.
 CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC FT DOMAIN 737 742 NEMO-BINDING.
 CC NP_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 145 145 BY SIMILARITY.
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 757 AA; 86866 MW; 3AFFE46A7DF91F9C CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 DB 737 LDWSWL 742
 RESULT 6
 CYOA_BUCAI STANDARD; PRT; 296 AA.
 AC P57544;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase Bo(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).
 GN CYOA OR BU472.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=1093077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RL Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE

CC GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) - Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC
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 CC
 CC EMBL: AP001119; BAB13169.1; -
 CC HSSP: P18400; 1CYW.
 CC InterPro: IPR001505; Copper_Cua.
 CC InterPro: IPR002429; Cyt_c_ox_2.
 CC InterPro: IPR000437; Prok_lipoprot.
 CC Pfam: PF00116; COX2; 1.
 CC PRODOM: PD000131; Copper_Cua; 1.
 CC PROSITE: PS00103; PROKAR_LIPOPROTEIN; FALSE_NEG.
 CC Oxidoreductase: Respiratory chain; Electron transport; Transmembrane;
 CC Signal; Lipoprotein; Complete proteome.
 CC FT SIGNAL 1 15 POTENTIAL.
 CC FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
 CC FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
 CC FT DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 34 54 POTENTIAL.
 CC FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 79 99 POTENTIAL.
 CC FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
 CC SQ SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FFBAC CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 296;
 Best Local Similarity 83.3%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 DB 125 LDWSWL 130
 RESULT 7
 QOX2_ACEAC STANDARD; PRT; 307 AA.
 ID QOX2_ACEAC
 AC P50653;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
 DE A1 subunit 2) (Oxidase BA(3) subunit 2).
 GN CYAB.
 OS Acetobacter aceti.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Acetobacter.
 OX NCBI_TaxID=435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1023;
 RX MEDLINE=9332308; PubMed=8392509;
 RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
 RA Kawamura Y., Horinouchi S., Beppu T.;
 RT "Characterization of a cytochrome a1 that functions as a ubiquinol
 RT oxidase in Acetobacter aceti.";
 RL J. Bacteriol. 175:4307-4314(1993).
 CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC
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 CC -----
 DR EMBL; D13185; BAA02480.1; -;
 DR HSSP; P18400; ICYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR ProSITE; PS000131; PROKAR_LIPOPROTEIN; 1.
 DR PROSITE; PS000131; PROKAR_LIPOPROTEIN; 1.
 DR Oxidoreductase; Respiratory chain; Signal; Transmembrane;
 KW Lipoprotein.
 KW SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT TRANSMEM 45 66 POTENTIAL.
 FT TRANSEM 87 107 POTENTIAL.
 SQ SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 307;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 Db 135 LDWKWL 140
 RESULT 8
 CYOA_PSEPU
 ID CYOA_PSEPU STANDARD; PRT; 314 AA.
 AC Q9WRL1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase B0(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).
 GN CYOA.
 OS Pseudomonas putida
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OC NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IH-2000;
 RX MEDLINE=99085656; PubMed=9868765;
 RA Hirayama H., Takami H., Inoue A., Horikoshi K.;
 RT "Isolation and characterization of toluene-sensitive mutants from
 RT Pseudomonas putida IH-2000.";
 RL FEMS Microbiol. Lett. 169:219-225(1998).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
 CC GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) - Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AB016787; BAA76356.1; -;
 DR HSSP; P18400; ICYW.

DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR ProSITE; PS000131; PROKAR_LIPOPROTEIN; 1.
 DR Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 KW Inner membrane; Signal; Lipoprotein.
 KW SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
 FT TRANSEM 43 63 POTENTIAL.
 FT DOMAIN 64 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 87 107 POTENTIAL.
 FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
 SQ SEQUENCE 314 AA; 34702 MW; 96E04FC3AA77F07 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 314;
 Best Local Similarity 83.3%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 Db 133 LDWKWL 138
 RESULT 9
 DCUP_YEAST
 ID DCUP_YEAST STANDARD; PRT; 362 AA.
 AC P32347;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
 GN HEM12 OR HEM6 OR POP3 OR YD9609.03.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92249304; PubMed=1576986;
 RA Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,
 RA Kushner J., Labbe P.;
 RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12
 RT gene sequence and evidence for two conserved glycines essential for
 RT enzymatic activity.";
 RL Eur. J. Biochem. 205:1011-1016(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93348774; PubMed=8346678;
 RA Diflumeri C., Laroque R., Keng T.;
 RT "Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the
 RT gene for uroporphyrinogen decarboxylase.";
 RL Yeast 9:613-623(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP MUTANTS.
 RX MEDLINE=93111946; PubMed=1471989;
 RA Chelstowska A., Zodek T., Garey J.R., Kushner J., Rytka J.,
 RA Labbe-Bois R.;
 RT "Identification of amino acid changes affecting yeast
 RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
 RT mutant alleles.";
 RL Biochem. J. 288:753-757(1992).
 CC -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III - coproporphyrinogen + 4
 CC CO(2).
 CC -1- PATHWAY: PORPHYRIN AND HEME BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC CC -1- SIMILARITY: BELONGS TO THE UROPORPHRINOGEN DECARBOXYLASE FAMILY.
 CC CC -----
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 CC CC -----
 CC DR EMBL; X63721; CAA45253.1; -
 CC DR EMBL; Z19089; CAA79514.1; -
 CC DR EMBL; Z49209; CAA89078.1; -
 CC DR PIR; S23471; S23471.
 CC DR PIR; S20190; S20190.
 CC DR PIR; S31312; S31312.
 CC DR HSSP; P06132; IURO.
 CC DR SGD; S0002454; HEM12.
 CC DR InterPro: IPR000257; Uro_decarboxyls.
 CC DR Pfam; PF01208; URO-D; 1.
 CC DR PROSITE; PS00906; UROD_1; 1.
 CC DR PROSITE; PS00907; UROD_2; 1.
 CC KW Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
 CC FT VARIANT 59 59 S -> F (IN HEM12-6 AND HEM12-12).
 CC FT VARIANT 62 62 T -> I (IN HEM12-14).
 CC FT VARIANT 107 107 L -> S (IN HEM12-3 AND HEM12-13).
 CC FT VARIANT 215 215 S -> N (IN HEM12-2 AND HEM12-11).
 CC FT MUTAGEN 33 33 G->D: INACTIVATION.
 CC FT MUTAGEN 300 300 G->D: INACTIVATION.
 CC SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48E62BC277 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSW 5
 |||||
 Db 279 LDWSW 283

RESULT 10
 EPA3_CHICK STANDARD; PRT; 983 AA.
 AC P29318;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (CEK4).
 GN EPA3 OR ETK1 OR CEK4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92031278; PubMed=1657122;
 RA Sajjadi F.G., Pasquale E.B., Subramani S.;
 RT "Identification of a new eph-related receptor tyrosine kinase gene
 RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor.";
 RL New Biol. 3:769-778(1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.

CC CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC CC RECEPTOR SUBFAMILY.
 CC CC -----
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 CC CC -----
 CC DR EMBL; M68514; AAA48666.1; -
 CC DR PIR; B45583; B45583.
 CC DR HSSP; P00523; 2PTK.
 CC DR InterPro: IPR000561; EGF-like.
 CC DR InterPro: IPR001090; Ephrin_receptor.
 CC DR InterPro: IPR000719; Euk_pkinase.
 CC DR InterPro: IPR003961; FN_III.
 CC DR InterPro: IPR003962; FNIII_repeat.
 CC DR InterPro: IPR001660; SAM.
 CC DR InterPro: IPR001245; Tyr_pkinase.
 CC DR InterPro: IPR001426; Ykase_receptorv.
 CC DR Pfam; PF00041; fn3; 2.
 CC DR Pfam; PF00069; pkinase; 1.
 CC DR Pfam; PF00536; SAM; 1.
 CC DR Pfam; PF01404; EPH_lbd; 1.
 CC DR PRINTS; PR00014; FNTYPEIII.
 CC DR PRINTS; PR00109; TYRKINASE.
 CC DR ProDom; PD000001; Euk_pkinase; 1.
 CC DR ProDom; PD001495; Ephrin_receptor; 1.
 CC DR SMART; SM00001; EGF_like; 1.
 CC DR SMART; SM00060; FN3; 2.
 CC DR SMART; SM00454; SAM; 1.
 CC DR SMART; SM00219; Tyrc; 1.
 CC DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC DR PROSITE; PS0105; SAM_DOMAIN; 1.
 CC KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 983
 CC FT DOMAIN 20 540
 CC FT TRANSMEM 541 564
 CC FT DOMAIN 565 983
 CC FT DOMAIN 188 321
 CC FT DOMAIN 322 431
 CC FT DOMAIN 432 529
 CC FT DOMAIN 621 882
 CC FT DOMAIN 911 975
 CC FT SITE 981 983
 CC FT NP_BIND 627 635
 CC FT BINDING 653 653
 CC FT ACT_SITE 746 746
 CC FT MOD_RES 596 596
 CC FT MOD_RES 602 602
 CC FT CARBOHYD 231 231
 CC FT CARBOHYD 336 336
 CC FT CARBOHYD 390 390
 CC FT CARBOHYD 403 403
 CC FT CARBOHYD 492 492
 CC SQ SEQUENCE 983 AA; 109910 MW; E8895F0BDF77651E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDWSW 5
Db      342 LDWSW 346

RESULT 11
EPA3_HUMAN
ID EPA3_HUMAN STANDARD; PRT; 983 AA.
AC P29320; Q9H2V4; Q9H2V3;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE EPHrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
DE Kinase receptor ETK1) (HEK) (HEK4).
GN EPA3 OR ETK1 OR ETK OR HEK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92179233; PubMed=1311845;
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
RT Kinase expressed by human lymphoid tumor cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
RN [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RA Chiari R., Hames G., Stroobant V., Maillere B., Texier C., Mach B.,
RA Boon T., Coulie P.G.;
RT "Identification of a tumor specific shared antigen derived from an
RT Eph-receptor and presented to CD4 T cells on HLA class II
RT molecules.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE=92147681; PubMed=1737782;
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
RA Welch K., Loudovaris M., Rockman S., Busmanis I.;
RT "Isolation and characterization of a novel receptor-type protein
RT tyrosine kinase (hek) from a human pre-B cell line.";
RL J. Biol. Chem. 267:3262-3267(1992).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
CC FUNCTION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
CC SECRETED (ISOFORM 2).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M83941; AAA58633.1;
CC EMBL: AF213459; AAG43576.1;
CC EMBL: AF213460; AAG43577.1;
CC EMBL: A28003; CAA01906.1;
CC PIR: A38224; A38224.
CC HSPP: P00523; 2PTK.
CC Genew: HGNC:3387; EPAH3.

MIM: 179611;
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_lbd; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TyTKC; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 983
FT DOMAIN 21 541
FT TRANSMEM 542 565
FT DOMAIN 566 983
FT DOMAIN 189 322
FT DOMAIN 323 432
FT DOMAIN 433 530
FT DOMAIN 621 882
FT DOMAIN 911 975
FT SITE 981 983
FT NP_BIND 627 635
FT BINDING 653 653
FT ACT_SITE 746 746
FT MOD_RES 596 596
FT MOD_RES 602 602
FT MOD_RES 779 779
FT CARBOHYD 232 232
FT CARBOHYD 337 337
FT CARBOHYD 391 391
FT CARBOHYD 404 404
FT CARBOHYD 493 493
FT VARSPLIC 532 539
FT VARSPLIC 540 540
FT CONFLICT 507 507
FT CONFLICT 724 724
FT CONFLICT 911 911
FT CONFLICT 924 924
SQ SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSW 5
Db      343 LDWSW 347

RESULT 12
EPA3_MOUSE
ID EPA3_MOUSE STANDARD; PRT; 983 AA.

```

P29319;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (NEK4).
EPHA3 OR ETK1 OR NEK4 OR TYRO4.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN-ICR X Swiss Webster; TISSUE=Embryo;
RX MEDLINE=92031278; PubMed=1657122;
RA Sajjadi F.G., Pasquale E.B., Subramani S.;
RT Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.;
RL New Biol. 3:769-778(1991).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM IS SECRETED.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE BRAIN. ALSO DETECTED IN TESTIS.
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.

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CC EMBL; M68513; AAA39521.1; -;
CC EMBL; M68515; AAA39522.1; ALT_SEQ.
CC PIR; A45583; A45583.
CC HSP; P00523; 2PTK.
CC MGD; MGI:99612; EphA3.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR001090; Ephrin_receptor.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003962; FNIII_repeat.
CC InterPro; IPR001660; SAM.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR001426; Ykase_receptor.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00536; SAM; 1.
CC Pfam; PF01404; EPH_lbd; 1.
CC PRINTS; PR00014; FNYPEP11.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Euk_pkinase; 1.
CC ProDom; PD001495; Ephrin_receptor; 1.
CC SMART; SM00060; FN3; 2.
CC SMART; SM00454; SAM; 1.
CC SMART; SM00219; TyrKc; 1.
CC PROSITE; PS01186; EGF_2; UNKNOWN.1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V.1; 1.
CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V.2; 1.

DR PROSITE; PS50105; SAM_DOMAIN; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 541 564 POTENTIAL.
FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 188 321 CYS-RICH.
FT DOMAIN 322 431 FIBRONECTIN TYPE-III 1.
FT DOMAIN 432 529 FIBRONECTIN TYPE-III 2.
FT DOMAIN 529 882 PROTEIN KINASE.
FT DOMAIN 911 975 SAM.
FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 627 635 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 746 746 BY SIMILARITY.
FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 779 779 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 492 492 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPIC 530 983 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 983 AA; 109955 MW; BB44A6655D8107A2 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDWSW 5
Db 342 LDWSW 346
|||||
RESULT 13
EPA3_RAT STANDARD; PRT; 984 AA.
AC 008680;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor REK4) (TYRO-4).
DE EPHA3 OR REK4 OR TYRO4.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=98120505; PubMed=9458884;
RA Li Y.Y., McTiernan C.F., Feldman A.M.;
RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene r-Epha3 in neonatal rat cardiomyocytes.";
RL Am. J. Physiol. 274:H331-H341(1998).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN AND LUNG.
CC -!- INDUCTION: DOWN-REGULATED BY IL1-BETA IN NEONATAL CARDIAC MYOCYTES.
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.

Db 540 DMSWL 544

RESULT 15

3MG2_ECOLI

ID 3MG2_ECOLI STANDARD; PRT; 282 AA.

AC P04395;

DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE DNA-3-methyladenine glycosylase II (EC 3.2.2.21) (3-methyladenine-DNA

DE glycosylase II, inducible) (TAG II) (DNA-3-methyladenine glycosylase

DE II).

GN ALKA OR AIDA OR B2068.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-12 AND 14-20.

RX MEDLINE-85054800; PubMed-6094528;

RA Nakabeppu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;

RT "Structure and expression of the alka gene of Escherichia coli

RT involved in adaptive response to alkylating agents.";

RL J. Biol. Chem. 259:13730-13736(1984).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-K12 / MG1655;

RX MEDLINE-97426617; PubMed-9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-K12;

RX MEDLINE-97251358; PubMed-9097040;

RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,

RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Mikl T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshina T.,

RA Saito N., Sempel G., Seki Y., Sivasubraman S., Tagami H.,

RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horluchi T.;

RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 40.1-50.0 min region on the linkage map.";

RL DNA Res. 3:379-392(1996).

RN [4]

RP CHARACTERIZATION.

RX MEDLINE-85054799; PubMed-6389535;

RA Nakabeppu Y., Kondo H., Sekiguchi M.;

RT "Cloning and characterization of the alka gene of Escherichia coli

RT that encodes 3-methyladenine DNA glycosylase II.";

RL J. Biol. Chem. 259:13723-13729(1984).

RN [5]

RP SEQUENCE OF 1-2 FROM N.A.

RX MEDLINE-86313568; PubMed-3529081;

RA Nakabeppu Y., Sekiguchi M.;

RT "Regulatory mechanisms for induction of synthesis of repair enzymes

RT in response to alkylating agents: ada protein acts as a

RT transcriptional regulator.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:6297-6301(1986).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS), AND MUTAGENESIS.

RX MEDLINE-96319733; PubMed-8706135;

RA Yamagata Y., Kato M., Odawara K., Tokuno Y., Nakashima Y.,

RA Matsushima N., Yasumura K., Tomita K.-I., Ihara K., Fujii Y.,

RA Nakabeppu Y., Sekiguchi M., Fujii S.;

RT "Three-dimensional structure of a DNA repair enzyme, 3-methyladenine

RT DNA glycosylase II, from Escherichia coli.";

RL Cell 86:311-320(1996).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RX MEDLINE-96319734; PubMed-8706136;

RA Labahn J., Schärer O.D., Long A., Ezaz-Nikpay K., Verdine G.L.,

RA Ellenberger T.E.;

RT "Structural basis for the excision repair of alkylation-damaged DNA.";

RL Cell 86:321-329(1996).

CC -!- FUNCTION: HYDROLYSIS OF THE DEOXYRIBOSE N-GLYCOSIDIC BOND TO

CC EXCISE 3-METHYLADEININE, 3-METHYLGUANINE, 7-METHYLGUANINE,

CC O2-METHYLTHYMINE, AND O2-METHYLCYTOSINE FROM THE DAMAGED DNA

CC POLYMER FORMED BY ALKYLATION LESIONS.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alkylated DNA, releasing 3-

CC methyladenine, 3-methylguanine, 7-methylguanine, and 7-

CC methyladenine.

CC -!- SUBUNIT: MONOMER.

CC -!- INDUCTION: WHEN E. COLI CELLS ARE EXPOSED TO DOSES OF DNA

CC ALKYLATING AGENT. IT IS NOT INHIBITED BY REACTION PRODUCTS.

CC -!- SIMILARITY: BELONGS TO THE ALKYLASE DNA GLYCOSIDASES ALKA FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; K02498; AAA23430.1; -

DR EMBL; AE000297; AAC75129.1; -

DR EMBL; D90844; BAA15921.1; -

DR EMBL; D90845; BAA15926.1; -

DR EMBL; M13827; -; NOT_ANNOTATED_CDS.

DR PIR; A00904; DGEEMA.

DR PDB; 1MPG; 28-JAN-98.

DR EcoGene; EG11222; alka.

DR InterPro; IPR000035; Alka_DNAGlylsids.

DR InterPro; IPR003265; Endo_3c.

DR Pfam; PF00730; HRR-GPD; 1.

DR SMART; SM00478; ENDO3c; 1.

DR PROSITE; PS00516; Alkylase_3D-structure; Complete proteome.

KW DNA repair; Hydrolase; 3D-structure; Complete proteome.

FT SITE 218 218 DETERMINANT FOR SUBSTRATE SPECIFICITY

FT AND/OR ACCEPTOR.

FT ACT_SITE 238 238 PROTON ACCEPTOR.

FT MUTAGEN 124 124 Q->A: METHYLMETHANE SULFONATE-RESISTANT.

FT MUTAGEN 218 218 W->A: NO CATALYTIC ACTIVITY,

FT MUTAGEN 237 237 METHYLMETHANE SULFONATE-SENSITIVE.

FT MUTAGEN 238 238 D->N: MORE THAN 30% CATALYTIC ACTIVITY,

FT MUTAGEN 238 238 METHYLMETHANE SULFONATE-RESISTANT.

FT MUTAGEN 238 238 D->N: NO CATALYTIC ACTIVITY,

FT MUTAGEN 238 238 METHYLMETHANE SULFONATE-SENSITIVE.

SQ SEQUENCE 282 AA: 31393 MW; B66BB5E23019899C CRC64;

Query Match 85.0%; Score 34; DB 1; Length 282;

Best Local Similarity 80.0%; Pred. No. 1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6

Db 11 DMSWL 15

Search completed: May 30, 2003, 15:48:47

Job time : 10.1184 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriaph.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	740	6 Q95KV1	Q95kv1 bos taurus
2	40	100.0	756	6 Q95KV0	Q95kv0 bos taurus
3	38	95.0	1139	16 Q8ZC91	Q8zcc91 yersinia pe
4	37	92.5	310	2 Q9XBS7	Q9xbs7 zymomonas m
5	37	92.5	322	16 Q8YK7	Q8y9k7 bruceella me
6	37	92.5	347	16 Q98KR3	Q98kr3 rhizobium l
7	37	92.5	645	2 Q9X6C6	Q9x6c6 thermus bro
8	36	90.0	205	16 Q9ACR5	Q9acr5 streptomyce
9	36	90.0	242	12 Q919K8	Q919k8 culicx nigri
10	36	90.0	261	2 Q8ACG7	Q8acg7 caldicellul
11	36	90.0	288	2 Q8VTT4	Q8vtt4 pseudomonas
12	36	90.0	313	2 Q8VUQ6	Q8vuq6 pseudomonas
13	36	90.0	318	16 Q8ZC58	Q8zcc58 yersinia pe
14	36	90.0	329	16 Q8XVB4	Q8xvb4 ralstonia s
15	36	90.0	331	16 Q91427	Q91427 pseudomonas
16	36	90.0	344	16 Q8YEH7	Q8yeh7 bruceella me

17	36	90.0	353	16 Q9A7F0	Q9a7f0 caulobacter
18	36	90.0	386	16 Q92027	Q92u27 rhizobium m
19	36	90.0	393	16 Q98721	Q987z1 rhizobium l
20	36	90.0	409	10 Q9M3F6	Q9m3f6 arabidopsis
21	36	90.0	452	4 Q96AB7	Q96ab7 homo sapien
22	36	90.0	477	11 Q9CYU6	Q9cyu6 mus musculu
23	36	90.0	484	4 Q9BTV6	Q9btv6 homo sapien
24	36	90.0	703	10 Q9FIS0	Q9fis0 arabidopsis
25	36	90.0	747	16 Q9G735	Q9g735 mycobacteri
26	36	90.0	803	17 Q97UH8	Q97uh8 sulfolobus
27	36	90.0	996	2 Q9AQH0	Q9aqh0 caldicellul
28	36	90.0	1329	16 Q9CD30	Q9cd30 mycobacteri
29	36	90.0	1426	2 Q9X3P6	Q9x3p6 caldicellul
30	36	90.0	1751	2 Q9AQ84	Q9aqq4 caldicellul
31	36	90.0	1770	2 Q9X3P5	Q9x3p5 caldicellul
32	35	87.5	162	16 Q53756	Q53756 mycobacteri
33	35	87.5	295	5 Q9VTL8	Q9vtl8 drosophila
34	35	87.5	347	16 Q920P5	Q92qp5 rhizobium m
35	35	87.5	348	16 Q8UFX0	Q8ufx0 agrobacteri
36	35	87.5	396	17 Q96X28	Q96xx28 sulfolobus
37	35	87.5	439	2 Q93Q61	Q93q61 klebsiella
38	35	87.5	443	16 Q8ZDM7	Q8zdm7 yersinia pe
39	35	87.5	481	10 Q96311	Q96311 arabidopsis
40	35	87.5	999	2 Q93JY2	Q93jy2 erwinia chr
41	34	85.0	82	17 Q26213	Q26213 methanobact
42	34	85.0	116	2 Q88039	Q88039 rhodobacter
43	34	85.0	135	2 Q05744	Q05744 mycobacteri
44	34	85.0	214	16 Q9KFX7	Q9kfx7 bacillus ha
45	34	85.0	282	16 Q8X7K0	Q8x7k0 escherichia

ALIGNMENTS

RESULT 1

Q95KV1	ID	Q95KV1	PRELIMINARY;	PRT;	740 AA.
AC	Q95KV1	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	Ikb kinase-alpha.				
GN	BIKKALPHA.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;				
RT	"Identification and characterisation of the bovine Ikb kinases (IKKS)				
RT	alpha, beta and gamma."				
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBAJ databases.				
DR	EMBL; AJ141555; CAC93686.1;				
DR	InterPro; IPR000719; Euk_pkinase.				
DR	InterPro; IPR002290; Ser_thr_pkinase.				
DR	Pfam; PF00069; pkinase; 1.				
DR	ProDom; PD000001; Euk_pkinase; 1.				
DR	SMART; SM00219; TyrKc; 1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.				
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.				
KW	ATP-binding; Kinase; Transferase.				
SQ	SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;				

Query Match 100.0%; Score 40; DB 6; Length 740;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
|||||

Db 733 LDWSWL 738

RESULT 2

Q95KVO PRELIMINARY; PRT; 756 AA.

ID Q95KVO PRELIMINARY; PRT; 756 AA.

AC Q95KVO; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Ikb kinase-beta.

GN BIKK9BETA.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

GN [1]

RP SEQUENCE FROM N.A.

RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;

RT "Identification and characterisation of the bovine Ikb kinases (IKKs) alpha, beta and gamma.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ414556; CAC93687.1; -

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR002290; Ser_thr_pkinase.

DR Pfam: PF00069; pkinase; 1.

DR ProDom: PD000001; Euk_pkinase; 1.

DR SMART: SM00219; TyrKc; 1.

DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.

KW ATP-binding; Kinase; Transferase.

SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 756;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 LDWSWL 6

|||||

Db 737 LDWSWL 742

RESULT 3

Q8ZC91 PRELIMINARY; PRT; 1139 AA.

ID Q8ZC91 PRELIMINARY; PRT; 1139 AA.

AC Q8ZC91; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Putative potassium efflux system.

GN YPO3129.

OS Yersinia pestis.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Yersinia.

OC NCBI_TaxID=632;

GN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-CO-92 / BIOVAR ORIENTALIS;

RX MEDLINE-21470413; PubMed-11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,

RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

RT "Genome sequence of Yersinia pestis, the causative agent of plague."

RL Nature 413:523-527(2001).

DR EMBL: AJ414155; CAC92364.1; -

DR InterPro: IPR001880; MS10n_channel.

DR Pfam: PF00924; MS_channel; 1.


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DR EMBL: AE009554; AAL52332.1; -
DR InterPro: IPR001694; Resp_NADH_dhl.
DR Pfam: PF001146; NADHdh; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 322 AA; 35966 MW; D5B5B123AB2C13E7 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 322;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
Db 174 LDWNWL 179

RESULT 6
ID Q98KR3 PRELIMINARY; PRT; 347 AA.
AC Q98KR3;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH-ubiquinone dehydrogenase chain 8.
GN MLL1361.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002997; BAB48751.1; -
DR InterPro: IPR001694; Resp_NADH_dhl.
DR Pfam: PF001146; NADHdh; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Ubiquinone; Complete proteome.
SQ SEQUENCE 347 AA; 38370 MW; 1092F351BD97EC57 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 347;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
Db 199 LDWNWL 204

RESULT 7
ID Q9X6C6 PRELIMINARY; PRT; 645 AA.
AC Q9X6C6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-galactosidase.
GN BGAT.
OS Thermus brockianus.
OC Bacteria; Thermus/deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=56956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ITI360;

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RX MEDLINE=99402735; PubMed=10473401;
RA Fridjonsson O., Watzlawick H., Gehweiler A., Rohrhirsch T., Mattes R.;
RT "Cloning of the gene encoding a novel thermostable alpha-galactosidase
RT from Thermus brockianus ITI360."
RL Appl. Environ. Microbiol. 65:3955-3963(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ITI360;
RX MEDLINE=20203878; PubMed=10741834;
RA Fridjonsson O., Watzlawick H., Mattes R.;
RT "The structure of the alpha-galactosidase gene loci in Thermus
RT brockianus ITI360 and Thermus thermophilus TH125."
RL Extremophiles 4:23-33(2000).
DR EMBL; AF135398; AAD33667.1; -
DR InterPro: IPR001554; GH_14.
DR Pfam: PF01373; Glyco_hydro_14; 1.
DR Pfam: PF02449; Glyco_hydro_42; 1.
SQ SEQUENCE 645 AA; 73420 MW; C79A9E1C0020EC40 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 645;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
Db 48 LDNAWL 53

RESULT 8
ID Q9ACR5 PRELIMINARY; PRT; 205 AA.
AC Q9ACR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SCPl.253.
GN SCPl.253.
OS Streptomyces coelicolor.
OC Plasmid SCPl.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Bartell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36779.1; -
KW Hypothetical protein; plasmid.
SQ SEQUENCE 205 AA; 23051 MW; 6602396CFF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
Db 11 DWSWL 15

RESULT 9
Q919K8

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ID Q919K8 PRELIMINARY; PRT; 242 AA.
AC Q919K8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FLORIDA1997;
RX MEDLINE=21488685; PubMed=11602755;
RA Alfonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RT Becnel J.J., Rock D.L., Kutish G.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF403738; AAK94146.1;
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 79 LDWSW 83

RESULT 10
Q9A0G7 PRELIMINARY; PRT; 261 AA.
ID Q9A0G7;
AC Q9A0G7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Glycosyl hydrolase 6 (Fragment).
OS Caldicellulosiruptor sp. Tok7B.1.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Syntrophomonadaceae; Caldicellulosiruptor.
OX NCBI_TaxID=80339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tok7B.1;
RX MEDLINE=20171169; PubMed=10706665;
RA Gibbs M.D., Reeves R.A., Farrington G.K., Anderson P., Williams D.P.,
RA Bergquist P.L.;
RT "Multidomain and multifunctional glycosyl hydrolases from the extreme
thermophile Caldicellulosiruptor isolate Tok7B.1.";
RL Curr. Microbiol. 40:333-340(2000).
DR EMBL: AF078040; AAK06391.1;
DR HSSP: Q06851; INBC.
DR InterPro: IPR001956; CBD_3.
DR Pfam: PF00942; CBM_3; 1.
DR ProDom: PD001947; CBD_3; 1.
KW Hydrolase.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 28759 MW; 4771744A36A6AE04 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 79 LDWSW 83

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Db 237 DWSWL 241

RESULT 11
Q8VTT4 PRELIMINARY; PRT; 288 AA.
ID Q8VTT4;
AC Q8VTT4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome o ubiquinol oxidase A (Fragment).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PML1;
RA Syn C.K.C., Liew C.F., Swarup S.;
RT "Pseudomonas putida cytochrome o ubiquinol oxidase A, B, C, and D
genes";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321090; AAL37192.1;
DR InterPro: IPR001505; Copper_CuA.
DR ProDom: PD000131; Copper_CuA; 1.
FT NON_TER 1
FT NON_TER 288
SQ SEQUENCE 288 AA; 31882 MW; 60E40B3A36516BFC CRC64;

Query Match 90.0%; Score 36; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 108 LDWSWL 113

RESULT 12
Q8VUQ6 PRELIMINARY; PRT; 313 AA.
ID Q8VUQ6;
AC Q8VUQ6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome o oxidase A.
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT2442;
RA Fukumori F., Kishii M.;
RT "Characterization of the toluene-sensitive mutants of Pseudomonas
putida KT2442TOL.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB066295; BAB83593.1;
DR InterPro: IPR001505; Copper_CuA.
DR InterPro: IPR002429; Cyt_c-ox_2.
DR Pfam: PF00116; COX2; 1.
DR ProDom: PD000131; Copper_CuA; 1.
SQ SEQUENCE 313 AA; 34557 MW; 193E3F7F8EBDA42B CRC64;

Query Match 90.0%; Score 36; DB 2; Length 313;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 133 LDWSWL 138

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RESULT 13

Q82C58 Q82C58 PRELIMINARY; PRT; 318 AA.
 AC Q82C58; 90.0%; Score 36; DB 16; Length 318;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-).
 GN CYOA OR YPO3164.
 OS Versinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague."
 RL Nature 413:523-527(2001).
 DR EMBL; AJ414155; CAC92399.1; -;
 DR InterPro; IPR001505; Copper_CuA.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR Oxidoreductase; Complete proteome.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 318 AA; 35049 MW; E2947941923016D3 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 318;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 DB 135 LDWKWL 140

RESULT 14

Q8XVB4 Q8XVB4 PRELIMINARY; PRT; 329 AA.
 AC Q8XVB4; 90.0%; Score 36; DB 16; Length 329;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)
 DE oxidoreductase protein (EC 1.10.3.-).
 GN CYOA OR RSC2917 OR RS00308.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,
 RA Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002).
 DR EMBL; AL646072; CAD16624.1; -;
 DR InterPro; IPR001505; Copper_CuA.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR Oxidoreductase; Complete proteome.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;

Query Match 90.0%; Score 36; DB 16; Length 331;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 DB 133 LDWKWL 138

Search completed: May 30, 2003, 14:38:36
 Job time : 17.7632 secs

DR Pfam; PF001116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;

Query Match 90.0%; Score 36; DB 16; Length 329;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 DB 133 LDWKWL 138

RESULT 15

Q91427 Q91427 PRELIMINARY; PRT; 331 AA.
 AC Q91427; 90.0%; Score 36; DB 16; Length 331;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cytochrome O ubiquinol oxidase subunit II.
 GN CYOA OR PA1317.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL; AE004561; AAG04706.1; -;
 DR HSP; P18400; ICYW
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR002429; Cyt_Cox_2.
 DR InterPro; IPR001092; HLH_basic.
 DR Pfam; PF001116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 331 AA; 36623 MW; DC4449ED0FF0BB66 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 331;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 DB 133 LDWKWL 138

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 91.9211 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: US-09-643-260-19

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	100.0	28	23 AAB08741	Mutated IKKbeta NE
2	148	100.0	28	23 AAM48524	NBD peptide SEQ ID
3	134	90.5	28	23 ABR08740	IKKbeta NEMO bindi
4	134	90.5	28	23 AAM48523	NBD peptide SEQ ID
5	100	67.6	36	23 AAU79345	Antennapedia-caveo
6	98	66.2	20	21 AAB13423	Synthetic alpha sm
7	98	66.2	26	18 AAW11630	Anti-apoptotic pro
8	98	66.2	41	22 AAB80924	Mixer SIM peptide
9	98	66.2	41	22 AAB80925	Mixer SIM mutant p
10	95	64.2	21	18 AAW45976	Cysteine protease

RESULT 1

ABB08741

ID ABB08741 standard; peptide; 28 AA.

XX ABB08741;

XX 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antisthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; muten.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 22 /note- "Wildtype Trp substituted by Ala"

FT Misc-difference 24 /note- "Wildtype Trp substituted by Ala"

XX WO200183547-A2.

XX 08-NOV-2001.

11 95 64.2 24 19 AAW82957 Oestrogen receptor
 12 95 64.2 36 21 AAY78416 Drosophila antenna
 13 95 64.2 230 21 AAY58610 Protein regulating
 14 94 63.5 27 18 AAW11629 Anti-apoptotic pro
 15 94 63.5 27 20 AAW27444 Antennapedia inter
 16 94 63.5 27 23 ABB83151 Transduction domai
 17 94 63.5 34 21 AAY79919 Human papillomavir
 18 94 63.5 36 23 AAU79344 Antennapedia-caveo
 19 94 63.5 60 20 AAY42291 Drosophila antenna
 20 94 63.5 60 20 AAY27403 D. melanogaster pA
 21 94 63.5 60 20 AAY04364 Drosophila antenna
 22 94 63.5 61 22 AAE00811 D. melanogaster an
 23 94 63.5 217 22 AAE10922 Human HOXB7 varian
 24 94 63.5 378 22 ABB72035 Drosophila melanog
 25 94 63.5 417 22 ABB57755 Drosophila melanog
 26 94 63.5 589 22 ABB58929 Internalization se
 27 93 62.8 22 20 AAW91049 Beta-catenin deriv
 28 93 62.8 22 21 AAB27063 Human nucleic acid
 29 93 62.8 106 21 AAB21030 Human colon cancer
 30 93 62.8 115 21 AAB53629 Human polypeptide
 31 93 62.8 220 22 AAW41487 Human polypeptide
 32 93 62.8 236 22 AAM39701 Human polypeptide
 33 93 62.8 243 19 AAW48885 Amino acid sequenc
 34 92.5 62.5 46 22 AAB80927 XFast-3 mutant SIM
 35 92 62.2 16 18 AAW45974 Cysteine protease
 36 92 62.2 16 18 AAW33410 D-form peptide 43-
 37 92 62.2 16 18 AAW33407 Peptide 43-58 of h
 38 92 62.2 16 19 AAW82958 Oestrogen receptor
 39 92 62.2 16 19 AAW71270 Antennapedia pepti
 40 92 62.2 16 19 AAW71316 Antennapedia pepti
 41 92 62.2 16 19 AAW30508 Drosophila membran
 42 92 62.2 16 19 AAW56397 Preferred signal s
 43 92 62.2 16 20 AAY52102 Peptide from the t
 44 92 62.2 16 20 AAY13509 Signal sequence of
 45 92 62.2 16 20 AAY00859 Peptide pAntp(43-5

ALIGNMENTS

XX PF 02-MAY-2001; 2001WO-US40654.
 XX XX 02-MAY-2000; 2000US-201261P.
 PR PR 22-AUG-2000; 2000US-0643260.
 XX XX (UYVA) UNIV YALE.
 PA May MJ, Ghosh S;
 PI WPI; 2002-179350/23.
 DR
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 PT
 PS Claim 23; Fig 5; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKBeta at the NEMO binding domain. Blockage of IKBeta-NEMO
 CC interaction results in inhibition of IKBeta kinase activation and
 CC subsequent decreased phosphorylation of Ikbappab. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKBeta.
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 148; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKWIFQNRMRKWKKTALDASALQTE 28
 Db 1 DRQIKWIFQNRMRKWKKTALDASALQTE 28
 RESULT 2
 AAM48524
 ID AAM48524 standard; Peptide; 28 AA.
 XX
 AC AAM48524;
 XX
 DT 20-MAR-2002 (first entry)
 XX

DE NBD peptide SEQ ID NO 19.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; Ikbappab kinase beta; IKBeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Example 5; Fig 5; 89pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of Ikbappab kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKBeta kinase
 CC activation and subsequent decreased phosphorylation of Ikbappab. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 148; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKWIFQNRMRKWKKTALDASALQTE 28
 Db 1 DRQIKWIFQNRMRKWKKTALDASALQTE 28
 RESULT 3
 ABB08740

ID XX ABB08740 standard; peptide; 28 AA.
 AC XX ABB08740;
 DT XX 14-JUN-2002 (first entry)
 DE XX IKKbeta NEMO binding domain peptide SEQ ID NO 18.
 DE XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nontropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer.
 OS Homo sapiens.
 XX
 XX WO200183547-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYUA) UNIV YALE.
 PA
 XX
 XX May MJ, Ghosh S;
 PI
 XX WPI; 2002-179350/23.
 DR
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Fig 5; 82pp; English.
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB07313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyoma, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or herpes simplex. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying

CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 28 AA;
 Query Match 90.5%; Score 134; DB 23; Length 28;
 Best Local Similarity 92.9%; Pred. No. 5.6e-13;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DROIKIWFQNRKMKKKTKALDASALQTE 28
 |||||
 DB 1 DROIKIWFQNRKMKKKTKALDASALQTE 28
 |||||
 RESULT 4
 AAM48523
 ID AAM48523 standard; Peptide; 28 AA.
 XX
 AC AAM48523;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE NBD peptide SEQ ID NO 18.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYUA) UNIV YALE.
 PI
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 WPI; 2002-121889/16.
 DR
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Example 5; Fig 5; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 28 AA;
 CC

Query Match 90.5%; Score 134; DB 23; Length 28;
 Best Local Similarity 92.9%; Pred. No. 5.6e-13;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DRQIKWIFQNRMRKWKKTALDASALQTE 28
 DB 1 DRQIKWIFQNRMRKWKKTALDWSLQTE 28

RESULT 5
 AAU79345
 ID AAU79345 standard; Peptide: 36 AA.
 AC AAU79345;
 DT 02-JUL-2002 (first entry)
 XX

DE Antennapedia-caveolin-X fusion peptide.
 XX
 KW Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;
 KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;
 KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;
 KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;
 KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;
 KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;
 KW spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav;
 KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
 KW human; fruit fly; antennapedia internalisation signal.

XX
 OS Drosophila melanogaster.
 OS Homo sapiens.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 1..16
 FT /label= Antennapedia_internalisation_signal
 FT /note= "Specifically claimed in claim 9"
 FT
 FT Misc-difference 17..32
 FT /label= Cav-X
 FT /note= "Control peptide based on a human caveolin-1
 FT scaffolding domain shown in AAU79340 residues
 FT 82-101"

XX
 PN WO200220768-A2.
 XX
 XX 14-MAR-2002.
 XX
 XX 10-SEP-2001; 2001WO-USA2069.
 XX
 XX 08-SEP-2000; 2000US-231327P.
 XX 07-DEC-2000; 2000US-0731023.
 XX
 XX (UYVA) UNIV YALE.
 XX
 XX Sessa WC;
 XX
 XX WPI; 2002-329877/36.
 XX
 XX New peptide having caveolin scaffolding domain, useful for modulating
 XX activity of endothelial nitric oxide synthase and inhibiting

PT inflammation and tumour cell angiogenesis proliferation -
 XX Claim 16; Page 72; 73pp; English.
 XX
 CC The invention describes an isolated caveolin scaffolding domain peptide
 CC (I). A fusion peptide (II) containing (I) and at least a membrane
 CC translocation sequence is useful for down regulating endothelial nitric
 CC oxide synthase (eNOS) activity in a cell, resulting in blockage of
 CC vasodilation. (II) is therefore useful for inhibiting inflammation and
 CC tumour cell angiogenesis/proliferation in an animal; and for blocking the
 CC interaction of caveolin with a protein in vivo. (II) may be useful in
 CC treatment of inflammatory conditions such as osteoporosis, rheumatoid
 CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)
 CC are also useful for treating pathological processes associated with a
 CC pro-inflammatory response including allergies such as allergic rhinitis,
 CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous
 CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,
 CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,
 CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and
 CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing
 CC corticosteroids useful for immunosuppression in transplant and cancer
 CC patients. When administered along with one or more antiinflammatory
 CC agent (I) and (II) are useful for inhibiting tumour growth or malignant
 CC neoplasm including cellular angiogenetics, proliferation, invasiveness,
 CC and metastasis in biological systems. This sequence represents a fusion
 CC peptide of the invention created from the fruit fly antennapedia
 CC internalisation signal and control sequence Cav-X, based on the human
 CC caveolin-1 scaffolding domain shown in AAU79340, residues 82-101.

XX Sequence 36 AA;
 CC

Query Match 67.6%; Score 100; DB 23; Length 36;
 Best Local Similarity 69.2%; Pred. No. 8.3e-08;
 Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 RQIKWIFQNRMRKWKKTALDASALQ 27
 DB 1 RQIKWIFQNRMRKWKKGIDKRAFT 26

RESULT 6
 AAB13423
 ID AAB13423 standard; peptide: 20 AA.
 XX
 XX AAB13423;
 XX
 XX 23-NOV-2000 (first entry)
 XX
 XX Synthetic alpha smooth muscle actin inhibitor # 3.
 XX
 XX Alpha smooth muscle actin; alpha-SM; wound contraction;
 XX hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;
 XX lung fibrosis.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 XX
 XX WO200038733-A1.
 XX
 XX 06-JUL-2000.
 XX
 XX 15-DEC-1999; 99WO-EP09964.
 XX
 XX 24-DEC-1998; 98EP-0204396.
 XX
 XX (UNIO) UCB-BIOPRODUCTS SA.
 XX
 XX Gabbiani G, Scarso A;
 XX
 XX WPI; 2000-452308/39.

CC extracellular matrix accumulation, a fibrotic condition, disease states
 CC associated with immunosuppression (such as different forms of malignancy,
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
 CC growth, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy
 CC or non-inflammatory renal disease) or renal fibrosis.

XX Sequence 41 AA;

Query Match 66.2%; Score 98; DB 22; Length 41;

Best Local Similarity 85.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 RQIKIWFONRRMKWKKTALD 21
 DB 1 RQIKIWFONRRMKWKKTALD 20

RESULT 9
 AAB80925
 ID AAB80925 standard; Protein; 41 AA.

XX AC AAB80925;

XX DT 04-JUN-2001 (first entry)

XX DE Mixer SIM mutant peptide.

XX SMad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
 KW Smad Interaction Motif; tissue repair; fibrotic condition;
 KW immunosuppression; diabetic nephropathy; tumour; muten.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "Biotin.Aminohexanoic acid-R"

FT Misc-difference 25 /note= "Wild-type Pro replaced by Ala. Wild-type sequence
 given in AAB80924."

FT Misc-difference 26 /note= "Wild-type Pro replaced by Ala"

XX WO200114413-A2.

XX PD 01-MAR-2001.

XX PF 25-AUG-2000; 2000WO-GB03265.

XX PR 25-AUG-1999; 99GB-0020000.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Germain SE, Hill CS, Howell MT;

XX WPI; 2001-265836/27.

XX Polypeptide capable of interacting with a Smad polypeptide, useful in
 the treatment of cancer and for tissue remodelling or healing of a
 wound, injury or surgery, comprises a Smad interaction motif and is
 less than 32 amino acids in length -

PS Example 2; Page 123; 179pp; English.

XX The present invention relates to peptides capable of interacting with a
 Smad protein, comprising a Smad interaction motif (SIM; amino acid
 sequence PP(T/N)K). The present sequence is one such Smad interacting
 peptide. Smad proteins are a family of highly conserved, intracellular
 proteins that signal cellular responses downstream of Transforming Growth
 Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
 is thought to be necessary for interaction with the MH2 domain of Smad2.
 The peptides of the present invention are useful in the manufacture of a
 medicament for the treatment of a patient in need of modulation of

CC activin or TGF-beta signalling; cancer; a patient in need of reducing
 CC extracellular matrix deposition, encouraging tissue repair and/or
 CC regeneration, tissue remodelling or healing of a wound, injury or
 CC surgery, or reducing scar tissue formation arising from injury to the
 CC brain; a patient with or at risk of end-stage organ failure, pathologic
 CC extracellular matrix accumulation, a fibrotic condition, disease states
 CC associated with immunosuppression (such as different forms of malignancy,
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
 CC growth, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy
 CC or non-inflammatory renal disease) or renal fibrosis.

XX Sequence 41 AA;

Query Match 66.2%; Score 98; DB 22; Length 41;

Best Local Similarity 85.0%; Pred. No. 1.9e-07;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 RQIKIWFONRRMKWKKTALD 21
 DB 1 RQIKIWFONRRMKWKKTALD 20

RESULT 10

AAB45976
 ID AAB45976 standard; peptide; 21 AA.

XX AC AAB45976;

XX DT 01-JUL-1998 (first entry)

XX DE Cysteine protease inhibiting peptide for preventing cell death.

XX KW Neuronal cell death; neurodegenerative disorder; inhibition;
 KW cysteine protease; cardiovascular; liver disease.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"

XX WO9735876-A1.

XX PD 02-OCT-1997.

XX PF 04-MAR-1997; 97WO-US04158.

XX PR 04-MAR-1996; 96US-0610220.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Troy CM;

XX WPI; 1997-489561/45.

XX New cysteine protease inhibiting peptide(s) for preventing cell
 death - in cases of neurodegenerative, cardiovascular and liver
 diseases, and their peptidomimetics, and general method for
 identifying enzyme inhibiting peptides

PS Claim 10; Page 68; 112pp; English.

XX This sequence represents a specifically claimed peptide of the formula:
 V-(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5;
 if n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more,
 CC (AA1)n = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value
 CC of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more,
 CC (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'',
 CC or all of which may be absent, = agent able to direct the compound
 CC to a specific cell. The peptides are inhibitors of cysteine proteases,
 CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit
 CC death of cells, particularly in humans, and can be used to treat
 CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,

Query Match 64.2%; Score 95; DB 19; Length 24;
Best Local Similarity 85.0%; pred. No. 2.9e-07;
Matches 17; Conservative 0; Mismatches 3; Indels

Key	Location/Qualifiers
XX	
FH	

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FT Modified-site 35 /note= "O-phosphorylated"
FT FT Modified-site 126
FT FT Modified-site 170 /note= "O-phosphorylated"
FT FT Modified-site 170 /note= "O-phosphorylated"
FT FT Peptide 119..124
FT FT Peptide /note= "signature sequence"
FT FT Peptide 131..188
FT FT Peptide /note= "signature sequence"
FT FT Peptide 163..186
FT FT Peptide /note= "signature sequence"
XX
PN WO9964596-A2.
XX
PD 16-DEC-1999.
XX
XX
PF 11-JUN-1999; 99WO-US13281.
XX
PR 12-JUN-1998; 98US-0089029.
PR 29-JUL-1998; 98US-0094575.
PR 14-OCT-1998; 98US-0104624.
XX
PA (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Yue H, Tang YT, Hillman JL, Bandman O, Corley NC;
PI Guegler KJ, Gorgone GA, Baughn MR, Patterson C, Lu DAM;
XX
DR WPI; 2000-116543/10.
DR N-PSDB; AAZ57841.
XX
XX New human polypeptides that regulate gene expression, for treatment,
PT prevention and diagnosis of, e.g. cancer -
PT
XX Claim 1; Page 84; 150pp; English.
XX
XX The present sequence is that of new human protein regulating gene
CC expression PRGE-3. It was deduced from Incyte clone 996352
CC obtained from a kidney tumour cDNA library. PRGE-3 is
CC characterised as a homeodomain protein. It is expressed in
CC reproductive, cardiovascular and urologic tissues associated with
CC cancer and trauma diseases, disorders or conditions. The
CC invention provides PRGE polypeptides (see AA58608-38) and
CC polynucleotides (see AA57839-69), expression vectors, host cells,
CC antibodies, agonists and antagonists. It also provides methods
CC for diagnosing, treating or preventing disorders associated with
CC expression of PRGE.
XX
XX Sequence 230 AA;
SQ
Query Match 64.2%; Score 95; DB 21; Length 230;
Best Local Similarity 81.0%; Pred. NO. 3.7e-06;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DRQIKWIFQNRMRKWKALD 21
DB :|||||
171 ERQIKWIFQNRMRKWKKEHD 191

RESULT 14
AAW11629
ID AAW11629 standard; peptide; 27 AA.
XX
AC AAW11629;
XX
XX 16-OCT-1997 (first entry)
XX
DE Anti-apoptotic protein blocking peptide FPI.
XX
XX Cell permeable; apoptosis; blocking; inhibition; tumour growth;
KW ex vivo purging; in vivo administration; Bcl-2.
XX
OS Synthetic.

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XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= sig_peptide
XX
PN DE19526174-A1.
XX
PD 23-JAN-1997.
XX
PF 18-JUL-1995; 95DE-1026174.
XX
PR 18-JUL-1995; 95DE-1026174.
XX
PA (BRAC/) BRACH M.
PA (HERR/) HERRMANN F.
PA (KIEH/) KIEHNTOPF M.
XX
PI Brach M, Herrmann F, Kiehnopf M;
XX
DR WPI; 1997-088160/09.
XX
XX Peptide(s) that block anti-apoptotic proteins - useful for
PT inhibiting tumour growth
PT
XX Claim 5; Page 7; 7pp; German.
XX
XX The present sequence is a cell permeable anti-apoptotic protein
CC blocking peptide, which can be used to inhibit tumour growth, e.g.
CC by ex vivo purging or (after stabilisation) in vivo
CC administration. The peptide preferably blocks Bcl-2, and comprises
CC a signal peptide mediating cell penetration and a functional
CC sequence corresponding to a Bcl-2 domain.
CC The effect of the peptide on dexamethasone (Dex) induced apoptosis
CC of Bcl-2 expressing tumour cells was examined. Results showed
CC synergistic apoptosis induction in the presence of Dex and the
CC peptide. The extent of apoptosis increased with increasing peptide
CC concentration, e.g. greater than 75% of cells were apoptotic in
CC the presence of Dex plus 100 microg/ml of the peptide. In the
CC presence of Dex plus 100 microg/ml of control peptide (signal
CC peptide), less than 25% of cells were apoptotic.
XX
XX Sequence 27 AA;
SQ
Query Match 63.5%; Score 94; DB 18; Length 27;
Best Local Similarity 94.1%; Pred. NO. 4.7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWIFQNRMRKWK 17
DB :|||||
1 ERQIKWIFQNRMRKWK 17

RESULT 15
AAW27444
ID AAY27444 standard; peptide; 27 AA.
XX
AC AAY27444;
XX
XX 26-NOV-1999 (first entry)
XX
DE Antennapedia internalization sequence in tandem with ezrin fragment.
XX
XX Pharmaceutical; ezrin; mutant; tumor; antennapedia internalization;
KW metastasis; human.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "biotinylated"
FT Modified-site 22
FT /note= "optionally phosphorylated"
XX

```

```

PN WO9947150-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-EF02054.
XX
PR 18-MAR-1998; 98US-0040725.
XX
XX (CURI-) INST CURIE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Arpin M, Crepaldi T, Gautreau A, Louvard D;
DR WPI; 1999-561851/47.
XX
PT New composition for prevention and treatment of tumors and metastasis
PT
XX
PS Example 5; Page 14; 31pp; English.
XX
CC The invention provides a pharmaceutical composition containing ezrin
CC protein, RNA or DNA mutated on tyrosine 353, or a functional fragment
CC or derivative of the ezrin mutant. The new composition is useful for
CC prevention and/or treatment of tumors, and especially metastasis. The
CC present sequence represents an antenapedia internalization sequence in
CC tandem with an ezrin fragment (residues 348-358). This is used in
CC experiments of p85 interaction with phosphorylated ezrin peptides.
XX
SQ Sequence 27 AA;
Query Match 63.5%; Score 94; DB 20; Length 27;
Best Local Similarity 89.5%; Pred. No. 4.7e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 RQIKIWFQNRRMKWKKKTAL 20
DB 1 RQIKIWFQNRRMKWKKLRL 19

```

Search completed: May 30, 2003, 14:50:03
Job time : 91.9766 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 48.8158 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: us-09-643-260-19
Perfect score: 148
Sequence: 1 DRQIKWFQNRMMKKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	100.0	28	9	US-09-847-940B-19
2	148	100.0	28	9	US-09-847-946A-19
3	134	90.5	28	9	US-09-847-940B-18
4	134	90.5	28	9	US-09-847-946A-18
5	101	68.2	26	9	US-10-097-175-101
6	100	67.6	36	10	US-09-731-023A-12
7	98	66.2	17	9	US-10-229-915-1
8	95	64.2	21	10	US-09-150-623-11
9	95	64.2	30	9	US-10-188-947-11
10	94	63.5	34	9	US-10-161-499-79
11	94	63.5	36	10	US-09-731-023A-11
12	94	63.5	217	9	US-10-097-340-129
13	93	62.8	28	10	US-09-214-371-9
14	93	62.8	115	9	US-09-925-299-1169
15	93	62.8	115	10	US-09-925-299-1169
16	92	62.2	16	9	US-09-902-432-32
17	92	62.2	16	9	US-10-007-363-3
18	92	62.2	16	9	US-09-953-031A-10
19	92	62.2	16	9	US-09-981-286A-3

20	92	62.2	16	9	US-09-962-967A-6	Sequence 6, Appli
21	92	62.2	16	9	US-09-912-414-6	Sequence 6, Appli
22	92	62.2	16	9	US-10-071-512A-2	Sequence 2, Appli
23	92	62.2	16	9	US-09-775-052-54	Sequence 54, Appli
24	92	62.2	16	9	US-10-239-804-3	Sequence 3, Appli
25	92	62.2	16	9	US-10-077-555-3	Sequence 3, Appli
26	92	62.2	16	9	US-09-295-189-4	Sequence 4, Appli
27	92	62.2	16	9	US-10-209-421-29	Sequence 29, Appli
28	92	62.2	16	9	US-10-229-915-2	Sequence 2, Appli
29	92	62.2	16	9	US-10-185-084-3	Sequence 3, Appli
30	92	62.2	16	9	US-09-965-876A-1	Sequence 1, Appli
31	92	62.2	16	10	US-09-214-371-43	Sequence 43, Appli
32	92	62.2	16	10	US-09-780-070-38	Sequence 38, Appli
33	92	62.2	16	10	US-09-150-623-9	Sequence 9, Appli
34	92	62.2	16	10	US-09-731-023A-10	Sequence 10, Appli
35	92	62.2	16	10	US-09-854-204-1	Sequence 1, Appli
36	92	62.2	16	10	US-09-900-147-8	Sequence 8, Appli
37	92	62.2	16	10	US-09-792-480-29	Sequence 29, Appli
38	92	62.2	16	10	US-09-785-802A-2	Sequence 2, Appli
39	92	62.2	16	10	US-09-785-802A-5	Sequence 5, Appli
40	92	62.2	16	12	US-10-024-935-12	Sequence 12, Appli
41	92	62.2	17	9	US-10-209-421-30	Sequence 30, Appli
42	92	62.2	17	10	US-09-854-204-19	Sequence 19, Appli
43	92	62.2	17	10	US-09-785-802A-3	Sequence 3, Appli
44	92	62.2	17	12	US-10-007-761-8	Sequence 8, Appli
45	92	62.2	18	10	US-09-785-802A-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-847-940B-19
; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19

Query Match	100.0%	Score 148;	DB 9;	Length 28;
Best Local Similarity	100.0%	Pred. No. 1.3e-14;		
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DRQIKWFQNRMMKKKTALDASALQTE 28		
Db	1	DRQIKWFQNRMMKKKTALDASALQTE 28		

RESULT 2
US-09-847-946A-19
; Sequence 19, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkel, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

Query Match 100.0%; Score 148; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFONRMRKWKKTALDASALQTE 28
|||||
DB 1 DRQIKWFONRMRKWKKTALDASALQTE 28

RESULT 3
US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-18

Query Match 90.5%; Score 134; DB 9; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.3e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKWFONRMRKWKKTALDASALQTE 28
|||||
DB 1 DRQIKWFONRMRKWKKTALDWSWLQTE 28

RESULT 4
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Firdels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18

Query Match 90.5%; Score 134; DB 9; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.3e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKWFONRMRKWKKTALDASALQTE 28
|||||
DB 1 DRQIKWFONRMRKWKKTALDWSWLQTE 28

RESULT 5
US-10-097-175-101
; Sequence 101, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VIBHA B.
; APPLICANT: FINDEIS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101

Query Match 68.2%; Score 101; DB 9; Length 26;
Best Local Similarity 73.9%; Pred. No. 6.1e-08;
Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWFONRMRKWKKTALDASA 24
|||||
DB 1 RQIKWFONRMRKWKKTLEISS 23

RESULT 6
US-09-731-023A-12
; Sequence 12, Application US/09731023A
; Patent No. US20020077283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1


```
; Publication No. US20030044427A1
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-499-79

Query Match      63.5%; Score 94; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 8.1e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRKWK 17
Db 1 ERQIKWFQNRMRKWK 17

RESULT 11
US-09-731-023A-11
; Sequence 11, Application US/09731023A
; Patent No. US20020077283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
; OTHER INFORMATION: Peptide
US-09-731-023A-11

Query Match      63.5%; Score 94; DB 10; Length 36;
Best Local Similarity 65.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKWFQNRMRKWKKTALDASALQT 27
Db 1 ROIKWFQNRMRKWKKGDIWKASFTT 26

RESULT 12
US-10-097-340-129
; Sequence 129, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS

; Publication No. US20030044427A1
; GENERAL INFORMATION:
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, JR.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-129

Query Match      63.5%; Score 94; DB 9; Length 217;
Best Local Similarity 94.1%; Pred. No. 5.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRKWK 17
Db 178 ERQIKWFQNRMRKWK 194

RESULT 13
US-09-214-371-9
; Sequence 9, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pinksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-209377A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
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US-09-214-371-9

Query Match 62.8%; Score 93; DB 10; Length 28;
Best Local Similarity 94.1%; Pred. No. 9.2e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIWIFQNRMRKWK 17
:|||||
DB 12 NRQIKWIFQNRMRKWK 28

RESULT 14

US-09-925-299-1169
; Sequence 1169, Application US/09925299
; Publication No. US2003040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1169
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1169

Query Match 62.8%; Score 93; DB 9; Length 115;
Best Local Similarity 88.2%; Pred. No. 4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIWIFQNRMRKWK 17
:|||||
DB 63 EROVKWIFQNRMRKWK 79

RESULT 15

US-09-925-299-1169
; Sequence 1169, Application US/09925299
; Patent No. US2002005627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1169
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1169

Query Match 62.8%; Score 93; DB 10; Length 115;
Best Local Similarity 88.2%; Pred. No. 4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIWIFQNRMRKWK 17
:|||||
DB 63 EROVKWIFQNRMRKWK 79

Search completed: May 30, 2003, 15:53:23
Job time : 48.8138 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 28.1842 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-19
Perfect score: 148
Sequence: 1 DRQIKWFOFNRKMKWKKTALDASALQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	64.2	24	US-09-419-826-34	Sequence 34, Appl
2	95	64.2	27	US-09-040-725A-2	Sequence 2, Appl
3	94	63.5	34	US-09-347-504-79	Sequence 79, Appl
4	94	63.5	61	US-08-202-044-3	Sequence 3, Appl
5	94	63.5	61	US-08-751-344B-3	Sequence 3, Appl
6	94	63.5	61	US-08-751-344B-6	Sequence 6, Appl
7	94	63.5	61	US-08-751-344B-9	Sequence 9, Appl
8	93	62.8	27	US-09-051-934-51	Sequence 51, Appl
9	93	62.8	27	US-09-051-934-52	Sequence 52, Appl
10	93	62.8	61	US-08-751-344B-7	Sequence 7, Appl
11	92	62.2	16	US-08-928-958-7	Sequence 7, Appl
12	92	62.2	16	US-08-810-540-3	Sequence 3, Appl
13	92	62.2	16	US-08-810-540-6	Sequence 6, Appl
14	92	62.2	16	US-09-072-429-7	Sequence 7, Appl
15	92	62.2	16	US-08-964-302A-6	Sequence 6, Appl
16	92	62.2	16	US-09-116-294-4	Sequence 4, Appl
17	92	62.2	16	US-08-964-614A-4	Sequence 4, Appl
18	92	62.2	16	US-08-849-486-1	Sequence 1, Appl
19	92	62.2	16	US-08-849-486-4	Sequence 4, Appl
20	92	62.2	16	US-09-208-966-54	Sequence 54, Appl
21	92	62.2	16	US-09-308-935-8	Sequence 8, Appl
22	92	62.2	16	US-09-441-416A-6	Sequence 6, Appl
23	92	62.2	16	US-09-296-089-33	Sequence 33, Appl
24	92	62.2	16	US-09-419-826-35	Sequence 35, Appl
25	92	62.2	16	US-09-302-305C-10	Sequence 10, Appl
26	92	62.2	18	US-08-838-545-20	Sequence 20, Appl
27	92	62.2	18	US-09-349-532-20	Sequence 20, Appl

28	92	62.2	20	4	US-09-466-772-3	Sequence 3, Appl
29	89	60.1	42	4	US-08-751-344B-4	Sequence 4, Appl
30	89	60.1	283	1	US-08-583-672-2	Sequence 2, Appl
31	89	60.1	283	2	US-08-202-044-2	Sequence 2, Appl
32	89	60.1	283	4	US-08-751-344B-2	Sequence 2, Appl
33	89	60.1	284	2	US-08-320-148B-2	Sequence 2, Appl
34	89	60.1	284	3	US-08-589-028-6	Sequence 6, Appl
35	89	60.1	284	3	US-08-784-582-6	Sequence 6, Appl
36	89	60.1	284	4	US-08-785-271-6	Sequence 6, Appl
37	89	60.1	284	4	US-09-031-898-2	Sequence 2, Appl
38	89	60.1	302	3	US-08-203-532F-4	Sequence 4, Appl
39	89	60.1	302	3	US-08-950-860-16	Sequence 16, Appl
40	89	60.1	302	4	US-09-078-455-4	Sequence 4, Appl
41	89	60.1	302	5	PCT-US95-01882A-4	Sequence 4, Appl
42	89	60.1	303	2	US-08-203-532F-2	Sequence 2, Appl
43	89	60.1	303	4	US-09-078-465-2	Sequence 2, Appl
44	89	60.1	303	5	PCT-US95-01882A-2	Sequence 2, Appl
45	88	59.5	349	4	US-09-162-524-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-419-826-34
; Sequence 34, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTISTROGEN COMPOSITIONS AND METHODS
; FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: /note= "X = Phosphotyrosine"
US-09-419-826-34

Query Match 64.2%; Score 95; DB 4; Length 24;
Best Local Similarity 85.0%; Pred. No. 8.6e-08;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 RQIKWFOFNRKMKWKKTALD 21
Db 1 RQIKWFOFNRKMKWKKTALD 20

RESULT 2
US-09-040-725A-2
; Sequence 2, Application US/09040725A
; Patent No. 6399584
; GENERAL INFORMATION:
; APPLICANT: Institut Curie
; APPLICANT: CNRS

APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gautreau, Alexis
APPLICANT: Louvard, Daniel
TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated
FILE REFERENCE: 39108200100
CURRENT APPLICATION NUMBER: US/09/040,725A
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (22)
OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2

Query Match 64.2%; Score 95; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 9.8e-08;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKKTALDASALQTE 28
:|||||:|||||:|
DB 1 RQIKWQNRRMKWKKLRQDXEETK 27

RESULT 3

US-09-347-504-79
Sequence 79, Application US/09347504
Patent No. 6399075

GENERAL INFORMATION:

APPLICANT: Howley, Peter M.
APPLICANT: Benson, John
APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
FILE REFERENCE: HMV-041.01
CURRENT APPLICATION NUMBER: US/09/347,504
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 79
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-504-79

Query Match 63.5%; Score 94; DB 4; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.8e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKK 17
:|||||:|||||:|
DB 1 ERQIKWQNRRMKWKK 17

RESULT 4

US-08-202-044-3
Sequence 3, Application US/08202044
Patent No. 5858973

GENERAL INFORMATION:

APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square

CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,044
FILING DATE: 23-FEB-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: MGH-124XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-202-044-3

Query Match 63.5%; Score 94; DB 2; Length 61;
Best Local Similarity 94.1%; Pred. No. 3.4e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKK 17
:|||||:|||||:|
DB 43 ERQIKWQNRRMKWKK 59

RESULT 5

US-08-751-344B-3
Sequence 3, Application US/08751344B
Patent No. 6210960

GENERAL INFORMATION:

APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-3

Query Match 63.5%; Score 94; DB 4; Length 61;
Best Local Similarity 94.1%; Pred. No. 3.4e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
DB 43 ERQIKIWFQNRMMKKK 59

RESULT 6

US-08-751-344B-6
Sequence 6, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-6

Query Match 63.5%; Score 94; DB 4; Length 61;
Best Local Similarity 94.1%; Pred. No. 3.4e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17

DB 43 ERQIKIWFQNRMMKKK 59

RESULT 7

US-08-751-344B-9
Sequence 9, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-9

Query Match 63.5%; Score 94; DB 4; Length 61;
Best Local Similarity 94.1%; Pred. No. 3.4e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
DB 43 ERQIKIWFQNRMMKKK 59

RESULT 8

US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384

;; EARLIER FILING DATE: 1996-01-22
;; EARLIER APPLICATION NUMBER: 60/005,944
;; EARLIER FILING DATE: 1995-10-27
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 51
;; LENGTH: 27
;; TYPE: PRT
;; ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match 62.8%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKKTALD 21
|||||
DB 1 RQIKWQNRRMKWKKHIE 20

RESULT 9

US-09-051-934-52
; Sequence 52, Application US/09051934C
; Patent No. 6028053

GENERAL INFORMATION:

;; APPLICANT: Van der Geer
;; TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/09/051,934C

;; EARLIER FILING DATE: 1998-04-22
;; EARLIER APPLICATION NUMBER: 60/011,799

;; EARLIER FILING DATE: 1996-02-20
;; EARLIER APPLICATION NUMBER: 60/010,384

;; EARLIER FILING DATE: 1996-01-22
;; EARLIER APPLICATION NUMBER: 60/005,944

;; EARLIER FILING DATE: 1995-10-27
;; NUMBER OF SEQ ID NOS: 60

;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 52

;; LENGTH: 27
;; TYPE: PRT

;; ORGANISM: phosphotyrosine binding domain
;; FEATURE:

;; NAME/KEY: MOD_RES
;; LOCATION: (24)

;; OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match 62.8%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKKTALD 21
|||||
DB 1 RQIKWQNRRMKWKKHIE 20

RESULT 10

US-08-751-344B-7
; Sequence 7, Application US/08751344B
; Patent No. 6210960

GENERAL INFORMATION:

;; APPLICANT: Habener M.D., Joel F.
;; APPLICANT: Miller Ph.D., Christopher P.

;; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
;; TITLE OF INVENTION: THEREFOR

;; NUMBER OF SEQUENCES: 29
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Banner & Witcoff, Ltd.
;; STREET: One Financial Center
;; CITY: Boston
;; STATE: MA

;; COUNTRY: US
;; ZIP: 02111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/751,344B
;; FILING DATE: 19-No. 6210960-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/202,044
;; FILING DATE: 23-Feb-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Williams Ph.D., Kathleen M.
;; REGISTRATION NUMBER: 34,380
;; REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)

TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617) 345-9100

;; TELEFAX: (617) 345-9111

;; INFORMATION FOR SEQ ID NO: 7:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 61 amino acids

;; TYPE: amino acid

;; TOPOLOGY: unknown

;; MOLECULE TYPE: peptide

;; HYPOTHETICAL: NO

;; ANTI-SENSE: NO

;; FRAGMENT TYPE: internal

US-08-751-344B-7

Query Match 62.8%; Score 93; DB 4; Length 61;
Best Local Similarity 88.2%; Pred. No. 4.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKK 17

DB 43 ERQVKWQNRRMKWKK 59

RESULT 11

US-08-928-958-7

; Sequence 7, Application US/08928958

; Patent No. 5877282

GENERAL INFORMATION:

;; APPLICANT: NADLER, STEVEN G.

;; APPLICANT: CLEAVELAND, JEFFREY S.

;; APPLICANT: BLAKE, JAMES

;; APPLICANT: HAFAR, OMAR K.

;; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN

;; TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND

;; TITLE OF INVENTION: METHODS OF USE THEREOF

;; NUMBER OF SEQUENCES: 24

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: ROBINS & ASSOCIATES

;; STREET: 90 MIDDLEFIELD ROAD, SUITE 200

;; CITY: MENLO PARK

;; STATE: CA

;; COUNTRY: USA

;; ZIP: 94025

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA: US/08/928,958

;; APPLICATION NUMBER: 12-SEP-1997

;; FILING DATE: 12-SEP-1997

;; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 60/026978

;; FILING DATE: 20-SEP-1996

;; ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWK 17
Db 1 RQIKWIFQNRMRKWK 16

RESULT 12
US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWK 17
Db 1 RQIKWIFQNRMRKWK 16

RESULT 13
US-08-810-540-6
Sequence 6, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-6

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWK 17
Db 1 RQIKWIFQNRMRKWK 16

RESULT 14
US-09-072-429-7
Sequence 7, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kleid, Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: ON0141b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-3714
TELEFAX: (609) 252-4526-
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-072-429-7

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKWK 17
|||||
Db 1 ROIKIWFQNRMRKWK 16

RESULT 15

US-08-964-302A-6
Sequence 6, Application US/08964302A
Patent No. 6015787

GENERAL INFORMATION:
APPLICANT: Potter, David A.
APPLICANT: Skolnik, Paul R.
TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,302A
FILING DATE: 04-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meikiejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 00398/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-302A-6

Query Match 62.2%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ROIKIWFQNRMRKWK 17
|||||
Db 1 ROIKIWFQNRMRKWK 16

Search completed: May 30, 2003, 14:41:33
Job time : 28.1842 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	103	69.6	81	2	B29585	homeotic protein H
2	103	69.6	96	2	A05266	homeotic protein H
3	103	69.6	97	2	C27176	homeotic protein H
4	103	69.6	224	2	S26400	homeotic protein H
5	103	69.6	224	2	A31324	homeotic protein H
6	100	67.6	105	2	A27471	homeotic protein R
7	100	67.6	119	2	A03314	homeotic protein M
8	100	67.6	229	2	A03329	homeotic protein H
9	99	66.9	75	2	I51341	homeo box protein
10	98	66.2	86	2	S08303	homeotic protein H
11	97	65.5	60	2	PC2399	antennapedia-like
12	97	65.5	60	2	PC3400	antennapedia-like
13	96.5	65.2	96	2	S08639	homeotic protein z
14	96	64.9	234	2	S00992	homeotic protein H
15	95	64.2	66	2	S15536	homeotic protein H
16	95	64.2	103	2	A32167	homeotic protein H
17	95	64.2	153	1	WJHU3C	homeotic protein H
18	95	64.2	153	1	WJMSX6	homeotic protein H
19	95	64.2	230	2	S00592	homeotic protein H
20	95	64.2	234	1	S02014	homeotic protein H
21	95	64.2	235	2	A56568	homeotic protein H
22	95	64.2	235	2	S72429	homeotic protein H
23	95	64.2	242	1	A39164	homeotic protein H
24	94.5	63.9	118	2	A24777	homeotic protein H
25	94.5	63.9	118	2	J02073	homeotic protein H
26	94.5	63.9	118	2	B24777	homeotic protein M
27	94.5	63.9	269	1	A43551	homeotic protein H
28	94.5	63.9	269	1	A45578	homeotic protein H
29	94.5	63.9	275	1	WJ2FX2	homeotic protein H

A:Gene: GDB:HXB6
A:Cross-references: GDB:120659; OMIM:142961
A:Map position: 17q21.3-17q21.3
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:19-75/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 96;
Best Local Similarity 70.0%; Pred. No. 5.3e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWFQNRMMKWKTA--LDASALQTE 28
DB 59 ERQIKWFQNRMMKWKESKLLSASQLSAE 88

RESULT 3

C27176
homeotic protein Hox 2.2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C:Accession: C27176
R:Hart, C.P.; Fainsod, A.; Ruddle, F.H.
Genomics 1, 182-195, 1987
A:Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary
A:Reference number: A27176; MUID:88085193; PMID:2891608
A:Accession: C27176
A:Molecule type: DNA
A:Residues: 1-97 <HAR>
A:Cross-references: GB:M18401; MID:g193936; PIDN:AAC27130.1; PID:g3335322
C:Genetics:
A:Gene: Hox-2.2
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:20-76/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 97;
Best Local Similarity 70.0%; Pred. No. 5.4e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWFQNRMMKWKTA--LDASALQTE 28
DB 60 ERQIKWFQNRMMKWKESKLLSASQLSAE 89

RESULT 4

S26400
homeotic protein Hox 2.2 (variant 1) - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
C:Accession: S26400; S26401
R:Shen, W.; Delmer, K.; Simonitch-Eason, T.A.; Lawrence, H.J.; Largman, C.
Nucleic Acids Res. 19, 539-545, 1991
A:Title: Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells
A:Reference number: S26400; MUID:91187672; PMID:1672751
A:Accession: S26400
A:Molecule type: DNA
A:Residues: 1-224 <SHR>
A:Cross-references: EMBL:X58431; NID:g32369; PIDN:CAA41335.1; PID:g32370
A:Experimental source: tissue-type placenta
A:Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60
A:Accession: S26401
A:Molecule type: DNA
A:Residues: 1-139, 'E' <SH2>
A:Cross-references: EMBL:X58431; NID:g32369; PIDN:CAA41336.1; PID:g32371
A:Experimental source: tissue-type placenta
A:Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60
A:Note: the authors did not translate the codons for residues 139, and 140
C:Genetics:
A:Introns: 139/1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation
F:147-203/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 224;
Best Local Similarity 70.0%; Pred. No. 1.3e-07;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWFQNRMMKWKTA--LDASALQTE 28
DB 187 ERQIKWFQNRMMKWKESKLLSASQLSAE 216

RESULT 5

A31324
homeotic protein Hox 2.2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C:Accession: A31324
R:Schughart, K.; Utset, M.F.; Angewiletsch, A.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
A:Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
A:Reference number: A31324; MUID:88289762; PMID:2899893
A:Accession: A31324
A:Molecule type: mRNA
A:Residues: 1-224 <SCH>
A:Cross-references: GB:J03782; MID:g193929; PIDN:AAA37843.1; PID:g387203
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:147-203/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 224;
Best Local Similarity 70.0%; Pred. No. 1.3e-07;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWFQNRMMKWKTA--LDASALQTE 28
DB 187 ERQIKWFQNRMMKWKESKLLSASQLSAE 216

RESULT 6

A27471
homeotic protein R5 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
C:Accession: A27471
R:Faizon, M.; Sanderson, N.; Chung, S.Y.
Gene 54, 23-32, 1987
A:Title: Cloning and expression of rat homeo-box-containing sequences.
A:Reference number: A91576; MUID:87277429; PMID:2886401
A:Accession: A27471
A:Molecule type: DNA
A:Residues: 1-105 <FAL>
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:6-62/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 105;
Best Local Similarity 70.4%; Pred. No. 1.6e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMMKWKKTALDASALQ 27
DB 46 ERQIKWFQNRMMKWKKEKDESOAPT 72

RESULT 7

A03314
homeotic protein m6 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997
C:Accession: A03314; S14043
R:Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
Nature 314, 713-718, 1985
A:Title: Structural analysis of murine genes containing homeo box sequences and their
A:Reference number: A03314; MUID:85188311; PMID:2986010

A:Accession: A03314
A:Molecule type: DNA
A:Residues: 1-119 <COL>
R:Breier, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.
EMBO J. 5, 2209-2215, 1986
A:Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation
A:Reference number: S13785; MUID:87053860; PMID:2877873
A:Accession: S14043
A:Molecule type: DNA
A:Residues: 19-48, 'RI', 51-87 <BRE>
C:Genetics:
A:Gene: m6
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:20-76/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 119;
Best Local Similarity 70.4%; Pred. No. 1.8e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRMKWKTALDASALQT 27
:|||||
Db 60 ERQIKWQNRMRMKWKTALDASALQT 86
:|||||

RESULT 8
A28329
N:Alternate names: homeotic protein Hox A7 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C:Accession: A28329; I49131
R:Kessel, M.; Schulze, F.; Fibi, M.; Gruss, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987
A:Title: Primary structure and nuclear localization of a murine homeodomain protein.
A:Reference number: A28329; MUID:87260976; PMID:2885847
A:Accession: A28329
A:Molecule type: mRNA
A:Residues: 1-229 <RES>
A:Cross-references: GB:M17192; NID:g193906; PIDN:AAA37833.1; PID:g309313
R:Parikh, H.; Shah, S.; Hilt, D.; Peterkofsky, A.
Gene 154, 237-242, 1995
A:Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.
A:Reference number: I49131; MUID:95197009; PMID:7890170
A:Accession: I49131
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42, 'GAG', 46-229 <RES>
A:Cross-references: EMBL:U15972; NID:g664757; PIDN:AAC52160.1; PID:g664758
C:Genetics:
A:Gene: Hoxa7
A:Introns: 126/1
C:Superfamily: homeotic protein Hox A7; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:130-186/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 229;
Best Local Similarity 70.4%; Pred. No. 3.6e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRMKWKTALDASALQT 27
:|||||
Db 170 ERQIKWQNRMRMKWKTALDASALQT 196
:|||||

RESULT 9
I51341
homeo box protein - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
A:Accession: I51341
R:Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988

A:Title: Molecular cloning and characterization of homeobox-containing genes from Atl
A:Reference number: I51341; MUID:88226009; PMID:2897318
A:Accession: I51341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-75 <EJO>
A:Cross-references: GB:M18903; NID:g213797; PIDN:AAA49559.1; PID:g213798
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match 66.9%; Score 99; DB 2; Length 75;
Best Local Similarity 75.0%; Pred. No. 1.6e-07;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRMKWKTALDASA 24
:|||||
Db 42 ERQIKWQNRMRMKWKTALDASA 65
:|||||

RESULT 10
S08303
homeotic protein Hox 2.2 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C:Accession: S08303
R:Wedden, S.E.; Pang, K.; Eichele, G.
Development 105, 639-650, 1989
A:Title: Expression pattern of homeobox-containing genes during chick embryogenesis.
A:Reference number: S08302; MUID:90126373; PMID:2575515
A:Accession: S08303
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WED>
A:Cross-references: EMBL:X16847
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:10-66/Domain: homeobox homology <HOX>

Query Match 66.2%; Score 98; DB 2; Length 86;
Best Local Similarity 66.7%; Pred. No. 2.6e-07;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWQNRMRMKWKTALDASALQTE 28
:|||||
Db 50 ERQIKWQNRMRMKWKTALDASALQTE 79
:|||||

RESULT 11
PC2399
antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)
C:Species: Styela clava
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
C:Accession: PC2399
R:Ge, T.; Lee, H.; Tomlinson, C.R.
Gene 147, 219-222, 1994
A:Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela
A:Reference number: PC2399; MUID:95011617; PMID:7926803
A:Accession: PC2399
A:Molecule type: DNA
A:Residues: 1-60 <GET>
A:Cross-references: GB:S73920; NID:g693714; PIDN:AAB33061.2; PID:g7387472
A:Note: The authors translated the codon ATT for residue 47 as Glu
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match 65.5%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. No. 2.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRMKWKT 17
:|||||

Db 42 DRQKIFQNRMRKWK 58

RESULT 12

PC2400

C:Species: Styela plicata

C:Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997

C:Accession: PC2400

R:Ge, T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A:Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela cl

A:Reference number: PC2399; MUID:95011617; PMID:7928803

A:Accession: PC2400

A:Molecule type: DNA

A:Residues: 1-60 <GET>

A:Note: The authors translated the codon ATA for residue 47 as Glu

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:2-58/Domain: homeobox homology <HOX>

Query Match 65.5%; Score 97; DB 2; Length 60;

Best Local Similarity 94.1%; Pred. No. 2.5e-07;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQKIFQNRMRKWK 17

|||||

Db 42 DRQKIFQNRMRKWK 58

RESULT 13

S08639

C:Species: Brachydanio rerio (zebra fish)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C:Accession: S08639

R:Njollstad, P.R.; Molven, A.; Apold, J.; Fjose, A.

EMBO J. 9, 515-524, 1990

A:Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory

A:Reference number: S08639; MUID:90151628; PMID:1968004

A:Accession: S08639

A:Molecule type: DNA

A:Residues: 1-96 <NJO>

A:Cross-references: EMBL:X17266; NID:962538; PIDN:CAA35170.1; PID:el6657; PID:g1334622

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:8-64/Domain: homeobox homology <HOX>

Query Match 65.2%; Score 96.5; DB 2; Length 96;

Best Local Similarity 69.0%; Pred. No. 4.8e-07;

Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQKIFQNRMRKWK-TALDASALOPE 28

|||||

Db 48 ERQKIFQNRMRKWKETLTSTVPGTE 76

RESULT 14

S00992

C:Species: Xenopus laevis (African clawed frog)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 11-Jan-2002

C:Accession: S00992; A03316; S00590; T01066

R:Cho, K.W.Y.; Goetz, J.; Wright, C.V.E.; Fritz, A.; Hardwicke, J.; de Robertis, E.M.

EMBO J. 7, 2139-2149, 1988

A:Title: Differential utilization of the same reading frame in a Xenopus homeobox gene

A:Reference number: S00991; MUID:88329002; PMID:2901347

A:Accession: S00992

A:Molecule type: DNA

A:Residues: 1-234 <CHO>

A:Cross-references: EMBL:X12500; NID:964743; PIDN:CAA31021.1; PID:g64744

A:Note: 216-Ser and 225-Gln were also found and are interpreted as minor allelic diff

A:Accession: S00993

A:Molecule type: DNA

A:Residues: 83-215, 'S', 217-224, 'O', 226-234 <CHW>

A:Cross-references: EMBL:X12499; NID:964740; PIDN:CAA31020.1; PID:g64742

R:Carasco, A.E.; McGinnis, W.; Gehring, W.J.; De Robertis, E.M.

Cell 37, 409-414, 1984

A:Title: Cloning of an Xenopus laevis gene expressed during early embryogenesis codin

A:Reference number: A03316; MUID:84205675; PMID:6327066

A:Accession: A03316

A:Molecule type: DNA

A:Residues: 134-138, 'S', 140-200 <CAR>

A:Cross-references: GB:K01943; NID:g214242; PIDN:AAA49743.1; PID:g214243

A:Note: the authors translated the codon AGC for residue 200 as Arg

R:Fritz, A.; de Robertis, E.M.

Nucleic Acids Res. 16, 1453-1469, 1988

A:Title: Xenopus homeobox-containing cDNAs expressed in early development.

A:Reference number: S00589; MUID:88157707; PMID:2894634

A:Accession: S00590

A:Molecule type: mRNA

A:Residues: 121-215, 'S', 217-224, 'O', 226-234 <FRI>

A:Cross-references: EMBL:X07101; NID:964738; PIDN:CAA30122.1; PID:g1334649

C:Genetics:

A:Gene: AC1

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:1-234/Product: homeotic protein Hbox1, allelic version PRII #status predicted <MAT1

F:83-215/Product: homeotic protein Hbox1, allelic version PRII #status predicted <MAT>

F:142-198/Domain: homeobox homology <HOX>

Query Match 64.9%; Score 96; DB 2; Length 234;

Best Local Similarity 72.0%; Pred. No. 1.4e-06;

Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQKIFQNRMRKWK-TALDASAL 25

|||||

Db 182 ERQKIFQNRMRKWKESNLSSTL 206

RESULT 15

S15536

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

C:Accession: S15536

R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.;

Genome 31, 745-756, 1989

A:Title: Organization of human class I homeobox genes.

A:Reference number: S15036; MUID:90215256; PMID:2576652

A:Accession: S15536

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-66 <BON>

C:Genetics:

A:Gene: GDB:HOXA7

A:Cross-references: GDB:120647; OMIM:142950

A:Map position: 7p15.3-7p15.3

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:2-58/Domain: homeobox homology <HOX>

Query Match 64.2%; Score 95; DB 2; Length 66;

Best Local Similarity 81.0%; Pred. No. 5.3e-07;

Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQKIFQNRMRKWK-TALD 21

|||||

Db 42 ERQKIFQNRMRKWKKEHD 62

Search completed: May 30, 2003, 14:53:01

Job time : 31.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 14.5526 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKIWFQNRMRKWKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	69.6	224	1	HXB6_HUMAN
2	103	69.6	224	1	HXB6_MOUSE
3	100	67.6	105	1	HXA7_RAT
4	100	67.6	229	1	HXA7_MOUSE
5	99	66.9	75	1	HMSA_SALSA
6	98	66.2	84	1	HXB6_CHICK
7	96.5	65.2	96	1	HXB6_BRARE
8	96	64.9	208	1	HXA7_HETFR
9	96	64.9	234	1	HXC6_XENLA
10	95	64.2	153	1	HXC6_SHEEP
11	95	64.2	230	1	HXA7_HUMAN
12	95	64.2	230	1	HXB5_XENLA
13	95	64.2	234	1	HXC6_NOTVI
14	95	64.2	235	1	HXC6_HUMAN
15	95	64.2	235	1	HXC6_MOUSE
16	95	64.2	242	1	HXA7_COTJA
17	94.5	63.9	81	1	HXA5_BRARE
18	94.5	63.9	269	1	HXB5_HUMAN
19	94.5	63.9	269	1	HXB5_MOUSE
20	94.5	63.9	275	1	HXB5_BRARE
21	94	63.5	48	1	HXB6_XENLA
22	94	63.5	49	1	HXB5_SHEEP
23	94	63.5	71	1	HXA7_SHEEP
24	94	63.5	71	1	HXC5_NOTVI
25	94	63.5	74	1	HM90_APTME
26	94	63.5	76	1	HXC4_RAT
27	94	63.5	78	1	HXA5_SALSA
28	94	63.5	80	1	HXA4_LINSA
29	94	63.5	82	1	HXB5_CHICK
30	94	63.5	86	1	SCR_APTME
31	94	63.5	87	1	HXC5_XENLA
32	94	63.5	93	1	HXB8_PIG
33	94	63.5	105	1	HXB4_BRARE

ALIGNMENTS

RESULT 1

ID	HXB6_HUMAN	STANDARD;	PRT;	224 AA.
AC	P17509; P09068; Q9UGH2; Q9HB11;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Homeobox protein Hox-B6 (Hox-2B) (Hox-2.2) (Hox-2).			
GN	HXB6 OR Hox2B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RC	TISSUE=Placenta;			
RX	MEDLINE=91187672; PubMed=1672751;			
RA	Shen W.-F., Detmer K., Simionitch-Eason T.A., Lawrence H.J.,			
RA	Largman C.;			
RT	"Alternative splicing of the HOX 2.2 homeobox gene in human			
RT	hematopoietic cells and murine embryonic and adult tissues.";			
RL	Nucleic Acids Res. 19:539-545(1991).			
[2]				
RP	SEQUENCE FROM N.A.			
RA	Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.;			
RT	"Expression of HOX genes in T lymphocytes and hairy leukemia cell			
RT	lines.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
[3]				
RP	SEQUENCE FROM N.A.			
RA	Kidd K.K., Busygina V., DeMille M.M.C., Speed W.C., Ruggeri V.,			
RA	Kidd J.R., Pakstis A.J.;			
RT	"Overall linkage disequilibrium in 33 populations for highly			
RT	informative multiallelic haplotypes spanning the HOXB gene cluster.";			
RL	Am. J. Hum. Genet. 67:235-235(2000).			
[4]				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
[5]				
RP	SEQUENCE OF 135-224 FROM N.A.			
RX	MEDLINE=90046832; PubMed=2573064;			
RA	Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,			
RA	Hauser C.A., Simionitch T.A., Hack F.M., Lawrence H.J.;			
RT	"Lineage-restricted expression of homeobox-containing genes in human			
RT	hematopoietic cell lines.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).			
[6]				
RP	PRELIMINARY SEQUENCE OF 136-240 FROM N.A.			
RX	MEDLINE=8504858; PubMed=6091895;			
RA	Levine M., Rubin G.M., Tjian R.;			
RT	"Human DNA sequences homologous to a protein coding region conserved			
RT	between homeotic genes of Drosophila.";			
RL	Cell 38:667-673(1984).			
CC	-1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF			

P18864 rattus norv
P50208 ambystoma m
P09071 xenopus lae
Q9tt89 bos taurus
P09629 homo sapien
P09024 mus musculu
Q31771 xenopus lae
Q04476 xenopus lae
Q00444 homo sapien
P32043 mus musculu
Q9pww4 morone saxa
P15861 brachydanio

34 94 63.5 112 1 HXB7_RAT
35 94 63.5 148 1 HXA5_AMBME
36 94 63.5 209 1 HXA7_XENLA
37 94 63.5 217 1 HXB7_BOVIN
38 94 63.5 217 1 HXB7_HUMAN
39 94 63.5 217 1 HXB7_MOUSE
40 94 63.5 220 1 HXB7_XENLA
41 94 63.5 220 1 HXB7_XENLA
42 94 63.5 222 1 HXC5_HUMAN
43 94 63.5 222 1 HXC5_MOUSE
44 94 63.5 225 1 HXA7_MORSA
45 94 63.5 228 1 HXB6_BRARE

CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -2- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Homeobox-
 CC less; are produced by alternative splicing.
 CC -3- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; X58431; CAA41335.1; -
 DR EMBL; X58431; CAA41336.1; -
 DR EMBL; AJ270993; CAB55909.1; -
 DR EMBL; AF287967; AAG31552.1; -
 DR EMBL; BC014651; AAH14651.1; -
 DR EMBL; M02597; AAA36004.1; -
 DR EMBL; M02571; -; NOT_ANNOTATED_CDS.
 DR PIR; A05266; A05266.
 DR PIR; S26400; S26400.
 DR HSP; P02833; IHOM.
 DR TRANSFAC; T01732; -
 DR Genew; HGNC:5117; HOXB6.
 DR MIM; 142961; -
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW transcription regulation; Alternative splicing.
 FT DOMAIN 127 132 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 146 205 HOMEBOX.
 FT DOMAIN 216 220 POLY-GLU.
 FT VARSPLIC 140 140
 FT VARSPLIC 141 224 MISSING (IN ISOFORM 2).
 FT CONFLICT 24 25 HV -> QL (IN REF. 3 AND 4).
 FT CONFLICT 33 33 A -> R (IN REF. 1).
 FT CONFLICT 60 60 P -> R (IN REF. 1).
 FT CONFLICT 73 73 D -> A (IN REF. 1).
 FT CONFLICT 149 150 GR -> A (IN REF. 5).
 SQ SEQUENCE 224 AA; 25427 MW; D8F96AFAC893D878 CRC64;
 Query Match 69.6%; Score 103; DB 1; Length 224;
 Best Local Similarity 70.0%; Pred. No. 8.1e-09;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;
 Qy 1 DRQIKWQNRMRKWKTA--LDASALQTE 28
 :|||||
 Db 187 ERQIKWQNRMRKWKESKLLSASQSAE 216
 :|||||
 RESULT 2
 HXB6_MOUSE
 ID HXB6_MOUSE STANDARD; PRT; 224 AA.
 AC P09023;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
 GN HOXB6 OR HOXB-6 OR HOX-2.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289762; PubMed=2899893;
 RA Schughart K., Utset M.F., Awgulewitsch A., Ruddle F.H.;
 RT "Structure and expression of Hox-2.2, a murine homeobox-containing
 gene";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91187672; PubMed=1672751;
 RA Shen W.F., Delmer K., Simonitch-Eason T.A., Lawrence H.J.,
 RA Largman C.;
 RT "Alternative splicing of the HOX 2.2 homeobox gene in human
 hematopoietic cells and murine embryonic and adult tissues";
 RL Nucleic Acids Res. 19:539-545(1991).
 RN [3]
 RP SEQUENCE OF 144-224 FROM N.A.
 RX MEDLINE=88054465; PubMed=2890503;
 RA Lonai P., Arman E., Czosnek H., Ruddle F.H., Blatt C.;
 RT "New murine homeoboxes: structure, chromosomal assignment, and
 RT differential expression in adult erythropoiesis";
 RL DNA 6:409-418(1987).
 RN [4]
 RP SEQUENCE OF 140-224 FROM N.A.
 RX MEDLINE=88085193; PubMed=2891608;
 RA Hart C.P., Fainsod A., Ruddle F.H.;
 RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes:
 RT evolutionary and structural comparisons";
 RL Genomics 1:182-195(1987).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -2- SUBCELLULAR LOCATION: Nuclear.
 CC -3- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; M8166; AAA37844.1; -
 DR EMBL; X56459; CAA39834.1; -
 DR EMBL; M18401; AAC27130.1; ALT_SEQ.
 DR EMBL; J03782; AAA37843.1; -
 DR PIR; A31324; A31324.
 DR PIR; B29585; B29585.
 DR PIR; C27176; C27176.
 DR HSP; P02833; IHOM.
 DR TRANSFAC; T01733; -
 DR MGB; MGI:96187; Hoxb6.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; Homeobox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW transcription regulation.
 FT DOMAIN 127 132 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 146 205 HOMEBOX.
 FT DOMAIN 216 220 POLY-GLU.
 FT CONFLICT 186 186 T -> P (IN REF. 3).
 SQ SEQUENCE 224 AA; 25310 MW; E8FC0BDEB57F5C3D CRC64;
 Query Match 69.6%; Score 103; DB 1; Length 224;

Best Local Similarity 70.0%; Pred. No. 8,1e-09;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIWFQNRMMKWKKA--LDASALQTE 28
:|||||
Db 187 ERQIKIWFQNRMMKWKKSLLSASLSAE 216

RESULT 3

HXA7_RAT STANDARD; PRT; 105 AA.
AC P09634;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).
GN HOXA7 OR HOXA-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=87277429; PubMed=2886401;
RA Falzon M., Sanderson N., Chung S.Y.;
RT "Cloning and expression of rat homeo-box-containing sequences.";
RL Gene 54:23-32(1987).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.

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CC EMBL; M16807; -; NOT_ANNOTATED_CDS.
CC PIR; A27471; A27471.
CC HSP; P02833; 9ANT.

DR TRANSFAC; T01707;
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DNA_BIND 1 1
FT NON_TER 1 1
FT DOMAIN 5 64 HOMEBOX.
FT DOMAIN 91 105 GLU-RICH (ACIDIC).
SQ SEQUENCE 105 AA; 12552 MW; 106C1DF938F2864B CRC64;

Query Match 67.6%; Score 100; DB 1; Length 105;
Best Local Similarity 70.4%; Pred. No. 1e-08;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMMKWKKA--LDASALQ 27
:|||||
Db 46 ERQIKIWFQNRMMKWKKEKDESAQT 72

RESULT 4

HXA7_MOUSE STANDARD; PRT; 229 AA.
ID HXA7_MOUSE

AC P02830;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).
GN HOXA7 OR HOXA-7 OR HOX-1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260976; PubMed=2885847;
RA Kessel M., Schulze F., Fibi M., Gruss P.;
RT "Primary structure and nuclear localization of a murine homeodomain
protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=95197009; PubMed=7890170;
RA Parikh H., Shah S., Hilt D., Peterkofsky A.;
RT "Organization, sequence and regulation of expression of the murine
Hoxa-7 gene.";
RL Gene 154:237-242(1995).
RN [3]
RP SEQUENCE OF 126-229 FROM N.A.
RX MEDLINE=85188311; PubMed=2986010;
RA Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;
RT "Structural analysis of murine genes containing homoeo box sequences
and their expression in embryonal carcinoma cells.";
RL Nature 314:713-718(1985).
RN [4]
RP SEQUENCE OF 129-197 FROM N.A.
RX MEDLINE=87053860; PubMed=2877873;
RA Breier G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;
RT "Sequential expression of murine homeo box genes during F9 EC cell
differentiation.";
RL EMBO J. 5:2209-2215(1986).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.

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CC EMBL; M17192; AAA37833.1;
CC EMBL; U15972; AAC52160.1;
CC PIR; A03314; A03314.
CC PIR; A28329; A28329.
CC PIR; S14043; S14043.
CC HSP; P02833; 9ANT.
CC TRANSFAC; T01278;
CC MGD; MGI:96179; Hoxa7.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.

```

FT DOMAIN 118 123 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 129 188 HOMEBOX.
FT DOMAIN 156 159 POLY-ARG.
FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 215 229 POLY-GLU.
FT CONFLICT 43 45 GAG -> APA (IN REF. 1).
SQ SEQUENCE 229 AA; 25682 MW; D36E6BD61D8D5C6F CRC64;

Query Match
Best Local Similarity 67.6%; Score 100; DB 1; Length 229;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWKKTALDASALQT 27
Db :|||||
170 ERQIKWPNRRMKWKKEKDESAQT 196

RESULT 5
HMSA_SALSA STANDARD; PRT; 75 AA.
AC P09636;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein S12-A (Fragment).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Mølven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes
from Atlantic salmon."
RL Gene 62:141-152(1988).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC -----
DR EMBL; M18903; AAA49559.1; -
DR HSPF; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND 1 60 HOMEBOX.
FT NON_TER 75 75
SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match
Best Local Similarity 66.9%; Score 99; DB 1; Length 75;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWKKTALDASA 24
Db :|||||
42 ERQIKWPNRRMKWKKEKDESS 65

RESULT 6
HXB6_CHICK STANDARD; PRT; 84 AA.
AC P14839;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (GHOX-2.2) (Fragment).
OS HOXB6 OR GHOX-2.2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90126373; PubMed=2575515;
RA Wedden S.E., Fang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
embryogenesis."
RL Development 105:639-650(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC -----
DR EMBL; X16847; CAA34744.1; -
DR PIR; S08303; S08303.
DR HSPF; P02833; IHOM.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEIDIA; PARTIAL.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX.
FT NON_TER 84 AA; 10279 MW; BC06B10165B19E71 CRC64;
SQ SEQUENCE 84 AA; 10279 MW; BC06B10165B19E71 CRC64;

Query Match
Best Local Similarity 66.2%; Score 98; DB 1; Length 84;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKKTALDASALQTE 28
Db :|||||
48 ERQIKWPNRRMKWKKEKLLSSQLSAE 77

RESULT 7
HXC6_BRARE STANDARD; PRT; 96 AA.
AC P15862;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (ZF-61) (fragment).
OS HOXC6 OR HOXC6A OR HOXC6 OR ZF-61.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.

```

OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90151628; PubMed=1968004;
RA Njolstad P.R., Molven A., Apold J., Fjose A.;
RT The zebrafish homeobox gene hox-2.2: transcription unit, potential
RL regulatory regions and in situ localization of transcripts.;
EMBO J. 9:515-524(1990).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
CC EMBL: X17266; CAA35170.1;
DR PIR: S08639; S08639.
DR HSP: P02833; 9ANT.
DR ZFIN: ZDB-GENE-990415-113; hoxc6a.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; Homeobox; 1.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; 1.
DR PROSITE: PS00071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66
SQ SEQUENCE 96 AA; 11638 MW; F1ED7AFAA3B640C0 CRC64;

Query Match 65.2%; Score 96.5; DB 1; Length 96;
Best Local Similarity 69.0%; Pred. No. 3.3e-08;
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DROIKWFQNRKMKWK-TALDASALQTE 28
:|||||
Db 48 ERQIKWIFQNRKMKWKTLTSTVPGTE 76

RESULT 8
HXAT_HETFR
ID HXA7_HETFR STANDARD; PRT; 208 AA.
AC Q9IA25;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Homeobox protein Hox-A7.
GN HoxA7.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144096; PubMed=10677514;
RA Kim C.B., Anemiyi C., Bailey W., Kawasaki K., Mezey J., Miller W.,
RA Minoshima S., Shimizu N., Wagner G., Ruddle F.;
RT "Hox cluster genomics in the horn shark, Heterodontus francisci.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1655-1660(2000).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH

CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
CC EMBL: AF224262; AAF44645.1;
DR HSP: P02833; 9ANT.
DR TRANSFAC: T04478;
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00025; ANTENNAPEDIA.
DR PRINTS: PR00024; HOMEOBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; 1.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS00071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 124 129 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 135 194 HOMEOBOX.
SQ SEQUENCE 208 AA; 23786 MW; 71B661AB78E064D0 CRC64;

Query Match 64.9%; Score 96; DB 1; Length 208;
Best Local Similarity 66.7%; Pred. No. 9.2e-08;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKWFQNRKMKWK-TALDASALQ 27
:|||||
Db 176 ERQIKWIFQNRKMKWKTRAGSSST 202

RESULT 9
HXC6_XENLA
ID HXC6_XENLA STANDARD; PRT; 234 AA.
AC P02832;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-c6 (XlHox-1) (AC1).
GN HoxC6 OR XlHox1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329002; PubMed=2901347;
RA Cho K.W.Y., Goetz J., Wright C.V.E., Fritz A., Hardwicke J.,
RA de Robertis E.M.;
RT "Differential utilization of the same reading frame in a Xenopus
RT homeobox gene encodes two related proteins sharing the same
RT DNA-binding specificity.";
RL EMBO J. 7:2139-2149(1988).
RN [2]
RP SEQUENCE OF 121-234 FROM N.A.
RX MEDLINE=88157707; PubMed=2894634;
RA Fritz A., de Robertis E.M.;
RT "Xenopus homeobox-containing cDNAs expressed in early development.";
RL Nucleic Acids Res. 16:1453-1469(1988).
RN [3]
RP SEQUENCE OF 134-200 FROM N.A.
RX MEDLINE=84205675; PubMed=6327066;

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RA Carrasco A.E., McGinnis W., Gehring W.J., de Robertis E.M.;
RT "Cloning of an X. laevis gene expressed during early embryogenesis
RT genes";
RL Cell 37:409-414(1984).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY XENOPUS
CC EMBRYOS.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC -----
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CC -----
DR EMBL; X12499; CAA31020.1; ALT_INIT.
DR EMBL; X12500; CAA31021.1; -.
DR EMBL; K01943; AAA49743.1; -.
DR EMBL; X07101; CAA30122.1; -.
DR PIR; A03316; A03316.
DR PIR; S00590; S00590.
DR PIR; S00992; S00992.
DR HSP; P02833; 9ANT.
DR TRANSFAC; T01745; -.
DR TRANSFAC; T01746; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT CHAIN 1 234 HOMEOBOX PROTEIN HOX-C6 PRII.
FT CHAIN 83 234 HOMEOBOX PROTEIN HOX-C6 PRI.
FT DOMAIN 122 127 ANTP-TYPE HEXAPEPTIDE.
FT DOMAIN 141 200 HOMEOBOX.
FT VARIANT 139 139 T -> S.
SQ SEQUENCE 234 AA; 26689 MW; 4C371CC5252D2C58 CRC64;

Query Match 64.9%; Score 96; DB 1; Length 234;
Best Local Similarity 72.0%; Pred. No. 1e-07;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKKTDAL 25
DB 182 ERQIKWQNRRMKWKKESLSTL 206
:|||||:
182 ERQIKWQNRRMKWKKESLSTL 206

RESULT 10
HXK6_SHEEP
ID HXK6_SHEEP STANDARD; PRT; 153 AA.
AC P49925;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6.
GN HOXC6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;

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[1]
RN SEQUENCE FROM N.A.
RP Cosby N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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CC -----
DR EMBL; U33049; AAA75473.1; -.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 40 45 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 59 118 HOMEOBOX.
FT DOMAIN 86 89 POLY-ARG.
FT DOMAIN 126 130 POLY-GLY.
FT DOMAIN 139 153 GLU/LYS-RICH.
SQ SEQUENCE 153 AA; 17804 MW; 291E24399159621E CRC64;

Query Match 64.2%; Score 95; DB 1; Length 153;
Best Local Similarity 72.0%; Pred. No. 9.4e-08;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKKTDAL 25
DB 100 ERQIKWQNRRMKWKKESLSTL 124
:|||||:
100 ERQIKWQNRRMKWKKESLSTL 124

RESULT 11
HXA7_HUMAN
ID HXA7_HUMAN STANDARD; PRT; 230 AA.
AC P31268; O43486; O43368; Q9UDM1; Q9NSC8; O95655;
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).
GN HOXA7 OR HOX1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Polakowska R., LaCelle P.T.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99023755; PubMed=9804983;
RA McIlhatton M.A., Bremner P.S., McMullin M.F., Maxwell A.P.,
RA Winter P.C., Lappin T.R.;
RT "Sequence characterisation and expression of homeobox HOX A7 in the
RT multi-potential erythroleukaemic cell line TF-1."
RL Biochim. Biophys. Acta 1442:329-333(1998).

```

RN [3] SEQUENCE FROM N.A.
 RA Bradshaw H., Hinds K., Keppler D.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-2036265; PubMed-10911612;
 RA Kim M.H., Jin H., Seol E.Y., Yoo M., Park H.W.;
 RL "Sequence analysis and tissue specific expression of human HOXA7";
 RL Mol. Biotechnol. 14:19-24(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Placenta;
 RC Abrechtsen R., Wewer U.;
 RA Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE OF 1-91 FROM N.A.
 RA Cho M., Kim M.H., Hwang C.Y., Min W.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN SEQUENCE OF 130-195 FROM N.A.
 RP MEDLINE-90215256; PubMed-2576652;
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaetano G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
 RL "Organization of human class I homeobox genes";
 RL Genome 31:745-756(1989).
 CC [1]- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC [2]- SUBCELLULAR LOCATION: Nuclear.
 CC [3]- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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 CC
 CC EMBL; AF026397; AB94604.1; -
 CC EMBL; AJ005814; CAA06713.1; -
 CC EMBL; AC004080; -; NOT ANNOTATED_CDS.
 CC EMBL; AF032095; AAD01939.2; -
 CC EMBL; U92543; AD00727.1; -
 CC EMBL; X84803; CAA59270.1; -
 CC EMBL; X84804; CAA59270.1; JOINED.
 CC PIR; S15536; S15536.
 CC HSP; P02833; 9ANT.
 CC TRANSFAC; T01705; -
 CC Genew; HGNC:5108; HOXA7.
 CC MIM; 142950; -
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox.1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEBOX.
 CC PRODom; PD000010; Homeobox.1.
 CC SMART; SM00389; HOX.1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00027; HOMEBOX_1; 1.
 CC PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 119 124 ANTP-TYPE HEXAPEPTIDE.
 FT DOMAIN 130 189 HOMEBOX.
 FT DOMAIN 157 160 POLY-ARG.
 FT DOMAIN 196 199 POLY-ALA.
 FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 223 230 POLY-GLU.
 FT CONFLICT 18 18 T -> A (IN REF. 3).
 FT CONFLICT 75 76 DA -> RR (IN REF. 6).
 FT CONFLICT 75 78 MISSING (IN REF. 5).
 FT

FT CONFLICT 174 174 I -> V (IN REF. 4).
 FT CONFLICT 194 195 PT -> RL (IN REF. 5).
 FT CONFLICT 195 195 T -> I (IN REF. 7).
 FT CONFLICT 222 222 D -> Y (IN REF. 5).
 SQ SEQUENCE 230 AA; 25385 MW; 682F1991F1BBED21 CRC64;
 Query Match 64.2%; Score 95; DB 1; Length 230;
 Best Local Similarity 81.0%; Pred. No. 1.5e-07;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DRQIKWIFQNRMRKWKKTALD 21
 :|||||
 DB 171 ERQIKWIFQNRMRKWKKEHD 191
 RESULT 12
 -HXB5_XENLA
 ID HXB5_XENLA STANDARD; PRT; 230 AA.
 AC P09019;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B5 (XlHox-4) (Xhox-1B) (Fragment).
 GN HXB5 OR XLHBOX4.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88157707; PubMed-2894634;
 RA Fritz A., de Robertis E.M.;
 RL "Xenopus homeobox-containing cDNAs expressed in early development.";
 RL Nucleic Acids Res. 16:1453-1469(1988).
 RN [2]
 RP SEQUENCE OF 155-214 FROM N.A.
 RX MEDLINE-86274626; PubMed-3015593;
 RA Harvey R.P., Tabin C.J., Melton D.A.;
 RL "Embryonic expression and nuclear localization of Xenopus homeobox
 (Xhox) gene products";
 RL EMBO J. 5:1237-1244(1986).
 CC [1]- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC [2]- SUBCELLULAR LOCATION: Nuclear.
 CC [3]- DEVELOPMENTAL STAGE: EMBRYO.
 CC [4]- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC
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 CC
 CC EMBL; X07104; CAA30125.1; -
 CC EMBL; M26883; AAA49755.1; -
 CC PIR; S00592; S00592.
 CC HSP; P02833; 1SAN.
 CC TRANSFAC; T03764; -
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox.1.
 CC PRODom; PD000010; Homeobox.1.
 CC SMART; SM00389; HOX.1.
 CC PROSITE; PS00027; HOMEBOX_1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT NON_TER 1 1

FT	DOMAIN	137	142	ANTP-TYPE HEXAPEPTIDE.
FT	DNA_BIND	155	214	HOMEBOX.
SQ	SEQUENCE	230 AA;	25276 MW;	AD040C030F85532B CRC64;

Query Match 64.2%; Score 95; DB 1; Length 230;
Best Local Similarity 58.8%; Pred. NO. 1.5e-07;
Matches 20; Conservative 2; Mismatches 4; Indels

Qy 1 DROIKIWFQNRMKWK -----TALDASALQ 26
:|||||:|||||:|:|
Db 196 EROIKIWFQNRMKWKDKNKLKMSLATGSSAFQ 229

RESULT 13

NCBI	HOMEBOX
HKX6_NOTVI	STANDARD; PRT; 234 AA.
ID	HXC6_NOTVI
AC	P14858; P14857;
DT	01-APR-1990 (Rel. 14, Created)
DT	01-APR-1990 (Rel. 14, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Homeobox protein Hox-C6 (NvHox-1) (FH-2).
DN	HXC6 OR NVHOXI.
GN	Notophthalmus viridescens (Eastern newt) (<i>Triturus viridescens</i>).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC	Notophthalmus.
OX	NCBI_TaxID=8316;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89210814; PubMed=2907476;
RA	Savard P., Gates P.B., Brookes J.P.;
RT	"Position dependent expression of a homeobox gene transcript in
RT	relation to amphibian limb regeneration.";
RL	EMBO J. 7:4275-4282(1988).
RL	[2]
RP	SEQUENCE OF 131-234 FROM N.A.
RX	MEDLINE=90091821; PubMed=2574663;
RA	Tabin C.J.;
RT	"Isolation of potential vertebrate limb-identity genes.";
RL	Development 105:813-820(1989).
CC	- I - FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC	A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC	SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC	- I - SUBCELLULAR LOCATION: Nuclear.
CC	- I - SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.

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CC
DR EMBL; X13957; CAA32139.1; -
DR EMBL; X16848; CAA34745.1; -

DR PIR; S02014; S02014.
DR PIR; S07819; S07819.
DB HSSD. P02023. 0 AMT

DR TRANSFAC; T01747; -.
DR InterPro; IPR001827;

DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.

DR PRINTS; PR00024; HOME0BOX.
DR Produm; PD000010; Homeobox; 1.
DR SWARM; SW00200; voc; 1

DR SMART; SM00389; HOA; 1.
DR PROSITE; PS00027; HOMEBOX_1;
DR PROSITE; PS00032; ANTENNAPEDIA

DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Development
KW Transcription regulation.

FT	DOMAIN	122	127

FT	DNA_BIND	141	200	HOMEBOX.
SQ	SEQUENCE	234	AA; 26901	MW; EA15EED91ED294B0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 234;
Best Local Similarity 72.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 2; Mismatches 5; Indels

QY	1	DRQIKWIFQRRRMKWKKTALDASAL	25
		:	
Db	182	ERQIKWIFQRRRMKWKKESLTL	206

RESULT 14

HC6_HUMAN	HC6_HUMAN	STANDARD;	PRT;	235 AA.
ID	HC6_HUMAN	STANDARD;	PRT;	235 AA.
AC	P09630;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Homeobox protein Hox-C6 (Hox-3C) (HHO.C6) (CP25).			
DE	HOXC6 OR HOXC3C.			
GN	HoxC6			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RA	[1]			
RA	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	MEDLINE=87260899; PubMed=2885844;			
RA	Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,			
RA	Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,			
RA	Peschle C.;			
RT	"Two human homeobox genes, cl and c8: structure analysis and			
RT	expression in embryonic development.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).			
RL	[2]			
RA	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	MEDLINE=88262550; PubMed=2898768;			
RA	Simeone A., Pannese M., Acampora D., D'Esposito M., Boncinelli E.;			
RA	"At least three human homeoboxes on chromosome 12 belong to the same			
RT	transcription unit.";			
RT	Nucleic Acids Res. 16:5379-5390(1988).			
RL	[3]			
RA	SEQUENCE FROM N.A. (ISOFORM 2).			
RA	MEDLINE=97024425; PubMed=8870663;			
RA	Chariot A., Castronovo V., Le P., Gillet C., Sobel M.E., Gielen J.;			
RT	"Cloning and expression of a new HOXC6 transcript encoding a			
RT	repressing protein.";			
RL	Biochem. J. 319:91-97(1996).			
RL	[4]			
RA	SEQUENCE OF 141-206 FROM N.A.			
RA	MEDLINE=90215256; PubMed=2576652;			
RA	Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,			
RA	Gaudino G., Stornaiuolo A., Carlero M., Faiella A., Simeone A.;			
RT	"Organization of human class I homeobox genes.";			
RL	Genome 31:745-756(1989).			
CC	-1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF			
CC	A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH			
CC	SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are			
CC	produced by alternative splicing.			
CC	-1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; S82986; AAA46892.1; -			
DR	EMBL; M16938; AAA36007.1; -			


```

DR PIR: B28030; WJHU3C.
DR HSP: P02833; 9ANT.
DR TRANSFAC: T01742; -.
DR Genew; HGNC:5128; HOXC6.
DR MIM; 142972; -.
DR InterPro; IPR001827; Antennapedia.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation; Alternative splicing.
FT DOMAIN 122 127 ANTP-TYPE HEXAPEPTIDE.
FT DOMAIN 141 200 HOMEBOX.
FT DOMAIN 168 171 POLY-ARG.
FT DOMAIN 208 212 POLY-GLY.
FT DOMAIN 221 235 GLU/LYS-RICH.
FT VARSPIC 1 82 MISSING (IN ISOFORM 1).
FT CONFLICT 218 218 M -> L (IN REF. 3).
SQ SEQUENCE 235 AA; 26933 MW; BD68870347CB71C0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 235;
Best Local Similarity 72.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRKWKKTALDASAL 25
Db 182 EROIKIWFQNRMRKWKKSNTL 206

RESULT 15
HXC6_MOUSE STANDARD; PRT; 235 AA.
AC P10629; O61683;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (Hox-3.3) (Hox-6.1).
GN HOXC6 OR HOXC-6 OR HOXC-3.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94131843; PubMed=7905473;
RA Shmied S.M., Gaunt S.J., Coletta P.L., Geada A.M., Sharpe P.T.;
RT "Spatial localisation of transcripts of the Hox-C6 gene.";
RL J. Anat. 183:515-523(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92102952; PubMed=1684715;
RA Coletta P.L., Shmied S.M., Chaudhuri C., Mueller U., Clarke J.P.,
RA Sharpe P.T.;
RT "Characterisation of the murine Hox-3.3 gene and its promoter.";
RL Mech. Dev. 35:129-142(1991).
RN [3]
RP SEQUENCE OF 15-235 FROM N.A.
RC TISSUE-Spleen, and Bone marrow;
RX MEDLINE=88329001; PubMed=2901346;
RA Kongsuwan K., Webb E., Housiaux P., Adams J.M.;
RT "Expression of multiple homeobox genes within diverse mammalian
RT haemopoietic lineages.";
RL EMBO J. 7:2131-2138(1988).
RN [4]
RP SEQUENCE OF 131-235 FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE=88328811; PubMed=2458223;
RA Sharpe P.T., Miller J.R., Evans E.P., Burtenshaw M.D., Gaunt S.J.;
RT "Isolation and expression of a new mouse homeobox gene.";

```

Search completed: May 30, 2003, 15:49:10

2.

GenCore.version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 68.8947 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: us-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKIWFONRRMKWKKTALDASALQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.5	74.7	274	5 Q9XYT7	Q9xyt7 cassiopea x
2	101.5	68.6	627	5 Q95YH8	Q95yh8 daphnia mag
3	98	66.2	93	5 Q9U9Z5	Q9u9z5 lingua ung
4	97	65.5	60	5 Q26375	Q26375 styela clav
5	97	65.5	181	5 Q26611	Q26611 styela plic
6	97	65.5	194	5 Q26478	Q26478 styela cliv
7	96.5	65.2	231	13 Q9PVM4	Q9pvm4 brachydanio
8	96	64.9	101	13 Q9PSD5	Q9psd5 gallus gall
9	95.5	64.5	82	13 Q9PVS0	Q9pvs0 oryzias lat
10	95	64.2	219	13 Q90VZ9	Q90vz9 gallus gall
11	94.5	63.9	43	13 Q57359	Q57359 brachydanio
12	94.5	63.9	80	5 Q05008	Q05008 artemia san
13	94.5	63.9	230	11 Q9CZV0	Q9czv0 mus musculus
14	94.5	63.9	276	13 Q9PWM0	Q9pwm0 brachydanio
15	94.5	63.9	348	5 Q8WRC6	Q8wrc6 artemia san
16	94	63.5	39	13 Q57368	Q57368 brachydanio

17	94	63.5	46	13 Q9PVR9	Q9pvr9 oryzias lat
18	94	63.5	51	5 Q26407	Q26407 ctenodrilus
19	94	63.5	51	5 Q23743	Q23743 ctenodrilus
20	94	63.5	51	5 Q27413	Q27413 ctenodrilus
21	94	63.5	57	13 Q9PVR8	Q9pvr8 oryzias lat
22	94	63.5	58	5 Q9Y188	Q9y188 priapulid c
23	94	63.5	58	5 Q25208	Q25208 junonia coe
24	94	63.5	58	13 Q57362	Q57362 brachydanio
25	94	63.5	59	5 Q8WRM9	Q8wrm9 lithobius a
26	94	63.5	59	5 Q9NB42	Q9nb42 anopheles g
27	94	63.5	59	13 Q9PVR5	Q9pvr5 oryzias lat
28	94	63.5	60	5 Q77139	Q77139 archegozete
29	94	63.5	60	5 Q77143	Q77143 archegozete
30	94	63.5	60	13 Q8QGL8	Q8qgl8 petromyzon
31	94	63.5	60	13 Q8QGL7	Q8qgl7 petromyzon
32	94	63.5	60	13 Q8QGL6	Q8qgl6 petromyzon
33	94	63.5	60	13 Q8QGL5	Q8qgl5 petromyzon
34	94	63.5	60	13 Q8QGL3	Q8qgl3 petromyzon
35	94	63.5	60	13 Q8QGL2	Q8qgl2 petromyzon
36	94	63.5	61	5 Q27910	Q27910 polyandroca
37	94	63.5	63	5 Q77138	Q77138 archegozete
38	94	63.5	66	13 Q57356	Q57356 brachydanio
39	94	63.5	69	5 Q9U9T4	Q9u9t4 nereis vire
40	94	63.5	69	5 Q9BMF7	Q9bmf7 haliotis as
41	94	63.5	70	5 Q967W5	Q967w5 folsomia ca
42	94	63.5	71	13 Q9PVS1	Q9pvs1 oryzias lat
43	94	63.5	71	13 Q9PVS3	Q9pvs3 oryzias lat
44	94	63.5	73	5 Q9Y186	Q9y186 priapulid c
45	94	63.5	74	13 Q57367	Q57367 brachydanio

ALIGNMENTS

RESULT 1

Q9XYT7 ID Q9XYT7 PRELIMINARY; PRT; 274 AA.

AC Q9XYT7; 01-NOV-1999 (TRENBLREL. 12, Created)
 DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
 DE SCOX-3 homeodomain protein (Fragment).
 GN SCOX-3.
 OS Cassiopea xamachana.
 OC Eukaryota; Metazoa; Cnidaria; Scyphozoa; Rhizostomeae; Cassiopeidae;
 OC Cassiopea.
 OX NCBI_TaxID=12993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuhn K., Streit B., Schlerwater B.;
 RT "Isolation of Hox genes from the scyphozoan Cassiopeia xamachana:
 RT Implications for the early evolution of Hox genes.";
 RL J. Exp. Zool. 0:0-0(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF124553; AAC32577.1;
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox.1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 274 AA; 31041 MW; 58EE91F6E540C3A9 CRC64;

Query Match 74.7%; Score 110.5; DB 5; Length 274;
 Best Local Similarity 67.7%; Pred. No. 9.6e-09;
 Matches 21; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

QY 1 DRQKIWFQNRMRMKWK---TALDASALQTE 28
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

RESULT 2

ID Q95YH8 PRELIMINARY; PRT; 627 AA.
AC Q95YH8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Homeotic protein.
OS Daphnia magna.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Diplostroca;
OC Cladocera; Anomopoda; Daphniidae; Daphnia.
OX NCBI_TaxID=35525;
RN [1]
RP SEQUENCE FROM N.A.
RA Shiga Y., Yasumoto R., Hayashi S., Yamagata H.;
RT "Functional diversification of homeotic protein Antennapedia in
RT arthropod evolution."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB069680; BAB64346.1; -
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR ProDom: PD000010; Homeobox; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; UNKNOWN_1.
DR PROSITE: PS00027; HOMEBOX_1; UNKNOWN_1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
SQ SEQUENCE 627 AA; 69425 MW; A3A7962761CB5D10 CRC64;

Query Match 68.6%; Score 101.5; DB 5; Length 627;
Best Local Similarity 69.0%; Pred. No. 5.2e-07;
Matches 20; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 DRQKIWFQNRMRMKWK---KTALDASALQ 26
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

RESULT 3

ID Q909Z5 PRELIMINARY; PRT; 93 AA.
AC Q909Z5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Sex combs reduced homeodomain protein (Fragment).
OS Lingula unguis.
OC Eukaryota; Metazoa; Brachiopoda; Linguliformea; Lingulata; Lingulida;
OC Linguloidea; Lingulidae; Lingula.
OX NCBI_TaxID=7574;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99318125; PubMed-10391241;
RX de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution."
RL Nature 399:772-776(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF144674; AAD45589.1; -
DR HSSP: P02833; 1SAN.
DR TRANSFAC: T03872; -
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR00047; HTH_repressr.
DR Pfam: PF00046; Homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.

DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

Query Match 66.2%; Score 98; DB 5; Length 93;
Best Local Similarity 67.9%; Pred. No. 2.5e-07;
Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMRMKWKKTALDASALQTE 28
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

RESULT 4

ID Q26375 PRELIMINARY; PRT; 60 AA.
AC Q26375;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE DNA binding protein Ahox2 (Fragment).
GN AHOX2.
OS Styela clava (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95011617; PubMed-7926803;
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an antennapedia-like homeobox gene in the ascidians
RT Styela clava and S. plicata."
RL Gene 147:219-222(1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: S73920; AB33061.2; -
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR00047; HTH_repressr.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 7630 MW; F506301E9679BA25 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 60;
Best Local Similarity 94.1%; Pred. No. 2.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMRMKWK 17
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2124 MW; 5DC0379A30DF0137 CRC64;

RESULT 5

ID Q26611 PRELIMINARY; PRT; 181 AA.
AC Q26611;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Homeobox protein (Fragment).
OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7726;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-ASCIDIAN;
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
RL Styela clava and plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05600; AAA16288.1; -.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_repressr.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 181;
Best Local Similarity 94.1%; Pred. No. 7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRMKWK 17
Db 80 DRQVKIWQNRMRMKWK 96

RESULT 6
Q26478
ID Q26478 PRELIMINARY; PRT; 194 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Homeobox protein (Fragment).
OS Styela clava (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ASCIDIAN;
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
RL Styela clava and plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05571; AAA16226.1; -.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_repressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 194 AA; 21886 MW; 8AD1B15B3E4800BC CRC64;

Query Match 65.5%; Score 97; DB 5; Length 194;
Best Local Similarity 94.1%; Pred. No. 7.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRMKWK 17
Db 80 DRQVKIWQNRMRMKWK 96

us-09-643-260-19.rspt

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Db 52 DRQVKIWQNRMRMKWK 68

RESULT 7
Q9PWW4
ID Q9PWW4 PRELIMINARY; PRT; 231 AA.
AC Q9PWW4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Homeobox protein.
GN HOXC6A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RT "Zebrafish hox clusters and vertebrate genome evolution.";
RL Science 282:1711-1714(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF071265; AAD15958.1; -.
DR HSP; P02833; 9ANT.
DR TRANSFAC; T03667; -.
DR ZFIN; ZDB-GENE-990415-113; hoxc6a.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 231 AA; 26733 MW; 65164A13541D7E8A CRC64;

Query Match 65.2%; Score 96.5; DB 13; Length 231;
Best Local Similarity 69.0%; Pred. No. 1.1e-06;
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQIKWIFQNRMRMKWK-TALDASALQTE 28
Db 183 ERQIKWIFQNRMRMKWKETNLTSTVPGTE 211

RESULT 8
Q9PSD5
ID Q9PSD5 PRELIMINARY; PRT; 101 AA.
AC Q9PSD5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE HOXC-6 product (HOXC-6 protein).
GN HOXC-6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-WHOLE 10 DAY OLD EMBRYO;
RX MEDLINE=95151548; PubMed=7848839;
RA Gaunt S.J.;
RT "Conservation in the Hox code during morphological evolution.";
RL Int. J. Dev. Biol. 38:549-552(1994).

```

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; X60114; CAB94115.1; -;
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 101 AA; 11592 MW; 9837DB0AAB85546D CRC64;

Query Match 64.9%; Score 96; DB 13; Length 101;
 Best Local Similarity 72.0%; Pred. No. 5.5e-07;
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

DT 1 DRQIKWFQNRMRKWKKTALDASAL 25
 DB 49 ERQIKWFQNRMRKWKKSLSSTL 73

RESULT 9
 Q9PVS0 PRELIMINARY; PRT; 82 AA.
 AC Q9PVS0;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TRENBLrel. 20, Last annotation update)
 DE HOXB5A (Fragment).
 GN HOXB5A.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RL "Hox genes of the medaka fish Oryzias latipes.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026959; BAA86242.1; -;
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 9939 MW; 6B6828D280511888 CRC64;

Query Match

Best Local Similarity 64.5%; Score 95.5; DB 13; Length 82;
 Matches 21; Conservative 1; Mismatches 4; Indels 9; Gaps 1;

DT 1 DRQIKWFQNRMRKWKKTALDASALQ 26
 DB 47 ERQIKWFQNRMRKWKKSLSLTAPGASHQ 81

RESULT 10

Q90VZ9 PRELIMINARY; PRT; 219 AA.
 AC Q90VZ9;

DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 GN HOXA-7 protein (Homeodomain transcription factor HOXA-7).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21255551; PubMed=11357191;
 RA Gaunt S.J.;
 RT "Gradients and forward spreading of vertebrate Hox gene expression
 detected using a Hox/lacZ transgene.";
 RL Dev. Dyn. 221:26-36(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oberg K.C., Eichele G.;
 RT "Hox gene expression and regulation in the presumptive wing region of
 the chick lateral plate mesoderm (Abstract # 286).";
 RL Dev. Biol. 210:228-228(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oberg K.C., Pira C.U., Creamer D.H., Revelli J.-P., Eichele G.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ291729; CAC37629.1; -;
 DR EMBL; AF408695; AAL01899.1; -;
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
 DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 SQ SEQUENCE 219 AA; 24952 MW; 4BAE9046D52C0705 CRC64;

Query Match 64.2%; Score 95; DB 13; Length 219;
 Best Local Similarity 70.8%; Pred. No. 1.7e-06;
 Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRKWKKTALDASA 24
 DB 170 ERQIKWFQNRMRKWKKEESS 193

RESULT 11

OS7359 PRELIMINARY; PRT; 43 AA.
 AC OS7359;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE HOXA5 protein (Fragment).
 GN HOXB5B OR HOXA5.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear
 expression patterns in the trunk.";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y14526; CAA74861.1; -;
 DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.

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DR PRODOM: PD000010; Homeobox; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DEA596 CRC64;

Query Match
Best Local Similarity 63.9%; Score 94.5; DB 13; Length 43;
Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DROIKWQNRKMKK-TALDASALQT 27
Db 9 ERQIKWQNRKMKKDKNKLKMSLAT 36

RESULT 12
ID Q05008 PRELIMINARY; PRT; 80 AA.
AC Q05008;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Antp protein (Fragment).
GN ANTP
OS Artemia franciscana (Brine shrimp) (Artemia franciscana).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=6661;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN-NORTH ARM OF GREAT SALT LAKE;
RA Averof M., Akam M.;
RT "HOM/HOX genes in a crustacean: implication for the origin of insect
and crustacean body plans.";
RL Curr. Biol. 3:73-78(1993).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: X70077; CAA45682.1;
DR HSP; P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_repressor.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR PRODOM: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9878 MW; 48472705C0EDFCB7 CRC64;

Query Match
Best Local Similarity 63.9%; Score 94.5; DB 5; Length 80;
Matches 18; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 DROIKWQNRKMKK---KTALDASAL 25
Db 42 ERQIKWQNRKMKKKNKSKYDSGL 69

RESULT 13
Q9CZV0 PRELIMINARY; PRT; 230 AA.
ID Q9CZV0;
AC Q9CZV0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Homeobox B5.
GN HOXB5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaic I., Pesole G., Quackenbush J.,
RA Schriml L. M., Staali F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M. F.,
RA Brownstein M. J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,
RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whittaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AK012146; BAB28059.1;
DR HSP; P02833; 1SAN.
DR MGD; MGI:96186; Hoxb5.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00025; ANTENNAPEDIA.
DR PRINTS: PR00024; HOMEBOX.
DR PRODOM: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; UNKNOWN_1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 230 AA; 25269 MW; CBF919E38F2196C6 CRC64;

Query Match
Best Local Similarity 63.9%; Score 94.5; DB 11; Length 230;
Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DROIKWQNRKMKK-TALDASALQT 27
Db 196 ERQIKWQNRKMKKDKNKLKMSLAT 223

RESULT 14
Q9PWW0 PRELIMINARY; PRT; 276 AA.
ID Q9PWW0;
AC Q9PWW0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Homeobox protein.
GN HOXB5.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA HO R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RT "Zebrafish box clusters and vertebrate genome evolution.";
RL Science 282:1711-1714(1998).

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CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL; AF071253; AAD15946.1; -

DR HSP; P02833; 1SAN.

DR TRANSFAC; T03633; -

DR ZFIN; ZDB-GENE-000823-6; hoxb5b.

DR InterPro; IPR001827; Antennapedia.

DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00025; ANTENNAPEDIA.

DR PRINTS; PR00024; HOMEBOX.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00032; ANTENNAPEDIA; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS00071; HOMEBOX_2; 1.

KW DNA-binding; Homeobox; Nuclear protein.

SQ SEQUENCE 276 AA; 30862 MW; C2DD9824CF2A1954 CRC64;

Query Match 63.9%; Score 94.5; DB 13; Length 276;

Best Local Similarity 67.9%; Pred. NO. 2.6e-06;

Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQIKWFQNRMRMKWK-TALDASALOT 27

Db :|||||:|||||:|||||:|||||:|||||

242 ERQIKWFQNRMRMKWKONKLSL 269

RESULT 15

Q8WRG6

ID Q8WRG6 PRELIMINARY; PRT; 348 AA.

AC Q8WRG6;

DT 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Antennapedia.

GN ANTP.

OS Artemia franciscana (Brine shrimp) (Artemia franciscana).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;

OC Artemiidae; Artemia.

OX NCBI_TaxID=6661;

RN [1]

RP SEQUENCE FROM N.A.

RA Ronshaugen M.R., McGinnis N., McGinnis W.;

RT "Hox protein mutation and evolution of the insect body plan.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF435786; AAL67685.1; -

DR InterPro; IPR001827; Antennapedia.

DR InterPro; IPR001356; Homeobox.

DR InterPro; IPR00047; HTH_repressr.

DR Pfam; PF00046; Homeobox; 1.

DR PRINTS; PR00025; ANTENNAPEDIA.

DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.

DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.

DR PROSITE; PS00071; HOMEBOX_2; 1.

SQ SEQUENCE 348 AA; 39554 MW; 38EC632F9AAFC13 CRC64;

Query Match

Best Local Similarity 64.3%; Score 94.5; DB 5; Length 348;

Matches 18; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 DRQIKWFQNRMRMKWK---KTALDASAL 25

Db :|||||:|||||:|||||:|||||:|||||

310 ERQIKWFQNRMRMKWKONKLSVDSGL 337

Search completed: May 30, 2003, 14:39:09
Job time : 69.8947 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 91.9211 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWFQNRKMKKTKALDWSWQTE 28

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: A_Geneseq_101002.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	28	ABB08740	IKKbeta NEMO bindi
2	162	100.0	28	AA448523	NBD peptide SEQ ID
3	134	82.7	28	ABB08741	Mutated IKKbeta NE
4	134	82.7	28	AA448524	NBD peptide SEQ ID
5	105	64.8	18	AA448628	Anti-inflammatory
6	105	64.8	18	AA448629	Anti-inflammatory
7	101	62.3	36	AAU79345	Antennapedia-caveo
8	100	61.7	41	AA80924	Mixer SIM peptide.
9	100	61.7	41	AA80925	Mixer SIM mutant p
10	98	60.5	20	AA813423	Synthetic alpha sm

11	98	60.5	26	18	AAW11630
12	97	59.9	34	21	AA79919
13	95	58.6	21	18	AAW45976
14	95	58.6	24	19	AAW82957
15	95	58.6	36	21	AAW78416
16	95	58.6	230	21	AAW58610
17	94	58.0	27	18	AAW11629
18	94	58.0	27	20	AAW27444
19	94	58.0	27	23	ABB83151
20	94	58.0	60	20	AAW42291
21	94	58.0	60	20	AAW27403
22	94	58.0	60	20	AAW04364
23	94	58.0	61	22	AAE00811
24	94	58.0	217	22	AAE10922
25	94	58.0	378	22	ABB72035
26	94	58.0	417	22	ABB57755
27	94	58.0	589	22	ABB58929
28	93	57.7	36	23	AAU79344
29	93	57.4	22	20	AAW91049
30	93	57.4	22	21	AAE27063
31	93	57.4	106	21	AAE21030
32	93	57.4	115	21	AAE53629
33	93	57.4	220	22	AAW41487
34	93	57.4	236	22	AAW39701
35	93	57.4	243	19	AAW48885
36	92.5	57.1	26	23	AAW47333
37	92	56.8	16	18	AAW45974
38	92	56.8	16	18	AAW33410
39	92	56.8	16	18	AAW33407
40	92	56.8	16	19	AAW82958
41	92	56.8	16	19	AAW71270
42	92	56.8	16	19	AAW71316
43	92	56.8	16	19	AAW30508
44	92	56.8	16	19	AAW56397
45	92	56.8	16	20	AAW52102

ALIGNMENTS

RESULT 1
ABB08740
ID ABB08740 standard; peptide; 28 AA.
XX ABB08740;
XX
XX
DT 14-JUN-2002 (first entry)
XX
DE IKKbeta NEMO binding domain peptide SEQ ID NO 18.
XX
XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer.
XX Homo sapiens.
XX
XX WO200183547-A2.
XX
XX PD 08-NOV-2001.
XX
XX PF 02-MAY-2001; 2001WO-US40654.
XX
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX
XX (UYUA) UNIV YALE.

Anti-apoptotic pro
Human papillomavir
Cysteine protease
Oestrogen receptor
Drosophila antenna
Protein regulating
Anti-apoptotic pro
Antennapedia inter
Transduction domai
Drosophila antenna
D. melanogaster PA
D. melanogaster an
Human HOXB7 varian
Drosophila melanog
Drosophila melanog
Antennapedia-caveo
Internalization se
Beta-catenin deriv
Human nucleic acid
Human colon cancer
Human polypeptide
Human polypeptide
Amino acid sequenc
Sensory organ tran
Cysteine protease
D-form peptide 43-
Peptide 43-58 of h
Oestrogen receptor
Antennapedia pepti
Antennapedia pepti
Drosophila membran
Preferred signal s
Peptide from the t

XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Fig 5; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (AB08725-AB08742) comprising at least one NEMO binding domain
 CC (AB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 162; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.8e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMMKKTKALDWSWLQTE 28
 |||||
 DB 1 DRQIKWFQNRMMKKTKALDWSWLQTE 28

RESULT 2

AA048523
 ID AA048523 standard; Peptide; 28 AA.

XX
 AC AA048523;

XX 20-MAR-2002 (first entry)

XX NBD peptide SEQ ID NO 18.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW

KW

KW

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OS

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PN

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PD

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PF

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rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 autoimmune disorder; multiple sclerosis; transplant rejection;
 osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 ataxia telangiectasia; allergy; anaphylaxis; arthritis.

Synthetic.

WO200183554-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US14346.

02-MAY-2000; 2000US-201261P.

22-AUG-2000; 2000US-0643260.

(PRAE-) PRAECIS PHARM INC.

(UYVA) UNIV YALE.

May MJ, Ghosh S, Findeis MA, Phillips K;

WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation
 domain fused to NEMO binding sequence, useful for blocking nuclear
 factor kappaB activation, and for treating asthma, lung inflammation,
 psoriasis

Example 5; Fig 5; 88pp; English.

The invention relates to an antiinflammatory compound (especially
 AA048628-AA048645), comprising a membrane translocation domain
 (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15
 amino acid residues, fused to a NEMO binding sequence
 (AA048525-AA048619). The antiinflammatory compounds have antiasthmatic,
 cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 antibacterial, immunosuppressive, antitumor, antidiabetic, osteopathic,
 nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 compounds act as selective inhibitors of cytokine-mediated NFkappaB
 activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 the NEMO binding domain that results in inhibition of IkappaB kinase
 activation and subsequent decreased phosphorylation of IkappaB. The
 compounds are useful for treating inflammatory disorders, e.g. asthma,
 lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 telangiectasia. The compounds are also useful for treating
 pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 arthritis.

Sequence 28 AA;

Query Match 100.0%; Score 162; DB 23; Length 28;

Best Local Similarity 100.0%; Pred. No. 6.8e-15;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMMKKTKALDWSWLQTE 28

|||||

DB 1 DRQIKWFQNRMMKKTKALDWSWLQTE 28

RESULT 3

AB08741

ID AB08741 standard; peptide; 28 AA.

XX AB08741;

XX 14-JUN-2002 (first entry)

XX Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; viricide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Misc-difference 22 /note= "Wildtype Trp substituted by Ala"
 FT Trp
 FT Misc-difference 24 /note= "Wildtype Trp substituted by Ala"
 FT Trp
 XX WO200183547-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (UYIA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Claim 23; Fig 5; 82pp; English.
 XX

The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying

CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX

SQ Sequence 28 AA;
 Query Match 82.7%; Score 134; DB 23; Length 28;
 Best Local Similarity 92.9%; Pred. No. 3.6e-11;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DRQIKWIFQNRMRMKTKTALDWSLQTE 28
 |||||
 Db 1 DRQIKWIFQNRMRMKTKTALDASALQTE 28
 |||||

RESULT 4
 AAM48524
 ID AAM48524 standard; Peptide; 28 AA.
 XX
 XX AC AAM48524;
 XX
 XX 20-MAR-2002 (first entry)
 XX
 XX NBD peptide SEQ ID NO 19.
 XX
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; viricide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IkappaB; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYIA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Example 5; Fig 5; 88pp; English.
 XX

The invention relates to an antiinflammatory compound (especially
 CC AAM48528-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, viricide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 28 AA;

Query Match 82.7%; Score 134; DB 23; Length 28;

Best Local Similarity 92.9%; Pred. No. 3.6e-11;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRKMKKKTALDWSWLTQTE 28

Db 1 DRQIKWFQNRKMKKKTALDASALQTE 28

RESULT 5

AAM48628

ID AAM48628 standard; Peptide; 18 AA.

XX AC AAM48628;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 131.

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX XX (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis

XX Claim 12; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 18 AA;

Query Match 64.8%; Score 105; DB 23; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RRMKWKKTALDWSWLTQTE 28

Db 1 RRMKWKKTALDWSWLTQTE 18

RESULT 6

AAM48629

ID AAM48629 standard; Peptide; 18 AA.

XX AC AAM48629;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 132.

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX XX (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 PS Claim 12; Page 63; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotatic, antiprosclerotic, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 18 AA;
 Query Match 64.8%; Score 105; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RRMKKKKTALDWSWLOTE 28
 DB 1 RRMKKKKTALDWSWLOTE 18

RESULT 7
 AAU79345
 ID AAU79345 standard; Peptide; 36 AA.
 XX AAU79345;
 AC AAU79345;
 DT 02-JUL-2002 (first entry)
 XX Antennapedia-caveolin-X fusion peptide.

XX Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;
 KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;
 KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;
 KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;
 KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;
 KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;
 KW spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav;
 KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
 KW human; fruit fly; antennapedia internalisation signal.

XX Drosophila melanogaster.
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1..16
 FT /label= Antennapedia_internalisation_signal
 FT /note= "Specifically claimed in claim 9"
 FT Misc-difference 17..32
 FT /label= Cav-X
 FT /note= "Control peptide based on a human caveolin-1
 FT scaffolding domain shown in AAU79340 residues
 FT 82-101"

XX WO200220768-A2.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-USA2069.

XX 08-SEP-2000; 2000US-231327P.
 PR 07-DEC-2000; 2000US-0731023.
 XX (UYVA) UNIV YALE.
 XX Sessa WC;
 XX WPI; 2002-329877/36.
 XX New peptide having caveolin scaffolding domain, useful for modulating
 XX activity of endothelial nitric oxide synthase and inhibiting
 XX inflammation and tumour cell angiogenesis proliferation -
 XX Claim 16; Page 72; 73pp; English.

XX The invention describes an isolated caveolin scaffolding domain peptide
 CC (I). A fusion peptide (II) containing (I) and at least a membrane
 CC translocation sequence is useful for down regulating endothelial nitric
 CC oxide synthase (eNOS) activity in a cell, resulting in blockage of
 CC vasodilation. (II) is therefore useful for inhibiting inflammation and
 CC tumour cell angiogenesis/proliferation in an animal; and for blocking the
 CC interaction of caveolin with a protein in vivo. (II) may be useful in
 CC treatment of inflammatory conditions such as osteoporosis, rheumatoid
 CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)
 CC are also useful for treating pathological processes associated with a
 CC pro-inflammatory response including allergies such as allergic rhinitis,
 CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous
 CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,
 CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,
 CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and
 CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing
 CC corticosteroids useful for immunosuppression in transplant and cancer
 CC patients. When administered along with one or more antiinflammatory
 CC agent (I) and (II) are useful for inhibiting tumour growth or malignant
 CC neoplasm including cellular angiogenesis, proliferation, invasiveness,
 CC and metastasis in biological systems. This sequence represents a fusion
 CC peptide of the invention created from the fruit fly antennapedia
 CC internalisation signal and control sequence Cav-X, based on the human
 CC caveolin-1 scaffolding domain shown in AAU79340, residues 82-101.

XX Sequence 36 AA;
 Query Match 62.3%; Score 101; DB 23; Length 36;
 Best Local Similarity 69.2%; Pred. No. 1.2e-06;
 Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWKKTALDWSWLOTE 27
 DB 1 RQIKWIFQNRMRKWKKTALDWSWLOTE 26

RESULT 8
 AAB80924
 ID AAB80924 standard; Protein; 41 AA.
 XX AAB80924;
 AC AAB80924;
 DT 04-JUN-2001 (first entry)
 XX Mixer SIM peptide.
 XX Smad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
 KW Smad Interaction Motif; tissue repair; fibrotic condition;
 KW immunosuppression; diabetic nephropathy; tumour.
 XX Unidentified.

XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Biotin.Aminohexanoic acid-R"

CC which competitively inhibits interaction of a papillomavirus (PV) E2
 CC protein with a PV E1 protein for treating a cell infected with PV or a
 CC mammal with a PV-induced condition. (A) has antiviral, virucide,
 CC cytostatic, antiproliferative and dermatological activities. Methods
 CC from the present invention can be used to treat PV-induced conditions
 CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
 CC lesions chosen from warts and other benign cutaneous lesions, plantar
 CC warts (verruca plantaris), common warts (verruca plana), Butcher's
 CC common warts, flat warts, genital warts (condyloma acuminatum) and
 CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
 CC oesophageal and other upper airway papilloma or vaginal, cervical,
 CC vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
 CC used to treat epithelial and internal fibropapillomas in animals.
 CC The present sequence represents a peptide sequence used in the
 CC exemplification of the present invention.

XX Sequence 34 AA;
 Query Match 59.9%; Score 97; DB 21; Length 34;
 Best Local Similarity 64.3%; Pred. No. 3.8e-06;
 Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWFQNRMRKWKKTALDWSLQTE 28
 DB 1 ERQIKWFQNRMRKWKKG--WKHMRLE 26

RESULT 13
 AAW45976
 ID AAW45976 standard; peptide; 21 AA.

XX AAW45976;

DT 01-JUL-1998 (first entry)

DE Cysteine protease inhibiting peptide for preventing cell death.

XX Neuronal cell death; neurodegenerative disorder; inhibition;
 KW cysteine protease; cardiovascular; liver disease.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"

FT WO9735876-A1.

PN 02-OCT-1997.

XX 04-MAR-1997; 97WO-US04158.

XX 04-MAR-1996; 96US-0610220.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM;

XX WPI; 1997-489561/45.

XX New cysteine protease inhibiting peptide(s) for preventing cell
 PT death - in cases of neurodegenerative, cardiovascular and liver
 PT diseases, and their peptidomimetics, and general method for
 PT identifying enzyme inhibiting peptides

PS Claim 10; Page 68; 112pp; English.

XX This sequence represents a specifically claimed peptide of the formula:
 CC V-(AA1)n-Cys(V')-(AA2)m-V' (1), in which n and m = 0-5, totalling 2-5;
 CC if n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more,
 CC (AA1)n = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value
 CC of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more,
 CC (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'',

CC any or all of which may be absent, - agent able to direct the compound
 CC to a specific cell. The peptides are inhibitors of cysteine proteases,
 CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit
 CC death of cells, particularly in humans, and can be used to treat
 CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,
 CC Parkinson's or Huntington's diseases, multiple sclerosis, muscular
 CC dystrophy, stroke), cardiovascular disease and liver disorders.
 CC The peptides should be more specific than pseudosubstrate inhibitors.

XX Sequence 21 AA;

Query Match 58.6%; Score 95; DB 18; Length 21;
 Best Local Similarity 94.4%; Pred. No. 4.2e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKWKKT 19
 DB 1 ROIKIWFQNRMRKWKQA 18

RESULT 14
 AAW82957
 ID AAW82957 standard; peptide; 24 AA.

XX AAW82957;

DT 04-FEB-1999 (first entry)

DE Oestrogen receptor activity inhibiting peptide #13.

XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;
 KW breast cancer; estrogen; tumour; phosphotyrosyl peptide;
 KW malonyltyrosyl peptide; steroid receptor co-activator-1.

OS Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 19 /note= "phosphotyrosine"

XX WO9846250-A1.

XX 22-OCT-1998.

XX 14-APR-1998; 98WO-US07711.

XX 14-APR-1997; 97US-0043545.

XX (REGC) UNIV CALIFORNIA.

XX Pietras RJ;

XX WPI; 1998-594522/50.

XX New anti-oestrogen peptide compositions - comprise sequences based
 PT on estrogen receptor and steroid receptor co-activator-1 sequences,
 PT used for treating cancers

PS Claim 11; Page 156; 182pp; English.

XX The present invention describes a composition comprising an isolated
 CC oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The
 CC peptides used in the composition comprise sequences of human oestrogen
 CC receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1
 CC (SRC-1). The peptide compositions, nucleic acids and vectors of the
 CC present invention can reduce OR activity in a cell, reduced OR
 CC polypeptide dimerisation in a cell and reduce the binding of SRC-1
 CC polypeptide to an OR polypeptide dimer in a cell. They can be used for
 CC killing cancer cells and treating cancers, particularly breast cancer.
 CC The present sequence represents a specifically claimed anti-oestrogen
 CC peptide.

Search completed: May 30, 2003, 14:50:03
Job time : 92.9766 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 48.8158 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-18
Perfect score: 162
Sequence: 1 DRQIKWFQNRKMKKKTALDWSWLQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications, AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	28	9	US-09-847-940B-18
2	162	100.0	28	9	US-09-847-946A-18
3	134	82.7	28	9	US-09-847-940B-19
4	134	82.7	28	9	US-09-847-946A-19
5	105	64.8	18	9	US-09-847-946A-131
6	101	62.3	36	10	US-09-731-023A-12
7	98	60.5	17	9	US-10-229-915-1
8	97	59.9	34	9	US-10-161-499-79
9	96	59.3	26	9	US-10-097-175-101
10	95	58.6	21	10	US-09-150-623-11
11	94	58.0	30	9	US-10-188-947-11
12	94	58.0	217	9	US-10-097-340-129
13	93.5	57.7	36	10	US-09-731-023A-11
14	93	57.4	28	10	US-09-214-371-9
15	93	57.4	115	9	US-09-925-299-1169
16	93	57.4	115	10	US-09-925-299-1169
17	92	56.8	16	9	US-09-902-432-32
18	92	56.8	16	9	US-10-007-363-3
19	92	56.8	16	9	US-09-953-031A-10

20	56.8	92	16	9	US-09-981-286A-3	Sequence 3, Appl
21	56.8	92	16	9	US-09-962-967A-6	Sequence 6, Appl
22	56.8	92	16	9	US-09-912-414-6	Sequence 6, Appl
23	56.8	92	16	9	US-10-071-512A-2	Sequence 2, Appl
24	56.8	92	16	9	US-09-775-052-54	Sequence 54, Appl
25	56.8	92	16	9	US-10-239-804-3	Sequence 3, Appl
26	56.8	92	16	9	US-10-077-555-3	Sequence 3, Appl
27	56.8	92	16	9	US-09-295-189-4	Sequence 4, Appl
28	56.8	92	16	9	US-10-209-421-29	Sequence 29, Appl
29	56.8	92	16	9	US-10-229-915-2	Sequence 2, Appl
30	56.8	92	16	9	US-10-185-084-3	Sequence 3, Appl
31	56.8	92	16	9	US-09-955-876A-1	Sequence 1, Appl
32	56.8	92	16	10	US-09-214-371-43	Sequence 43, Appl
33	56.8	92	16	10	US-09-780-070-38	Sequence 38, Appl
34	56.8	92	16	10	US-09-150-623-9	Sequence 9, Appl
35	56.8	92	16	10	US-09-731-023A-10	Sequence 10, Appl
36	56.8	92	16	10	US-09-854-204-1	Sequence 1, Appl
37	56.8	92	16	10	US-09-900-147-8	Sequence 8, Appl
38	56.8	92	16	10	US-09-792-480-29	Sequence 29, Appl
39	56.8	92	16	10	US-09-785-802A-2	Sequence 2, Appl
40	56.8	92	16	10	US-09-785-802A-5	Sequence 5, Appl
41	56.8	92	16	12	US-10-024-935-12	Sequence 12, Appl
42	56.8	92	17	9	US-10-209-421-30	Sequence 30, Appl
43	56.8	92	17	10	US-09-854-204-19	Sequence 19, Appl
44	56.8	92	17	10	US-09-785-802A-3	Sequence 3, Appl
45	56.8	92	17	12	US-10-007-761-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-18

Query Match 100.0%; Score 162; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRKMKKKTALDWSWLQTE 28
Db 1 DRQIKWFQNRKMKKKTALDWSWLQTE 28

RESULT 2
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-18

Query Match 100.0%; Score 162; DB 9; Length 28;

Best Local Similarity 100.0%; Pred. No. 3,1e-14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKWFOQRNRKMKKTALDWSWLQTE 28

Db 1 DRQIKWFOQRNRKMKKTALDWSWLQTE 28

RESULT 3

US-09-847-940B-19

; Sequence 19, Application US/09847940B

; Patent No. US2002015600A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sankar

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-117CP

; CURRENT APPLICATION NUMBER: US/09/847,940B

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides

US-09-847-940B-19

Query Match 82.7%; Score 134; DB 9; Length 28;

Best Local Similarity 92.9%; Pred. No. 1,1e-10;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DRQIKWFOQRNRKMKKTALDWSWLQTE 28

Db 1 DRQIKWFOQRNRKMKKTALDASALQTE 28

RESULT 4

US-09-847-946A-19

; Sequence 19, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; CURRENT FILING DATE: 2001-05-02

; CURRENT FILING DATE: 2001-05-02

; CURRENT FILING DATE: 2001-05-02

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; CURRENT FILING DATE: 2001-05-02

; CURRENT FILING DATE: 2001-05-02

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-19

Query Match 82.7%; Score 134; DB 9; Length 28;

Best Local Similarity 92.9%; Pred. No. 1,1e-10;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DRQIKWFOQRNRKMKKTALDWSWLQTE 28

Db 1 DRQIKWFOQRNRKMKKTALDASALQTE 28

RESULT 5

US-09-847-946A-131

; Sequence 131, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 131

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial

; OTHER INFORMATION: Sequence:anti-inflammatory compound

US-09-847-946A-131

Query Match 64.8%; Score 105; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 3,4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RRMKWKKTALDWSWLQTE 28

Db 1 RRMKWKKTALDWSWLQTE 18

RESULT 6

US-09-731-023A-12

; Sequence 12, Application US/09731023A

; Patent No. US20020077283A1

; GENERAL INFORMATION:

; APPLICANT: Sessa, William

; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics

; FILE REFERENCE: 44574-5076-US

; CURRENT APPLICATION NUMBER: US/09/731,023A

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/231,327

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-cav-x fusion peptide
US-09-731-023A-12

Query Match 62.38; Score 101; DB 10; Length 36;
Best Local Similarity 69.28; Pred. No. 2.1e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 RQIKWQNRRMKWKTALDWSLQT 27
:|||||:|||||:|:|
Db 1 RQIKWQNRRMKWKGIDKAFETT 26

RESULT 7
US-10-229-915-1
; Sequence 1, Application US/10229915
; Publication No. US20030083262A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: PPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; CURRENT FILING DATE: 2002-08-27
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-1

Query Match 60.58; Score 98; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKWQNRRMKWKK 17
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Db 1 DRQIKWQNRRMKWKK 17

RESULT 8
US-10-161-499-79
; Sequence 79, Application US/10161499
; Publication No. US2003004427A1
; GENERAL INFORMATION:
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-161-499-79

Query Match 59.98; Score 97; DB 9; Length 34;
Best Local Similarity 64.38; Pred. No. 6.5e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DRQIKWQNRRMKWKTALDWSLQTE 28
:|||||:|||||:|:|
Db 1 ERQIKWQNRRMKWKKGG--WKHMRLE 26

RESULT 9
US-10-097-175-101
; Sequence 101, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VIBHA B.
; APPLICANT: FINDEIS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101

Query Match 59.38; Score 96; DB 9; Length 26;
Best Local Similarity 77.38; Pred. No. 6.7e-06;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RQIKWQNRRMKWKTALDWS 23
:|||||:|||||:|:|
Db 1 RQIKWQNRRMKWKTLESS 22

RESULT 10
US-09-150-623-11
; Sequence 11, Application US/09150623
; Patent No. US2002004931A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/150,623
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/610,220
 ; FILING DATE: MAR-04-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-150-623-11

Query Match 58.6%; Score 95; DB 10; Length 21;
 Best Local Similarity 94.4%; Pred. No. 7.3e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ROIKWFQNRMRKWKKA 19
 DB 1 ROIKWFQNRMRKWKKA 18

RESULT 11
 US-10-188-947-11
 ; Sequence 11, Application US/1018947
 ; Publication No. US20030023993A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MEDHITOV, Ruslan
 ; APPLICANT: BARTON, Gregory
 ; APPLICANT: HORN, Tiffany
 ; TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
 ; FILE REFERENCE: 044574-5101US
 ; CURRENT APPLICATION NUMBER: US/10/188,947
 ; CURRENT FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: 60/289,738
 ; PRIOR FILING DATE: 2001-05-09
 ; PRIOR APPLICATION NUMBER: 60/289,815
 ; PRIOR FILING DATE: 2001-05-09
 ; PRIOR APPLICATION NUMBER: 60/289,866
 ; PRIOR FILING DATE: 2001-05-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; OTHER INFORMATION: TIRAP/Antennapedia fusion protein
 ; US-10-188-947-11

Query Match 58.0%; Score 94; DB 9; Length 30;
 Best Local Similarity 89.5%; Pred. No. 1.4e-05;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKWFQNRMRKWKKTAL 20
 DB 1 ROIKWFQNRMRKWKKLQL 19

RESULT 12
 US-10-097-340-129
 ; Sequence 129, Application US/10097340
 ; Publication No. US20030087250A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John MONAHAN

; APPLICANT: Manjula GANNAVAPU
 ; APPLICANT: Sebastian HOERSCH
 ; APPLICANT: Shubhangi KAMATKAR
 ; APPLICANT: Steve G. KOVATS
 ; APPLICANT: Rachel E. MEYERS
 ; APPLICANT: Michael MORRISSEY
 ; APPLICANT: Peter OLANDT
 ; APPLICANT: Ami SEN
 ; APPLICANT: Peter VEIBY
 ; APPLICANT: Gordon B. MILLS
 ; APPLICANT: Robert C. BAST, Jr.
 ; APPLICANT: Karen LU
 ; APPLICANT: Rosemarie SCHMANDT
 ; APPLICANT: Xumei ZHAO
 ; APPLICANT: Karen GLATT
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
 ; FILE REFERENCE: MRI-030
 ; CURRENT APPLICATION NUMBER: US/10/097,340
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,025
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/325,149
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/276,026
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/324,967
 ; PRIOR FILING DATE: 2001/09/26
 ; PRIOR APPLICATION NUMBER: 60/311,732
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/325,102
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/323,580
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 129
 ; LENGTH: 217
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-097-340-129

Query Match 58.0%; Score 94; DB 9; Length 217;
 Best Local Similarity 94.1%; Pred. No. 9.4e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRKWK 17
 DB 178 ERQIKWFQNRMRKWK 194

RESULT 13
 US-09-731-023A-11
 ; Sequence 11, Application US/09731023A
 ; Patent No. US20020077283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sessa, William
 ; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
 ; FILE REFERENCE: 44574-5076-US
 ; CURRENT APPLICATION NUMBER: US/09/731,023A
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/231,327
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
 ; OTHER INFORMATION: peptide

US-09-731-023A-11

Query Match 57.7%; Score 93.5; DB 10; Length 36;
Best Local Similarity 81.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 2 RQIKIWFQNRMRMKKKTALDW 22
Db 1 RQIKIWFQNRMRMKKKTALDW 20

RESULT 14

US-09-214-371-9
; Sequence 9, Application US/09214371B
; Patent No. US2001001851A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pinksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214, 371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-9

Query Match 57.4%; Score 93; DB 10; Length 28;
Best Local Similarity 94.1%; Pred. No. 1.7e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRMRMKK 17
Db 12 NRQIKIWFQNRMRMKK 28

RESULT 15

US-09-925-299-1169
; Sequence 1169, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1169
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1169

Query Match 57.4%; Score 93; DB 9; Length 115;
Best Local Similarity 88.2%; Pred. No. 6.8e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DRQIKIWFQNRMRMKK 17
Db 63 ERQVKIWFQNRMRMKK 79
Search completed: May 30, 2003, 15:53:23
Job time : 49.8158 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 28.1842 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: us-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKIWFQNRMMKKKTALDWSWLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	59.9	34	4	US-09-347-504-79
2	95	58.6	24	4	US-09-419-826-34
3	94	58.0	27	4	US-09-040-725A-2
4	94	58.0	61	2	US-08-202-044-3
5	94	58.0	61	4	US-08-751-344B-3
6	94	58.0	61	4	US-08-751-344B-6
7	94	58.0	61	4	US-08-751-344B-9
8	93	57.4	27	3	US-09-051-934-51
9	93	57.4	27	3	US-09-051-934-52
10	93	57.4	61	4	US-08-751-344B-7
11	92	56.8	16	2	US-08-928-958-7
12	92	56.8	16	2	US-08-810-540-3
13	92	56.8	16	2	US-08-810-540-6
14	92	56.8	16	2	US-09-072-429-7
15	92	56.8	16	3	US-08-964-302A-6
16	92	56.8	16	3	US-09-116-294-4
17	92	56.8	16	3	US-08-964-614A-4
18	92	56.8	16	3	US-08-849-486-1
19	92	56.8	16	3	US-08-849-486-4
20	92	56.8	16	4	US-09-208-966-54
21	92	56.8	16	4	US-09-308-935-8
22	92	56.8	16	4	US-09-441-416A-6
23	92	56.8	16	4	US-09-296-089-33
24	92	56.8	16	4	US-09-419-826-35
25	92	56.8	16	4	US-09-302-305C-10
26	92	56.8	18	3	US-08-838-545-20
27	92	56.8	18	4	US-09-349-532-20

Sequence 3, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 16, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli

28 56.8 20 4 US-09-466-772-3
29 54.9 42 4 US-08-751-344B-4
30 54.9 283 1 US-08-583-672-2
31 54.9 283 2 US-08-202-044-2
32 54.9 283 4 US-08-751-344B-2
33 54.9 284 2 US-08-320-148B-2
34 54.9 284 3 US-08-589-028-6
35 54.9 284 3 US-08-784-582-6
36 54.9 284 4 US-08-785-271-6
37 54.9 284 4 US-09-031-898-2
38 54.9 302 2 US-08-203-532F-4
39 54.9 302 3 US-08-950-860-16
40 54.9 302 4 US-09-078-465-4
41 54.9 302 5 PCT-US95-01882A-4
42 54.9 303 2 US-08-203-532F-2
43 54.9 303 4 US-09-078-465-2
44 54.9 303 5 PCT-US95-01882A-2
45 53.7 15 2 US-08-810-540-4

ALIGNMENTS

RESULT 1

US-09-347-504-79
; Sequence 79, Application US/09347504
; Patent No. 639075
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-504-79

Query Match 59.9%; Score 97; DB 4; Length 34;
Best Local Similarity 64.3%; Pred. No. 1.5e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKIWFQNRMMKKKTALDWSWLQTE 28
Db 1 ERQIKIWFQNRMMKKKG--WKHMRLE 26
:|||||:|||||:|::|

RESULT 2

US-09-419-826-34
; Sequence 34, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTITESTROGEN COMPOSITIONS AND METHODS
; FILE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998

APPLICATION NUMBER: US 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /note= "X - Phosphotyrosine"
US-09-419-826-34

Query Match 58.6%; Score 95; DB 4; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWKKTALD 21
DB 1 RQIKWIFQNRMRKWKKPLXD 20

RESULT 3

US-09-040-725A-2
Sequence 2, Application US/09040725A
Patent No. 6395584
GENERAL INFORMATION:
APPLICANT: Institut Curie
APPLICANT: CNRS
APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gautreau, Alexis
APPLICANT: Louvard, Daniel
TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated
FILE REFERENCE: 391082000100
CURRENT APPLICATION NUMBER: US/09/040,725A
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (22)
OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2

Query Match 58.0%; Score 94; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWKKTAL 20
DB 1 RQIKWIFQNRMRKWKKRL 19

RESULT 4

US-08-202-044-3
Sequence 3, Application US/08202044
Patent No. 5858973
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square

CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,044
FILING DATE: 23-FEB-1994
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: MGH-124XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-202-044-3

Query Match 58.0%; Score 94; DB 2; Length 61;
Best Local Similarity 94.1%; Pred. No. 6.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKWIFQNRMRKWK 17
DB 43 ERQIKWIFQNRMRKWK 59

RESULT 5

US-08-751-344B-3
Sequence 3, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-3

Query Match 58.0%; Score 94; DB 4; Length 61;
Best Local Similarity 94.1%; Pred. No. 6.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMMKKK 17
DB 43 ERQIKWIFQNRMMKKK 59

RESULT 6

US-08-751-344B-6
Sequence 6, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-6

Query Match 58.0%; Score 94; DB 4; Length 61;
Best Local Similarity 94.1%; Pred. No. 6.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMMKKK 17

DB 43 ERQIKWIFQNRMMKKK 59

RESULT 7

US-08-751-344B-9
Sequence 9, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-9

Query Match 58.0%; Score 94; DB 4; Length 61;
Best Local Similarity 94.1%; Pred. No. 6.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMMKKK 17
DB 43 ERQIKWIFQNRMMKKK 59

RESULT 8

US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051.934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384

EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match 57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWKKTALD 21
|||||
DB 1 RQIKWIFQNRMRKWKKHIE 20

RESULT 9
US-09-051-934-52
Sequence 52, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (24)
OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match 57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRKWKKTALD 21
|||||
DB 1 RQIKWIFQNRMRKWKKHIE 20

RESULT 10
US-08-751-344B-7
Sequence 7, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA

COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NO. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-7

Query Match 57.4%; Score 93; DB 4; Length 61;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKWK 17
:|||||
DB 43 ERQVKWIFQNRMRKWK 59

RESULT 11
US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFAR, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

RESULT 12
US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

RESULT 13
US-08-810-540-6
Sequence 6, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-6

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

US-08-810-540-6
Sequence 6, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

US-08-810-540-6
Sequence 6, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

US-08-810-540-6
Sequence 6, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWQNRRMKWKK 17
Db 1 RQIKWQNRRMKWKK 16

US-08-810-540-6
Sequence 6, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: ON0141b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-3714
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-072-429-7

Query Match 56.8%; Score 92; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3e-06; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRMKKK 17
|||||
Db 1 ROIKIWFQNRMRMKKK 16

RESULT 15

US-08-964-302A-6
Sequence 6, Application US/08964302A
Patent No. 6015787
GENERAL INFORMATION:
APPLICANT: Potter, David A.
APPLICANT: Skolnik, Paul R.
TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,302A
FILING DATE: 04-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 00398/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-302A-6

Query Match 56.8%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ROIKIWFQNRMRMKKK 17
|||||
Db 1 ROIKIWFQNRMRMKKK 16

Search completed: May 30, 2003, 14:41:33
Job time : 29.1842 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 30.7632 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWIFQNRMRKWKKTALDWSWLQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	59.9	60	2	PC2399
2	97	59.9	60	2	PC2400
3	97	59.9	105	2	A27471
4	97	59.9	119	2	A03314
5	97	59.9	229	2	A28329
6	96	59.3	75	2	I51341
7	95	58.6	66	2	S15336
8	95	58.6	81	2	B29585
9	95	58.6	96	2	A05266
10	95	58.6	97	2	C27176
11	95	58.6	224	2	S26400
12	95	58.6	224	2	A31324
13	94	58.0	33	2	S57235
14	94	58.0	42	2	I65241
15	94	58.0	45	2	PC1216
16	94	58.0	48	2	I51439
17	94	58.0	66	2	S15538
18	94	58.0	71	2	JC1161
19	94	58.0	71	2	A60084
20	94	58.0	74	2	D34510
21	94	58.0	75	2	S58852
22	94	58.0	76	2	D43559
23	94	58.0	78	2	I51342
24	94	58.0	81	2	S47605
25	94	58.0	82	2	S08302
26	94	58.0	83	2	S47603
27	94	58.0	83	2	S50066
28	94	58.0	86	2	A34510
29	94	58.0	86	2	JT0489

30	94	58.0	86	2	S08303	homeotic protein H
31	94	58.0	87	2	S00589	homeotic protein H
32	94	58.0	88	2	A03317	homeotic protein M
33	94	58.0	96	2	S08639	homeotic protein z
34	94	58.0	97	2	A24779	homeotic protein m
35	94	58.0	103	2	A32167	homeotic protein H
36	94	58.0	105	2	S47602	homeotic protein H
37	94	58.0	106	2	S36448	homeotic protein s
38	94	58.0	107	2	B61045	homeotic protein t
39	94	58.0	113	2	T10775	homeobox protein -
40	94	58.0	118	2	A24777	homeotic protein H
41	94	58.0	118	2	JT0273	homeotic protein H
42	94	58.0	118	2	B24777	homeotic protein M
43	94	58.0	138	2	S20087	homeotic protein b
44	94	58.0	148	2	PC4071	homeobox A5 protei
45	94	58.0	153	1	WJHU3C	homeotic protein H

ALIGNMENTS

RESULT 1

PC2399

antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)

C;Species: Styela clava

C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000

C;Accession: PC2399

R;Ge, T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela

A;Reference number: PC2399; MUID:95011617; PMID:7926803

A;Accession: PC2399

A;Molecule type: DNA

A;Residues: 1-60 <GET>

A;Cross-references: GB:S73920; NID:g693714; PIDN:AAB33061.2; PID:g7387472

A;Note: The authors translated the codon ATT for residue 47 as Glu

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. No. 1.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKWK 17

Db 42 DRQIKWIFQNRMRKWK 58

RESULT 2

PC2400

antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)

C;Species: Styela plicata

C;Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997

C;Accession: PC2400

R;Ge, T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela

A;Reference number: PC2399; MUID:95011617; PMID:7926803

A;Accession: PC2400

A;Molecule type: DNA

A;Residues: 1-60 <GET>

A;Note: The authors translated the codon ATA for residue 47 as Glu

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. No. 1.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKWK 17

Db 42 DRQIKWIFQNRMRKWK 58

Db 42 DRQIKWIFQNRMMKWK 58

RESULT 3

A27471

homeotic protein R5 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997

C:Accession: A27471

R:Faizon, M.; Sanderson, N.; Chung, S.Y.

Gene 54, 23-32, 1987

A:Title: Cloning and expression of rat homeo-box-containing sequences.

A:Reference number: A91576; MUID:87277429; PMID:2886401

A:Accession: A27471

A:Molecule type: DNA

A:Residues: 1-105 <FAL>

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:6-62/Domain: homeobox homology <HGX>

Query Match

Best Local Similarity 59.9%; Score 97; DB 2; Length 105;

Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DRQIKWIFQNRMMKWKKTALDWSWLTQ 27

Db 46 ERQIKWIFQNRMMKWKKEKDESQAPT 72

RESULT 4

A03314

homeotic protein m6 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997.

C:Accession: A03314; S14043

R:Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.

Nature 314, 713-718, 1985

A:Title: Structural analysis of murine genes containing homeo box sequences and their

A:Reference number: A03314; MUID:85188311; PMID:2986010

A:Accession: A03314

A:Molecule type: DNA

A:Residues: 1-119 <COL>

R:Breier, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.

EMBO J. 5, 2209-2215, 1986

A:Title: Sequential expression of murine homeo box genes during F9 EC cell differentiat

A:Reference number: S13785; MUID:87053860; PMID:2877873

A:Accession: S14043

A:Molecule type: DNA

A:Residues: 19-48, 'RI', 51-87 <BRE>

C:Genetics:

A:Gene: m6

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:20-76/Domain: homeobox homology <HGX>

Query Match

Best Local Similarity 59.9%; Score 97; DB 2; Length 119;

Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DRQIKWIFQNRMMKWKKTALDWSWLTQ 27

Db 60 ERQIKWIFQNRMMKWKKEKDESQAPT 86

RESULT 5

A28329

homeotic protein Hox A7 - mouse

N:Alternate names: homeotic protein Hox 1.1; m6 homeotic protein

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999

C:Accession: A28329; I49131

R:Kessel, M.; Schulze, F.; Fibi, M.; Gruss, P.

Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987

A:Title: Primary structure and nuclear localization of a murine homeodomain protein.

A:Reference number: A28329; MUID:87260976; PMID:2885847

A:Accession: A28329

A:Molecule type: mRNA

A:Residues: 1-229 <KES>

A:Cross-references: GB:M17192; NID:9193906; PIDN:AAA37833.1; PID:9309313

R:Parikh, H.; Shah, S.; Hilt, D.; Peterkofsky, A.

Gene 154, 237-242, 1995

A:Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gen

A:Reference number: I49131; MUID:95197009; PMID:7890170

A:Accession: I49131

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-42, 'GAG', 46-229 <RES>

A:Cross-references: EMBL:U15972; NID:9664757; PIDN:AAC52160.1; PID:9664758

C:Genetics:

A:Gene: Hoxa7

A:Introns: 126/1

C:Superfamily: homeotic protein Hox A7; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:130-186/Domain: homeobox homology <HGX>

Query Match

Best Local Similarity 59.9%; Score 97; DB 2; Length 229;

Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DRQIKWIFQNRMMKWKKTALDWSWLTQ 27

Db 170 ERQIKWIFQNRMMKWKKEKDESQAPT 196

RESULT 6

I51341

homeo box protein - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999

C:Accession: I51341

R:Fjose, A.; Molven, A.; Eiken, H.G.

Gene 62, 141-152, 1988

A:Title: Molecular cloning and characterization of homeobox-containing genes from Atl

A:Reference number: I51341; MUID:88226009; PMID:2897318

A:Accession: I51341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-75 <FJO>

A:Cross-references: GB:M18903; NID:9213797; PIDN:AAA49559.1; PID:g213798

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:2-58/Domain: homeobox homology <HGX>

Query Match

Best Local Similarity 59.3%; Score 96; DB 2; Length 75;

Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRQIKWIFQNRMMKWKKTALDWS 23

Db 42 ERQIKWIFQNRMMKWKKEKDESD 64

RESULT 7

S15336

homeotic protein Hox A7 - human (fragment)

N:Alternate names: homeotic protein Hox 1A

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

C:Accession: S15536

R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.;

Genome 31, 745-756, 1989

A:Title: Organization of human class I homeobox genes.

A:Reference number: S15036; MUID:90215256; PMID:2576652

A:Accession: S15536

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-66 <BON>

C:Genetics:

A:Gene: GDB:HOXA7

A:Cross-references: GDB:120647; OMIM:142950

A:Map position: 7p15.3-7p15.3

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 66;

Best Local Similarity 81.0%; Pred. No. 3.1e-06;

Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKWKKTALD 21

:|||||

Db 42 ERQIKWIFQNRMRKWKKEHKD 62

RESULT 8

B29585

homeotic protein Hox 2.2 precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997

C:Accession: B29585

R:Loni, P.; Arman, E.; Crosnek, H.; Ruddle, F.H.; Blatt, C.

DNA 6, 409-418, 1987

A:Title: New murine homeoboxes: structure, chromosomal assignment, and differential expression

A:Reference number: A29585; MUID:88054465; PMID:2890503

A:Accession: B29585

A:Molecule type: DNA

A:Residues: 1-81 <LON>

A:Cross-references: GB:M18167

A>Note: the authors translated the codon CAG for residue 69 as Glu

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;4-60/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 81;

Best Local Similarity 66.7%; Pred. No. 3.8e-06;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWIFQNRMRKWKKTALD 28

:|||||

Db 44 ERQIKWIFQNRMRKWKKSLSASLSAE 73

RESULT 9

A05266

homeotic protein Hox B6 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 05-Jun-1987 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997

C:Accession: A05266; S15537

R:Levine, M.; Rubin, G.M.; Tjian, R.

Cell 38, 667-673, 1984

A:Title: Human DNA sequences homologous to a protein coding region conserved between hom

A:Reference number: A05265; MUID:85024858; PMID:6091895

A:Accession: A05266

A:Molecule type: DNA

A:Residues: 1-96 <LEV>

A:Cross-references: EMBL:X02571

A>Note: this reading frame extends between two stop codons and does not begin with a sta

R:Boncinelli, E.; Acampora, D.; Fannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc

Genome 31, 745-756, 1989

A:Title: Organization of human class I homeobox genes.

A:Reference number: S15036; MUID:90215256; PMID:2576652

A:Accession: S15537

A:Molecule type: DNA

A:Residues: 18-19, 'R', 21-83 <BON>

C:Genetics:

A:Gene: GDB:HOXB6

A:Cross-references: GDB:120659; OMIM:142961

A:Map position: 17q21.3-17q21.3

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;19-75/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 96;

Best Local Similarity 66.7%; Pred. No. 4.6e-06;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWIFQNRMRKWKKTALD 28

:|||||

Db 59 ERQIKWIFQNRMRKWKKSLSASLSAE 88

RESULT 10

C27176

homeotic protein Hox 2.2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999

C:Accession: C27176

R:Hart, C.P.; Fainsod, A.; Ruddle, F.H.

Genomics 1, 182-195, 1987

A:Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolution

A:Reference number: A27176; MUID:88085193; PMID:2891608

A:Accession: C27176

A:Molecule type: DNA

A:Residues: 1-97 <HAR>

A:Cross-references: GB:M18401; NID:g193936; PIDN:AAC27130.1; PID:g3335322

C:Genetics:

A:Gene: Hox-2.2

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;20-76/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 97;

Best Local Similarity 66.7%; Pred. No. 4.6e-06;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWIFQNRMRKWKKTALD 28

:|||||

Db 60 ERQIKWIFQNRMRKWKKSLSASLSAE 89

RESULT 11

S26400

homeotic protein Hox 2.2 (variant 1) - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Nov-2000

C:Accession: S26400; S26401

R:Shen, W.; Detmer, K.; Simonitch-Eason, T.A.; Lawrence, H.J.; Largman, C.

Nucleic Acids Res. 19, 539-545, 1991

A:Title: Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cel

A:Reference number: S26400; MUID:91187672; PMID:1672751

A:Accession: S26400

A:Molecule type: DNA

A:Residues: 1-224 <SHE>

A:Cross-references: EMBL:X58431; NID:g33369; PIDN:CAA41335.1; PID:g32370

A:Experimental source: tissue-type placenta

A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 6

A:Accession: S26401

A:Molecule type: DNA

A:Residues: 1-139, 'E', <SH2>

A:Cross-references: EMBL:X58431; NID:g33369; PIDN:CAA41336.1; PID:g32371

A:Experimental source: tissue-type placenta

A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 6

A>Note: the authors did not translate the codons for residues 139, and 140

C:Genetics:

A:Introns: 139/1

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regul

F;147-203/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 224;

Best Local Similarity 66.7%; Pred. No. 1.1e-05;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKTA--LDWSWLQTE 28
:|||||
Db 187 ERQIKWPNRRMKWKESKLLSASQLSAE 216

RESULT 12

A31324
homeotic protein Hox 2.2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C:Accession: A31324
R:Schughart, K.; Uset, M.F.; Avgulevitch, A.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
A:Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
A:Reference number: A31324; MUID:88289762; PMID:2899893
A:Accession: A31324
A:Molecule type: mRNA
A:Residues: 1-224 <SCH>
A:Cross-references: GB:J03782; NID:g193929; PIDN:AAA37843.1; PID:g387203
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:147-203/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 224;
Best Local Similarity 66.7%; Pred. No. 1.1e-05;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKTA--LDWSWLQTE 28
:|||||
Db 187 ERQIKWPNRRMKWKESKLLSASQLSAE 216

RESULT 13

S57235
antennapedia protein (clone pl105) - fruit fly (Drosophila pseudoobscura) (fragment)
C:Species: Drosophila pseudoobscura
C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999
C:Accession: S57235
R:Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecill, J.K.; Kaufman, T.C.
Genetics 133, 319-330, 1993
A:Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.
A:Reference number: S57224
A:Accession: S57235
A:Molecule type: DNA
A:Residues: 1-33 <RAN>
A:Cross-references: EMBL:X77711
C:Genetics:
A:Gene: FlyBase:Antp
A:Cross-references: FlyBase:FBgn0012693
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 58.0%; Score 94; DB 2; Length 33;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWK 17
:|||||
Db 6 ERQIKWPNRRMKWK 22

RESULT 14

I65241
homeotic protein Hox-A - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
C:Accession: I65241
R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
Biochem. Genet. 32, 351-360, 1994
A:Title: Cloning of rat homeobox genes.

A:Reference number: I52340; MUID:95217128; PMID:7702549
A:Accession: I65241
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: GB:S76290; NID:g913077
C:Genetics:
A:Gene: Hox-A; Hox-1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 58.0%; Score 94; DB 2; Length 42;
Best Local Similarity 94.1%; Pred. No. 2.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWK 17
:|||||
Db 24 ERQIKWPNRRMKWK 40

RESULT 15

PC1216
homeotic protein Dtbx1 - planarian (Dugesia tigrina) (fragment)
C:Species: Dugesia tigrina
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
C:Accession: PC1216
R:Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehr
Gene 121, 337-342, 1992
A:Title: Homeoboxes in flatworms.
A:Reference number: JC1386; MUID:93077050; PMID:1359988
A:Accession: PC1216
A:Molecule type: DNA
A:Residues: 1-45 <OLI>
A:Cross-references: EMBL:X66822
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-45/Domain: homeobox homology (fragment) <HOX>

Query Match 58.0%; Score 94; DB 2; Length 45;
Best Local Similarity 94.1%; Pred. No. 2.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWK 17
:|||||
Db 29 ERQIKWPNRRMKWK 45

Search completed: May 30, 2003, 14:53:00
Job time : 31.7632 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	97	59.9	105	HXA7_RAT	P06834 rattus norv
2	97	59.9	229	HXA7_MOUSE	P02830 mus musculu
3	96	59.3	75	HMSA_SALSA	P09636 salmo salar
4	95	58.6	224	HXB6_HUMAN	P17509 homo sapien
5	95	58.6	224	HXB6_MOUSE	P09023 mus musculu
6	95	58.6	230	HXA7_HUMAN	P31268 homo sapien
7	94	58.0	48	HXB6_XENLA	P31256 xenopus lae
8	94	58.0	49	HXA7_SHEEP	Q28599 ovis aries
9	94	58.0	71	HXA7_SHEEP	Q28600 ovis aries
10	94	58.0	71	HXC5_NOTVI	P31262 notophthalm
11	94	58.0	74	HM90_APIME	P15860 apis mellif
12	94	58.0	76	HXC4_RAT	P18865 rattus norv
13	94	58.0	78	HXA5_SALSA	P09637 salmo salar
14	94	58.0	80	HXA4_LINSA	P81192 lineus sang
15	94	58.0	81	HXS1_BRARE	P09013 brachydanio
16	94	58.0	82	HXB5_CHICK	P14838 gallus gall
17	94	58.0	84	HXB6_CHICK	P14839 gallus gall
18	94	58.0	86	HXC3_APIME	P15859 apis mellif
19	94	58.0	87	HXC5_XENLA	P09020 xenopus lae
20	94	58.0	93	HXB8_PTIG	P09078 sus scrofa
21	94	58.0	96	HXC6_BRARE	P15862 brachydanio
22	94	58.0	105	HXB4_BRARE	P22574 brachydanio
23	94	58.0	112	HXB7_RAT	P18864 rattus norv
24	94	58.0	148	HXA5_AMBME	P50208 ambystoma m
25	94	58.0	153	HXC6_SHEEP	P49925 ovis aries
26	94	58.0	208	HXA7_HETFR	Q91a25 heterodontu
27	94	58.0	209	HXA7_XENLA	P09071 xenopus lae
28	94	58.0	217	HXB7_BOVIN	Q9tt89 bos taurus
29	94	58.0	217	HXB7_HUMAN	P09629 homo sapien
30	94	58.0	217	HXB7_MOUSE	P09024 mus musculu
31	94	58.0	220	HB7A_XENLA	Q911771 xenopus lae
32	94	58.0	220	HB7B_XENLA	P04476 xenopus lae
33	94	58.0	222	HXC5_HUMAN	Q00444 homo sapien

Best local similarity 70.4%, Fied: 1:
Matches 19: Conservative 1: Mism

Query Match 59.9%; Score 97; DB 1; Length 105;
Best Local Similarity 70.4%; Pred. No. 8.6e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Caps 0;

QY 1 DRQIKWIFONRRMKWKKTALDMSWLQT 27
 DB :|||||
 46 ERQIKWIFONRRMKWKKEHKSQAPT 72

RESULT 2
 HXA7_MOUSE STANDARD; PRT; 229 AA.
 AC P02830;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).
 GN HOXA7 OR HOXA-7 OR HOX-1.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260976; PubMed=2885847;
 RA Kessel M., Schulze F., Fibi M., Gruss P.;
 RT "Primary structure and nuclear localization of a murine homeodomain
 protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RX MEDLINE=95197009; PubMed=7890170;
 RA Parikh H., Shah S., Hilt D., Peterkofsky A.;
 RT "Organization, sequence and regulation of expression of the murine
 Hoxa-7 gene.";
 RL Gene 154:237-242(1995).
 RN [3]
 RP SEQUENCE OF 126-229 FROM N.A.
 RX MEDLINE=85188311; PubMed=2986010;
 RA Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;
 RT "Structural analysis of murine genes containing homeo box sequences
 and their expression in embryonal carcinoma cells.";
 RL Nature 314:713-718(1985).
 RN [4]
 RP SEQUENCE OF 129-197 FROM N.A.
 RX MEDLINE=87053860; PubMed=2877873;
 RA Breiter G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;
 RT "Sequential expression of murine homeo box genes during F9 EC cell
 differentiation.";
 RL EMBO J. 5:2209-2215(1986).
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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 DR EMBL; M17192; AAC37833.1; -;
 DR EMBL; U15972; AAC52160.1; -;
 DR PIR; A03314; A03314.
 DR PIR; A28329; A28329.
 DR PIR; S14043; S14043.
 DR HSSP; P02833; 9ANT.
 DR TRANSFAC; T01278; -;
 DR MGD; MGI:96179; Hoxa7.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PRO0025; ANTENNAPEDIA.
 DR PRINTS; PRO0024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 KW Transcription regulation.
 FT DOMAIN 118 123 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 129 188 HOMEBOX.
 FT DOMAIN 156 159 POLY-ARG.
 FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 215 229 POLY-GLU.
 FT CONFLICT 43 45 GAG -> APA (IN REF. 1).
 SQ SEQUENCE 229 AA; 25682 MW; D36E6BD61D8D5C6F CRC64;
 Query Match 59.9%; Score 97; DB 1; Length 229;
 Best Local Similarity 70.4%; Pred. No. 2e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFONRRMKWKKTALDMSWLQT 27
 DB :|||||
 170 ERQIKWIFONRRMKWKKEHKSQAPT 196

RESULT 3
 HMSA_SALSA STANDARD; PRT; 75 AA.
 ID HMSA_SALSA
 AC P09636;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Homeobox protein S12-A (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88226009; PubMed=2897318;
 RA Fjose A., Molven A., Eiken H.G.;
 RT "Molecular cloning and characterization of homeo-box-containing genes
 from Atlantic salmon.";
 RL Gene 62:141-152(1988).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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 CC -----
 DR EMBL; M18903; AAA49559.1; -;
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DNA_BIND 1 60 HOMEBOX.
 FT NON_TER 75 75
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;
 Query Match 59.3%; Score 96; DB 1; Length 75;
 Best Local Similarity 78.3%; Pred. No. 8.3e-07;

Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMMKKKTALDWS 23
:|||||
Db 42 ERQIKWQNRMMKKKHDKDES 64

RESULT 4

HXB6_HUMAN STANDARD; PRT; 224 AA.
AC P17509; P09068; Q9UGH2; Q9HB11;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2.2) (HOX-2).
GN HOXB6 OR HOXB2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Placenta;
RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.-F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
Largman C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human
hematopoietic cells and murine embryonic and adult tissues.";
RL Nucleic Acids Res. 19:539-545(1991).
[2]
RN SEQUENCE FROM N.A.
RA Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.;
RT "Expression of HOX genes in T lymphocytes and hairy leukemia cell
lines.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA Kidd K.K., Busygina V., DeMille M.M.C., Speed W.C., Ruggeri V.,
Kidd J.R., Fakis A.J.;
RT "Overall linkage disequilibrium in 33 populations for highly
informative multistate haplotypes spanning the HOXB gene cluster.";
RL Am. J. Hum. Genet. 67:235-235(2000).
[4]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE OF 135-224 FROM N.A.
RX MEDLINE=90046832; PubMed=2573064;
RA Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,
Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
RT "Lineage-restricted expression of homeobox-containing genes in human
hematopoietic cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
[6]
RN PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
RX MEDLINE=85024858; PubMed=6091895;
RA Levine M., Rubin G.M., Tjian R.;
RT "Human DNA sequences homologous to a protein coding region conserved
between homeotic genes of Drosophila.";
RL Cell 38:667-673(1984).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Homeobox-
less; are produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.

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EMBL; X58431; CAA41335.1; -;
EMBL; X58431; CAA41336.1; -;
EMBL; AJ270993; CAB65909.1; -;
EMBL; AF287967; AAG31552.1; -;
EMBL; BC014651; AAH14651.1; -;
EMBL; M30597; AAA36004.1; -;
EMBL; K02571; -; NOT_ANNOTATED_CDS.
PIR; A05266; A05266.
PIR; S26400; S26400.
DR HSSP; P02833; 1HOM.
DR TRANSFAC; T01732; -;
DR Genew; HGNC:5117; HOXB6.
MIW; 142961; -;
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation; Alternative splicing.
FT DOMAIN 127 132 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 146 205 HOMEBOX.
FT DOMAIN 216 220 POLY-GLU.
FT VARSPLIC 140 140 S -> E (IN ISOFORM 2).
FT VARSPLIC 141 224 MISSING (IN ISOFORM 2).
FT CONFLICT 24 25 HV -> OL (IN REF. 3 AND 4).
FT CONFLICT 33 33 A -> R (IN REF. 1).
FT CONFLICT 60 60 P -> R (IN REF. 1).
FT CONFLICT 73 73 D -> A (IN REF. 1).
FT CONFLICT 149 150 GR -> A (IN REF. 5).
SQ SEQUENCE 224 AA; 25427 MW; D8F96AFAC893D878 CRC64;

Query Match 58.6%; Score 95; DB 1; Length 224;
Best Local Similarity 66.7%; Pred. No. 3.6e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWQNRMMKKKTA--LDWSWLQTE 28
:|||||
Db 187 ERQIKWQNRMMKKKLLSASQSAE 216

RESULT 5
HXB6_MOUSE STANDARD; PRT; 224 AA.
ID HXB6_MOUSE
AC P09023;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
GN HOXB6 OR HOXB-6 OR HOX-2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98289762; PubMed=2899893;
RA Schughart K., Utset M.F., Awgulewitsch A., Ruddle F.H.;
RT "Structure and expression of Hox-2.2, a murine homeobox-containing
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
[2]
RN SEQUENCE FROM N.A.
RP

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RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
RA Larmann C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human
RT hematopoietic cells and murine embryonic and adult tissues.";
RL Nucleic Acids Res. 19:539-545(1991).
RN [3]
RP SEQUENCE OF 144-224 FROM N.A.
RX MEDLINE=88054465; PubMed=2890503;
RA Lonai P., Arman E., Czosnek H., Ruddle F.H., Blatt C.;
RA "New murine homeoboxes: structure, chromosomal assignment, and
RT differential expression in adult erythropoiesis.";
RL DNA 6:409-418(1987).
RN [4]
RP SEQUENCE OF 140-224 FROM N.A.
RX MEDLINE=8805193; PubMed=2891608;
RA Hart C.P., Fainsod A., Ruddle F.H.;
RA "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes:
RT evolutionary and structural comparisons.";
RL Genomics 1:182-195(1987).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC -----
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CC -----
DR EMBL; M18166; AAA37844.1; -
DR EMBL; X56459; CAA39834.1; -
DR EMBL; M18401; AAC27130.1; ALT_SEQ.
DR EMBL; J03782; AAA37843.1; -
DR PIR; A31324; A31324.
DR PIR; B29585; B29585.
DR PIR; C27176; C27176.
DR HSSP; P02833; 1HOM.
DR TRANSFAC; T01733; -
DR MGD; MGI:96187; Hoxb6.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 127 132 ANTP-TYPE HEXAPEPTIDE.
FT HOMEBOX.
FT DOMAIN 146 205 HOMEBOX.
FT DOMAIN 216 220 POLY-GLU.
FT CONFLICT 186 T -> P (IN REF. 3).
SQ SEQUENCE 224 AA; 25310 MW; E8FC0BDEB57F5C3D CRC64;
Query Match 58.6%; Score 95; DB 1; Length 224;
Best Local Similarity 66.7%; Pred. NO. 3.6e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
QY 1 DRQIKFQNRMRMKKTA--LDWSLQTE 28
Db 187 ERQIKFQNRMRMKKESKLLSASQLSAE 216
RESULT 6
HXA7_HUMAN

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HXA7_HUMAN STANDARD; PRT; 230 AA.
P31268; O43486; O43368; Q9UDMI; Q9NSC8; O95655;
01-JUL-1993 (Rel. 26, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).
GN HXA7 OR HOX1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Polakowska R., LaCelle P.T.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99023755; PubMed=9804983;
RA McIlhatten M.A., Brenner P.S., McMullin M.F., Maxwell A.P.,
RA Winter P.C., Lappin T.R.;
RT "Sequence characterisation and expression of homeobox HOX A7 in the
RT multi-potential erythroleukaemic cell line TF-1.";
RL Biochim. Biophys. Acta 1442:329-333(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Bradshaw H., Hinds K., Keppler D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20369265; PubMed=10911612;
RA Kim W.H., Jin H., Seol E.Y., Yoo M., Park H.W.;
RT "Sequence analysis and tissue specific expression of human HOXA7.";
RL Mol. Biotechnol. 14:19-24(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Albrechtsen R., Wewer U.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE OF 1-91 FROM N.A.
RA Cho M., Kim M.H., Hwang C.Y., Min W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE OF 130-195 FROM N.A.
RX MEDLINE=90215256; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA Gaetano G., Stornaiuolo A., Cafiero M., Falella A., Simeone A.;
RT "Organization of human class I homeobox genes.";
RL Genome 31:745-756(1989).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC -----
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CC -----
DR EMBL; AF026397; AAB94604.1; -
DR EMBL; AJ005814; CAA06713.1; -
DR EMBL; AC004080; -; NOT_ANNOTATED_CDS.
DR EMBL; AF032095; AAD01939.2; -
DR EMBL; U92543; AAD00727.1; -
DR EMBL; X84803; CAA59270.1; -
DR EMBL; X84804; CAA59270.1; JOINED.
DR PIR; S15536; S15536.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T01705; -

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DR Genew: HGNC:5108; HOXA7.
DR MM: 142950;
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00025; ANTENNAPEDIA.
DR PRINTS: PR00024; HOMEBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 119 124 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 130 189 HOMEBOX.
FT DOMAIN 157 160 POLY-ARG.
FT DOMAIN 196 199 POLY-ALA.
FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 223 230 POLY-GLU.
FT CONFLICT 18 18 T -> A (IN REF. 3).
FT CONFLICT 75 76 DA -> RR (IN REF. 6).
FT CONFLICT 78 78 MISSING (IN REF. 5).
FT CONFLICT 174 174 I -> V (IN REF. 4).
FT CONFLICT 194 195 PT -> RL (IN REF. 5).
FT CONFLICT 195 195 T -> I (IN REF. 7).
FT CONFLICT 222 222 D -> Y (IN REF. 5).
SQ SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;

Query Match 58.6%; Score 95; DB 1; Length 230;
Best Local Similarity 81.0%; Pred. No. 3.7e-06;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKWKALD 21
DB 171 ERQIKWIFQNRKMKWKEKD 191

RESULT 7
ID HXB6_XENLA STANDARD; PRT; 48 AA.
AC P31256;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).
GN HOXB6 OR XLHox-2.2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=93043517; PubMed=1384809;
RA Leroy P., de Robertis E.M.;
RT "Effects of lithium chloride and retinoic acid on the expression of
RL genes from the Xenopus laevis Hox 2 complex.";
Dev. Dyn. 194:21-32(1992).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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-----
EMBL; U61978; AAB04754.1;
DR HSSP: P02833; LHOM.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
FT NON_TER 1 1
FT DNA_BIND <1 49 HOMEBOX.
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;

EMBL; M91587; AAA49750.1;
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND <1 29 HOMEBOX.
SQ SEQUENCE 48 AA; 5716 MW; BC39E36822EDD2A CRC64;

Query Match 58.0%; Score 94; DB 1; Length 48;
Best Local Similarity 94.1%; Pred. No. 9.8e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKWK 17
DB 11 ERQIKWIFQNRKMKWK 27

RESULT 8
ID HXA5_SHEEP STANDARD; PRT; 49 AA.
AC Q28599;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (Fragment).
GN HOXA5 OR HOXA-5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
[1]
SEQUENCE FROM N.A.
RA Roche P.J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC 5'-CYNNATTA[GTG]-3'.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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-----
EMBL; U61978; AAB04754.1;
DR HSSP: P02833; LHOM.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
FT NON_TER 1 1
FT DNA_BIND <1 49 HOMEBOX.
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;
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Query Match      58.0%; Score 94; DB 1; Length 49;
Best Local Similarity 94.1%; Pred. No. 1e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMRKWK 17
DB 31 ERQIKWFQNRMRKWK 47

RESULT 9
HXA7 SHEEP
ID HXA7 SHEEP STANDARD; PRT; 71 AA.
AC Q28600;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Fragment).
GN HXA7 OR HOXA-7.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Roche P.J.J.
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC -----
DR EMBL; M44001; AAA49397.1; ALT_INIT.
DR PIR; JCL1161; JCL1161.
DR HSP; P02833; 1SANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1. PARTIAL.
DR PROSITE; PS00032; ANTENNAPEPIA; 1.
DR PROSITE; PS00711; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 4 63 HOMEBOX.
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8888 MW; 931049FAC1BAACB7 CRC64;

Query Match      58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMRKWK 17
DB 45 ERQIKWFQNRMRKWK 61

RESULT 10
HXC5 NOTVI
ID HXC5 NOTVI STANDARD; PRT; 71 AA.
AC P31262;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C5 (NvHox-3.4) (Fragment).

```

```

OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-92290273; PubMed-1351019;
RX Belleville S., Beauchemin M., Tremblay M., Noisieux N., Savard P.;
RT "Homeobox-containing genes in the newt are organized in clusters
RT similar to other vertebrates."
RL Gene 114:179-186(1992).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC -----
DR EMBL; M44001; AAA49397.1; ALT_INIT.
DR PIR; JCL1161; JCL1161.
DR HSP; P02833; 1SANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1. PARTIAL.
DR PROSITE; PS00032; ANTENNAPEPIA; 1.
DR PROSITE; PS00711; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 4 63 HOMEBOX.
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8979 MW; 07999FDE89995B42 CRC64;

Query Match      58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMRKWK 17
DB 45 ERQIKWFQNRMRKWK 61

RESULT 11
HM90 APIME
ID HM90 APIME STANDARD; PRT; 74 AA.
AC P15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein H90 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Apoidea; Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-90099384; PubMed-2574865;
RX Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).

```



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CC CC -1- SUBCELLULAR LOCATION: Nuclear (Potential);
CC CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; M29493; AAA27728.1; -
CC CC PIR; D34510; D34510.
CC CC HSSP; P02833; 1HOM.
CC CC InterPro; IPR001356; Homeobox.
CC CC Pfam; PF00046; homeobox; 1.
CC CC ProDom; PD000010; Homeobox; 1.
CC CC SMART; SM00389; HOX; 1.
CC CC PROSITE; PS00027; HOMEBOX_1; 1.
CC CC PROSITE; PS00071; HOMEBOX_2; 1.
CC CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
CC CC KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
CC CC FT NON_TER 1 1
CC CC FT DNA_BIND 8 67 HOMEBOX.
CC CC FT NON_TER 74 74
CC CC SQ SEQUENCE 74 AA; 9263 MW; 5FC8FB4F723D3837 CRC64;
CC CC
CC CC Query Match 58.0%; Score 94; DB 1; Length 74;
CC CC Best Local Similarity 94.1%; Pred. No. 1.5e-06;
CC CC Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC CC
CC CC QY 1 DROIKIWFQNRMRKWK 17
CC CC Db 49 EROIKIWFQNRMRKWK 65
CC CC
CC CC RESULT 12
CC CC HKC4_RAT STANDARD; PRT; 76 AA.
CC CC AC P18865;
CC CC DT 01-NOV-1990 (Rel. 16, Created)
CC CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
CC CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC CC DE Homeobox protein Hox-c4 (R3) (Fragment).
CC CC GN HOXC4 OR HOXC-4.
CC CC OS Rattus norvegicus (Rat).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC CC OX NCBI_TaxID=10116;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RC STRAIN-Sprague-Dawley;
CC CC RX MEDLINE=89231502; PubMed=2907739;
CC CC RA Falzon M., Chung S.Y.;
CC CC RT "The expression of rat homeobox-containing genes is developmentally
CC CC regulated and tissue specific.";
CC CC RL Development 103:601-610(1989).
CC CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC CC -1- TISSUE SPECIFICITY: PREDOMINANTLY SPINAL CORD AND KIDNEY.
CC CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC CC "DEFORMED" SUBFAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; M37567; AAA1343.1; -
CC CC
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DR PIR; C43559; C43559.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND 11 70 HOMEBOX.
SQ SEQUENCE 76 AA; 9293 MW; 5235F665C0672385 CRC64;
Query Match 58.0%; Score 94; DB 1; Length 76;
Best Local Similarity 94.1%; Pred. No. 1.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DROIKIWFQNRMRKWK 17
Db 52 EROIKIWFQNRMRKWK 68
RESULT 13
HXAS_SALSA STANDARD; PRT; 78 AA.
AC P09637;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (S12-B) (Fragment).
GN HOXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes
RT from Atlantic salmon.";
RL Gene 62:141-152(1988).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC CC -----
CC CC EMBL; M18904; AAA49560.1; -
CC CC HSSP; P02833; 9ANT.
CC CC InterPro; IPR001827; Antennapedia.
CC CC InterPro; IPR001356; Homeobox.
CC CC Pfam; PF00046; homeobox; 1.
CC CC ProDom; PD000010; Homeobox; 1.
CC CC SMART; SM00389; HOX; 1.
CC CC PROSITE; PS00027; HOMEBOX_1; 1.
CC CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC CC PROSITE; PS00071; HOMEBOX_2; 1.
CC CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
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FT  DNA_BIND 1 60 HOMEBOX.
SQ  SEQUENCE 78 AA; 9489 MW; 828DEBDDF78AC820 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 78;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMRKWK 17
DB 42 ERQIKWFQNRMRKWK 58

RESULT 14
HXA4_LINSA
ID HXA4_LINSA STANDARD; PRT; 80 AA.
AC P81192;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A4 (LsHox 4) (Fragment).
GN HXA4.
OS Lineus sanguineus (Ribbon worm).
OC Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;
OC Lineus.
OX NCBI_TaxID=48190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98163491; PubMed=9501210;
RA Kmita-Cunisse M., Loebl F., Bierne J., Gehring W.J.;
RT "Homeobox genes in the ribbonworm Lineus sanguineus: evolutionary
RT implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC "DEFORMED" SUBFAMILY.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00032; ANTENNAPEIDIA; PARTIAL.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 21 80 HOMEBOX.
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 80;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMRKWK 17
DB 52 ERQIKWFQNRMRKWK 68

RESULT 15
HX5L_BRARE
ID HX5L_BRARE STANDARD; PRT; 81 AA.
AC P09013;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 like (ZF-54) (Fragment).
GN HOXB5 OR ZF54 OR ZF-54.

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OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89016617; PubMed=2902580;
RA Njolstad P.R., Molven A., Hordvik I., Apold J., Fjose A.;
RT "Primary structure, developmentally regulated expression and
RT potential duplication of the zebrafish homeobox gene zF-21.";
RL Nucleic Acids Res. 16:9097-9113(1988).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC -----
DR EMBL; X12803; CAA31291.1; -
DR HSSP; P02833; 1SAN.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 6 65 HOMEBOX.
FT NON_TER 65 65
SQ SEQUENCE 81 AA; 9977 MW; B7698AEFFEB3C6B4 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 81;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWFQNRMRKWK 17
DB 47 ERQIKWFQNRMRKWK 63

Search completed: May 30, 2003, 15:49:09
Job time : 14.5526 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 68.8947 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWFORRMKWKKTALDWSWLQTE 28

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101.5	62.7	274	5 Q9XYT7	Q9XYT7 cassiopea x
2	97	59.9	60	5 Q26375	Q26375 styela clav
3	97	59.9	181	5 Q26611	Q26611 styela plic
4	97	59.9	194	5 Q26478	Q26478 styela clav
5	94	58.0	39	13 Q57368	Q57368 brachydanio
6	94	58.0	43	13 Q57359	Q57359 brachydanio
7	94	58.0	46	13 Q9PVR9	Q9PVR9 oryzias lat
8	94	58.0	51	5 Q26407	Q26407 ctenodrilus
9	94	58.0	51	5 Q23743	Q23743 ctenodrilus
10	94	58.0	51	5 Q27413	Q27413 ctenodrilus
11	94	58.0	57	13 Q9PVR8	Q9PVR8 oryzias lat
12	94	58.0	58	5 Q9Y188	Q9Y188 priapulid c
13	94	58.0	58	5 Q25208	Q25208 junonia coe
14	94	58.0	58	13 Q57362	Q57362 brachydanio
15	94	58.0	59	5 Q8WRM9	Q8WRM9 lithobius a
16	94	58.0	59	5 Q9NB42	Q9NB42 anopheles g

17	94	58.0	59	13 Q9PVR5	Q9PVR5 oryzias lat
18	94	58.0	60	5 Q77139	Q77139 archegozete
19	94	58.0	60	5 Q77143	Q77143 archegozete
20	94	58.0	60	13 Q8QGL8	Q8QGL8 petromyzon
21	94	58.0	60	13 Q8QGL7	Q8QGL7 petromyzon
22	94	58.0	60	13 Q8QGL6	Q8QGL6 petromyzon
23	94	58.0	60	13 Q8QGL5	Q8QGL5 petromyzon
24	94	58.0	60	13 Q8QGL3	Q8QGL3 petromyzon
25	94	58.0	60	13 Q8QGL2	Q8QGL2 petromyzon
26	94	58.0	61	5 Q27910	Q27910 polyandroca
27	94	58.0	63	5 Q77138	Q77138 archegozete
28	94	58.0	66	13 Q57356	Q57356 brachydanio
29	94	58.0	69	5 Q9U9T4	Q9U9T4 nereis vire
30	94	58.0	69	5 Q9BMF7	Q9BMF7 haliotis as
31	94	58.0	70	5 Q967W5	Q967W5 folsomia ca
32	94	58.0	71	13 Q9PVS3	Q9PVS3 oryzias lat
33	94	58.0	71	13 Q9PVS1	Q9PVS1 oryzias lat
34	94	58.0	73	5 Q9Y186	Q9Y186 priapulid c
35	94	58.0	74	13 Q57367	Q57367 brachydanio
36	94	58.0	75	5 Q25209	Q25209 junonia coe
37	94	58.0	75	13 Q9PVR6	Q9PVR6 oryzias lat
38	94	58.0	76	5 Q44257	Q44257 ethmostigm
39	94	58.0	77	5 Q44260	Q44260 ethmostigm
40	94	58.0	77	5 Q9U9Z4	Q9U9Z4 lingula ung
41	94	58.0	77	5 Q9Y187	Q9Y187 priapulid c
42	94	58.0	79	5 Q9U9T9	Q9U9T9 nereis vire
43	94	58.0	79	5 Q967V2	Q967V2 lithobius f
44	94	58.0	80	5 Q05008	Q05008 artemia san
45	94	58.0	81	5 Q17142	Q17142 brachioiost

ALIGNMENTS

RESULT 1

Q9XYT7	Q9XYT7	PRELIMINARY;	PRT;	274 AA.
AC	Q9XYT7;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Scx-3 homeodomain protein (Fragment).			
DE	SCOX-3.			
GN	Cassiopea xamachana.			
OS	Eukaryota; Metazoa; Cnidaria; Scyphozoa; Rhizostomeae; Cassiopeidae;			
OC	Cassiopea.			
OC	NCBI_TaxID=12993;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kuhn K., Streit B., Schierwater B.;			
RT	"Isolation of Hox genes from the scyphozoan Cassiopeia xamachana:			
RT	Implications for the early evolution of Hox genes."			
RL	J. Exp. Zool. 0:0-0(1999).			
CC	- - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
DR	EMBL; AF124593; A032577.1;			
DR	HSSP; P02833; 9ANT.			
DR	InterPro; IPR001356; Homeobox.			
DR	InterPro; IPR000047; HTH_repressr.			
DR	Pfam; PF00046; homeobox; 1.			
DR	PRINTS; PR00024; HOMEBOX.			
DR	PRINTS; PR00031; HTHREPRESSR.			
DR	ProDom; PD000010; Homeobox; 1.			
DR	SMART; SM00389; Hox; 1.			
DR	PROSITE; PS00027; HOMEBOX_1; 1.			
DR	PROSITE; PS00071; HOMEBOX_2; 1.			
KW	DNA-binding; Homeobox; Nuclear protein.			
FT	NON_TER 1			
SQ	SEQUENCE 274 AA; 31041 MW; 58EE91F6E540C3A9 CRC64;			

Query Match 62.7%; Score 101.5; DB 5; Length 274;
Best Local Similarity 64.5%; Pred. No. 5.2e-06;
Matches 20; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

RESULT	ID	PRELIMINARY	PRT	181 AA.
3	Q26611			
AC	Q26611;			
DT	01-NOV-1996	(trEMBLrel. 01, Created)		
DT	01-NOV-1996	(trEMBLrel. 01, Last sequence update)		
DT	01-MAR-2002	(trEMBLrel. 20, Last annotation update)		
DE	Homeobox protein (Fragment).			
DE	Styela plicata (Sea squirt).			
OS	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;			
OC	Stolidobranchia; Styelidae; Styela.			
OC	NCBI_TaxID=7726;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=ASCIDIAN;			
RA	Ge T., Lee H., Tomlinson C.R.;			
RA	"Identification of an Antennapedia-like Homeobox Gene ;			
RT	Styela clave and plicata.,"			
RT	Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	EMBL; U05600; AAA16288.1; "			
DR	HSSP; P02833; 9ANT.			

01-JUN-1998 (TREMBLrel. 06, Last s

RESULT 3
Q26611
ID Q26611 PRELIMINARY; PRT; 181 AA.
AC Q26611;
DT 01-NOV-1996 (trEMBLrel. 01, Created)
DT 01-NOV-1996 (trEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (trEMBLrel. 20, Last annotation update)
DE Homeobox protein (Fragment).
DS Styela plicata (Sea squirt).
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ASCIDIAN;
RT Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
RL Styela clavae and plicata.";
RL Submitted (JAN-1984) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL; U05600; AAA16288.1; -
DR HSSP; P02833; 9ANT.

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Hoxc5 protein (Fragment).
 GN HOXC5A OR HOXC5.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear
 expression patterns in the trunk";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y14526; CAA74874.1; -
 DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12E58860 CRC64;

 Query Match 58.0%; Score 94; DB 13; Length 39;
 Best Local Similarity 94.1%; Pred. No. 7.5e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DRQIKIWFQNRKMKWK 17
 Db :|||||
 13 ERQIKIWFQNRKMKWK 29

 RESULT 6
 057359 PRELIMINARY; PRT; 43 AA.
 ID Q57359
 AC Q57359
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Hoxc5 protein (Fragment).
 GN HOXC5B OR HOXC5.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear
 expression patterns in the trunk";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y14526; CAA74861.1; -
 DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

 Query Match 58.0%; Score 94; DB 13; Length 43;
 Best Local Similarity 94.1%; Pred. No. 8.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRKMKWK 17
 Db :|||||
 9 ERQIKIWFQNRKMKWK 25

 RESULT 7
 09PVR9 PRELIMINARY; PRT; 46 AA.
 ID Q9PVR9
 AC Q9PVR9
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE HOXC5A (Fragment).
 GN HOXC5A.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medakafish Oryzias latipes";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026960; BAA86243.1; -
 DR HSSP; P02833; IHOM.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 46 AA; 5955 MW; 60399999ED4294DD3 CRC64;

 Query Match 58.0%; Score 94; DB 13; Length 46;
 Best Local Similarity 94.1%; Pred. No. 8.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DRQIKIWFQNRKMKWK 17
 Db :|||||
 22 ERQIKIWFQNRKMKWK 38

 RESULT 8
 026407 PRELIMINARY; PRT; 51 AA.
 ID Q26407
 AC Q26407
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE CTS-Dfd protein (Fragment).
 GN CTS-DFD.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OX NCBI_TaxID=40316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94356262; PubMed-7915607;
 RA Dick M.H., Buss L.W.;
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
 (Annelida: Polychaeta).";
 RL Mol. Phylogenet. Evol. 3:146-158(1994).
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; S76416; AAB31775.1; -

DR HSP: P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 51;
 Best Local Similarity 94.1%; Pred. No. 9.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRKWK 17
 DB 22 ERQIKWQNRMRKWK 38

RESULT 9

Q23743 ID Q23743 PRELIMINARY; PRT; 51 AA.
 AC Q23743;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Deformed ortholog homeobox (Fragment).
 GN CTS-DFD.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OX NCBI_TaxID=40316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356262; PubMed=7915607;
 RA Dick M.H., Buss L.W.;
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
 (Annelida: Polychaeta).";
 RL Mol. Phylogenet. Evol. 3:146-158(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dick M.H., Buss L.W.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U26627; AAC46849.1; -
 DR HSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 51;
 Best Local Similarity 94.1%; Pred. No. 9.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRKWK 17
 DB 22 ERQIKWQNRMRKWK 38

RESULT 10
 Q27413 ID Q27413 PRELIMINARY; PRT; 51 AA.
 AC Q27413;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE LOX5 ORTHOLOG homeobox (Fragment).
 GN CTS-LOX5.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OX NCBI_TaxID=40316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356262; PubMed=7915607;
 RA Dick M.H., Buss L.W.;
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
 (Annelida: Polychaeta).";
 RL Mol. Phylogenet. Evol. 3:146-158(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dick M.H., Buss L.W.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U26629; AAC46851.1; -
 DR EMBL; S76226; AAB31777.1; -
 DR HSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 51;
 Best Local Similarity 94.1%; Pred. No. 9.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWQNRMRKWK 17
 DB 22 ERQIKWQNRMRKWK 38

RESULT 11

Q9PVR8 ID Q9PVR8 PRELIMINARY; PRT; 57 AA.
 AC Q9PVR8;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE HOXA5A (Fragment).
 GN HOXA5A.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medakafish Oryzias latipes.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026961; BAA86244.1; -

DR HSSP: P02833; IHOM.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_repressor.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;

Query Match 58.0%; Score 94; DB 13; Length 57;
Best Local Similarity 94.1%; Pred. No. 1.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMMKKK 17
Db 22 ERQIKIWFQNRMMKKK 38

RESULT 12

ID Q9Y188 PRELIMINARY; PRT; 58 AA.
AC Q9Y188;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hbl homeodomain protein (Fragment).
GN Hbl.
OS Priapulus caudatus.
OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulidae.
OX NCBI_TaxID=37621;
RN [1]
RX MEDLINE=99318125; PubMed=10391241;
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution."
RL Nature 399:772-776(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF144888; RAD40644.1; -.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_repressor.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A613 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 58;
Best Local Similarity 94.1%; Pred. No. 1.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMMKKK 17
Db 23 ERQIKIWFQNRMMKKK 39

RESULT 13

ID Q25208 PRELIMINARY; PRT; 58 AA.
AC Q25208;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Antennapedia protein (Fragment).
GN ANTENNAPEIDIA.
OS Junonia coenia (Peacock butterfly) (Precis coenia).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
OX NCBI_TaxID=39708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95075456; PubMed=7840822;
RA Warren R.W., Nagy L., Selegue J., Gates J., Carroll S.;
RT "Evolution of homeotic gene regulation and function in flies and
butterflies."
RL Nature 372:458-461(1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: L42135; AAA68461.1; -.
DR HSSP: P02833; IHOM.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_repressor.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 7583 MW; BD69B4875BAE565E CRC64;

Query Match 58.0%; Score 94; DB 5; Length 58;
Best Local Similarity 94.1%; Pred. No. 1.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMMKKK 17
Db 42 ERQIKIWFQNRMMKKK 58

RESULT 14

ID O57362 PRELIMINARY; PRT; 58 AA.
AC O57362;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hoxb7 protein (Fragment).
GN HOXB7A OR HOXB7.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
expression patterns in the trunk."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: Y14533; CAA74868.1; -.
DR TRANSFAC: T03635;
DR ZFIN: ZDB-GENE-000329-2; hoxb7a.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.

FT NON_TER 1 1
 SQ SEQUENCE 58 AA; 6863 MW; 41EAGF14488DA1E5 CRC64;
 Query Match 58.0%; Score 94; DB 13; Length 58;
 Best Local Similarity 94.1%; Pred. No. 1.1e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRKWK 17
 :|||||
 Db 13 ERQIKWFQNRMRKWK 29

RESULT 15

Q8WRM9 PRELIMINARY; PRT; 59 AA.
 AC Q8WRM9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Antennapedia (Fragment).
 GN ANTP.
 OS Lithobius atkinsoni.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius.
 OX NCBI_TaxID-177213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hughes C.L., Kaufman T.C.;
 RT "Exploring the myriapod body plan: expression patterns of the ten Hox
 genes in a centipede."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF434996; AAL36901.1; .
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
 DR PROSITE; PS0071; HOMEBOX_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 59 AA; 7093 MW; 9E60036CE0D515C1 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 59;
 Best Local Similarity 94.1%; Pred. No. 1.1e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRKWK 17
 :|||||
 Db 22 ERQIKWFQNRMRKWK 38

Search completed: May 30, 2003, 14:39:08
 Job time : 69.8947 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2.6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
 - 3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
 - 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
 - 5: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
 - 6: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
 - 7: /cgn2.6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
 - 8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
 - 9: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
 - 10: /cgn2.6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
 - 11: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
 - 12: /cgn2.6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
 - 13: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
 - 14: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	6	9	US-09-847-940B-17
2	41	100.0	6	9	US-09-847-946A-17
3	41	100.0	6	9	US-09-847-946A-45
4	41	100.0	6	9	US-09-847-946A-117
5	41	100.0	7	9	US-09-847-946A-121
6	41	100.0	8	9	US-09-847-946A-114
7	41	100.0	8	9	US-09-847-946A-122
8	41	100.0	9	9	US-09-847-946A-113
9	41	100.0	9	9	US-09-847-946A-116
10	41	100.0	9	9	US-09-847-946A-119
11	41	100.0	9	9	US-09-847-946A-120
12	41	100.0	10	9	US-09-847-946A-115
13	41	100.0	10	9	US-09-847-946A-118
14	41	100.0	11	9	US-09-847-946A-112
15	37	90.2	70	10	US-09-864-761-46514
16	37	90.2	354	9	US-10-166-087-6
17	36	87.8	6	9	US-09-847-940B-2
18	36	87.8	6	9	US-09-847-946A-2
19	36	87.8	6	9	US-09-847-946A-33

20	36	87.8	7	9	US-09-847-946A-37	Sequence 37, Appl
21	36	87.8	8	9	US-09-847-946A-30	Sequence 30, Appl
22	36	87.8	8	9	US-09-847-946A-38	Sequence 38, Appl
23	36	87.8	9	9	US-09-847-946A-29	Sequence 29, Appl
24	36	87.8	9	9	US-09-847-946A-32	Sequence 32, Appl
25	36	87.8	9	9	US-09-847-946A-35	Sequence 35, Appl
26	36	87.8	9	9	US-09-847-946A-36	Sequence 36, Appl
27	36	87.8	10	9	US-09-847-946A-31	Sequence 31, Appl
28	36	87.8	10	9	US-09-847-946A-34	Sequence 34, Appl
29	36	87.8	11	9	US-09-847-946A-28	Sequence 28, Appl
30	36	87.8	11	9	US-09-847-946A-132	Sequence 132, App
31	36	87.8	11	9	US-09-847-946A-140	Sequence 140, App
32	36	87.8	13	9	US-09-847-946A-143	Sequence 143, App
33	36	87.8	13	9	US-09-847-946A-144	Sequence 144, App
34	36	87.8	13	9	US-09-847-946A-145	Sequence 145, App
35	36	87.8	13	9	US-09-847-946A-148	Sequence 148, App
36	36	87.8	17	9	US-09-847-946A-141	Sequence 141, App
37	36	87.8	17	9	US-09-847-946A-142	Sequence 142, App
38	36	87.8	17	9	US-09-847-946A-146	Sequence 146, App
39	36	87.8	17	9	US-09-847-946A-147	Sequence 147, App
40	36	87.8	18	9	US-09-847-946A-131	Sequence 131, App
41	36	87.8	18	9	US-09-847-946A-135	Sequence 135, App
42	36	87.8	18	9	US-09-847-946A-136	Sequence 136, App
43	36	87.8	22	9	US-09-847-946A-133	Sequence 133, App
44	36	87.8	22	9	US-09-847-946A-134	Sequence 134, App
45	36	87.8	22	9	US-09-847-946A-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-09-847-940B-17
; Sequence 17, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-17

Query Match 100.0%; Score 41; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 2
US-09-847-946A-17
; Sequence 17, Application US/09847946A
; Publication No. US20030034999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-17

Query Match 100.0%; Score 41; DB 9; Length 6;
Best Local Similarity 100.0%; Pred.No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 3
US-09-847-946A-45
; Sequence 45, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-45

Query Match 100.0%; Score 41; DB 9; Length 6;
Best Local Similarity 100.0%; Pred.No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 4
US-09-847-946A-117
; Sequence 117, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-117

Query Match 100.0%; Score 41; DB 9; Length 6;
Best Local Similarity 100.0%; Pred.No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 5
US-09-847-946A-121
; Sequence 121, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-121

Query Match 100.0%; Score 41; DB 9; Length 7;
Best Local Similarity 100.0%; Pred.No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 6
US-09-847-946A-114
; Sequence 114, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 114
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-114

Query Match 100.0%; Score 41; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 3 LDWEWL 8

RESULT 7
US-09-847-946A-122
Sequence 122, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 122
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-122

Query Match 100.0%; Score 41; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 8
US-09-847-946A-113

Sequence 113, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 113
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-113

Query Match 100.0%; Score 41; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 9
US-09-847-946A-116
Sequence 116, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 116
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-116

Query Match 100.0%; Score 41; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 10

US-09-847-946A-119
; Sequence 119, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 60/201,261
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-119

Query Match 100.0%; Score 41; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 3 LDWEWL 8

RESULT 11

US-09-847-946A-120
; Sequence 120, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 60/201,261
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-120

Query Match 100.0%; Score 41; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6

Db 2 LDWEWL 7

RESULT 12

US-09-847-946A-115
; Sequence 115, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 60/201,261
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-115

Query Match 100.0%; Score 41; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 2 LDWEWL 7

RESULT 13

US-09-847-946A-118
; Sequence 118, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 60/201,261
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-118

Query Match 100.0%; Score 41; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||||

Db 3 LDWEWL 8

RESULT 14

US-09-847-946A-112
; Sequence 112, Application US/09847946A
; Publication No. US2003005499A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Flindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 112
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding

US-09-847-946A-112
Query Match 100.0%; Score 41; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
|||||

Db 3 LDWEWL 8

RESULT 15

US-09-864-761-46514
; Sequence 46514, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

Query Match 90.2%; Score 37; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
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Db 43 DWEWL 47

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Job time : 11.4605 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: us-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	6	23	Mutated IKKbeta NE
2	41	100.0	6	23	NBD mutant peptide
3	41	100.0	6	23	Anti-inflammatory
4	41	100.0	6	23	Anti-inflammatory
5	41	100.0	7	23	Anti-inflammatory
6	41	100.0	8	23	Anti-inflammatory
7	41	100.0	8	23	Anti-inflammatory
8	41	100.0	9	23	Anti-inflammatory
9	41	100.0	9	23	Anti-inflammatory
10	41	100.0	9	23	Anti-inflammatory

11	41	100.0	9	23	Anti-inflammatory
12	41	100.0	10	23	Anti-inflammatory
13	41	100.0	10	23	Anti-inflammatory
14	41	100.0	11	23	Anti-inflammatory
15	41	100.0	756	23	Human IKKbeta muta
16	38	92.7	12	21	Human peptido-mime
17	38	92.7	243	22	Propionibacterium
18	37	90.2	20	23	Insulin/insulin-li
19	37	90.2	70	22	Human bone marrow
20	37	90.2	70	22	Peptide #1807 enco
21	37	90.2	70	23	Human peptidase enco
22	37	90.2	210	20	Schizosaccharomyce
23	37	90.2	379	22	Putative P. abyssi
24	37	90.2	408	22	Putative P. abyssi
25	37	90.2	692	22	Micromonospora eve
26	37	90.2	1291	22	Drosophila melanog
27	36	87.8	6	23	IKKbeta NEMO bindi
28	36	87.8	6	23	Anti-inflammatory
29	36	87.8	6	23	NBD mutant peptide
30	36	87.8	7	23	Anti-inflammatory
31	36	87.8	8	23	Anti-inflammatory
32	36	87.8	8	23	Anti-inflammatory
33	36	87.8	9	20	IKK-alpha polypept
34	36	87.8	9	23	Anti-inflammatory
35	36	87.8	9	23	Anti-inflammatory
36	36	87.8	9	23	Anti-inflammatory
37	36	87.8	9	23	Anti-inflammatory
38	36	87.8	10	23	IKKbeta NEMO bindi
39	36	87.8	10	23	Anti-inflammatory
40	36	87.8	10	23	Anti-inflammatory
41	36	87.8	11	23	Human NBD peptide
42	36	87.8	11	23	Human IKKbeta pept
43	36	87.8	11	23	Anti-inflammatory
44	36	87.8	11	23	NBD peptide. Synt
45	36	87.8	13	23	Anti-inflammatory

ALIGNMENTS

RESULT 1
ABB08739

ID ABB08739 standard; peptide; 6 AA.

XX ABB08739;

XX 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 17.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX autoimmunity disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; antineoplastic; immunosuppressive;
XX osteopathic; cytotoxic; neutropenic; neuroprotective; anti-HIV; human;
XX antiarteriosclerotic; virucide; antiallergic; antiallergic;
XX dermatological; antibacterial; antipsoriatic; antineoplastic;
XX antiarthritic; osteopathic; antitumor; mutant; mutagen.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 4 /note= "Wildtype Ser substituted by Glu"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYVA) UNIV YALE.
 XX May MJ, Ghosh S;
 PI WPI; 2002-179350/23.
 DR
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 XX Claim 23; Page 45; 82pp; English.
 PS
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 1 LDWEWL 6
 RESULT 2
 ID AAM48522
 XX AAM48522 standard; Peptide; 6 AA.
 AC AAM48522;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 17.
 XX

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Example 6; Page 48; 88pp; English.
 CC
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 1 LDWEWL 6
 RESULT 3
 ID AAM48542
 XX AAM48542 standard; Peptide; 6 AA.
 XX

AA48542;
 20-MAR-2002 (first entry)
 Anti-inflammatory peptide SEQ ID NO 45.

Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 autoimmune disorder; multiple sclerosis; transplant rejection;
 osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 Synthetic.
 WO200183554-A2.
 08-NOV-2001.
 02-MAY-2001; 2001WO-US14346.
 02-MAY-2000; 2000US-201261P.
 22-AUG-2000; 2000US-0643260.
 (PRAE-) PRAECIS PHARM INC.
 (UYVA) UNIV YALE.
 May MJ, Ghosh S, Findeis MA, Phillips K;
 WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation
 domain fused to NEMO binding sequence, useful for blocking nuclear
 factor kappaB activation, and for treating asthma, lung inflammation,
 psoriasis

Claim 6; Page 61; 88pp; English.

The invention relates to an antiinflammatory compound (especially
 AA48628-AA48645), comprising a membrane translocation domain
 (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 amino acid residues, fused to a NEMO binding sequence
 (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 antibacterial, immunosuppressive, dermatological, neuroprotective,
 compounds act as selective inhibitors of cytokine-mediated NFkappaB
 activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 the NEMO binding domain that results in inhibition of IKKbeta kinase
 activation and subsequent decreased phosphorylation of IkappaB. The
 compounds are useful for treating inflammatory disorders, e.g. asthma,
 lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 telangiectasia. The compounds are also useful for treating
 pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 arthritis.

Sequence 6 AA;

Query Match 100.0%; Score 41; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6

Db 1 LDWEWL 6

RESULT 4

AA48614

ID AA48614 standard; Peptide; 6 AA.

XX AC AA48614;

XX AC 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 117.

XX DE Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 Antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
 immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 autoimmune disorder; multiple sclerosis; transplant rejection;
 osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 Synthetic.

OS WO200183554-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation
 domain fused to NEMO binding sequence, useful for blocking nuclear
 factor kappaB activation, and for treating asthma, lung inflammation,
 psoriasis

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially
 AA48628-AA48645), comprising a membrane translocation domain
 (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 amino acid residues, fused to a NEMO binding sequence
 (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 antibacterial, immunosuppressive, dermatological, neuroprotective,
 compounds act as selective inhibitors of cytokine-mediated NFkappaB
 activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 the NEMO binding domain that results in inhibition of IKKbeta kinase
 activation and subsequent decreased phosphorylation of IkappaB. The
 compounds are useful for treating inflammatory disorders, e.g. asthma,
 lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 telangiectasia. The compounds are also useful for treating
 pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 arthritis.

Sequence 6 AA;

Query Match 100.0%; Score 41; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
XX arthritis.
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 1 LDWEWL 6

RESULT 5
AAM48618
ID AAM48618 standard; Peptide; 7 AA.
XX
AC AAM48618;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 121.
XX
KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRACIS PHARM INC.
PA (UYVA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
PI WPI; 2002-121889/16.
XX
PS Claim 6; Page 62; 89pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
CC antibacterial, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

RESULT 6
AAM48611
ID AAM48611 standard; Peptide; 8 AA.
XX
AC AAM48611;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 114.
XX
KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRACIS PHARM INC.
PA (UYVA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
PI WPI; 2002-121889/16.
XX
PS Novel antiinflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis
XX
XX Claim 6; Page 62; 89pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
CC antibacterial, immunosuppressive, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 41; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 Db 3 LDWEWL 8
 |||||

RESULT 7
 AAM48619
 ID AAM48619 standard; Peptide; 8 AA.
 AC AAM48619;
 XX
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 122.
 XX
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX PD 08-NOV-2001.
 XX
 XX PD 02-MAY-2001; 2001WO-US14346.
 XX
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYVA) UNIV YALE.
 XX
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 PS Claim 6; Page 62; 88pp; English.

XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 41; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 Db 1 LDWEWL 6
 |||||

RESULT 8
 AAM48610
 ID AAM48610 standard; Peptide; 9 AA.
 AC AAM48610;
 XX
 XX DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 113.
 XX
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX PD 08-NOV-2001.
 XX
 XX PD 02-MAY-2001; 2001WO-US14346.
 XX
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYVA) UNIV YALE.
 XX
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 PS Novel antiinflammatory compound comprising membrane translocation
 PS domain fused to NEMO binding sequence, useful for blocking nuclear
 PS factor kappaB activation, and for treating asthma, lung inflammation,
 PS psoriasis -
 PS
 PS Claim 6; Page 62; 88pp; English.

XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytotstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWEWL 6
 D 1 LDWEWL 6

RESULT 9
 AAM48613
 ID AAM48613 standard; Peptide; 9 AA.
 XX AC AAM48613;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 116.
 KW Anti-inflammatory; antiasthmatic; cytotstatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX OS Synthetic.
 XX PN WO200183554-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US14346.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYIA) UNIV YALE.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPT: 2002-121889/16.
 XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -
 XX Claim 6; Page 62; 88pp; English.
 CC The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytotstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWEWL 6
 D 1 LDWEWL 6

RESULT 10
 AAM48616
 ID AAM48616 standard; Peptide; 9 AA.
 XX AC AAM48616;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 119.
 KW Anti-inflammatory; antiasthmatic; cytotstatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX OS Synthetic.
 XX PN WO200183554-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US14346.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYIA) UNIV YALE.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PA Novel antiinflammatory compound comprising membrane translocation

XX PT domain fused to NEMO binding sequence, useful for blocking nuclear

XX PT factor kappaB activation, and for treating asthma, lung inflammation,

XX PT psoriasis

XX PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWEWL 6

Db 3 LDWEWL 8

RESULT 11

AAM48617

ID AAM48617 standard; Peptide; 9 AA.

XX AC AAM48617;

XX DT 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 120.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

XX autoimmune disorder; multiple sclerosis; transplant rejection;

XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX WO200183554-A2.

XX PD 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX PA (UYIA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

DR Novel antiinflammatory compound comprising membrane translocation

XX domain fused to NEMO binding sequence, useful for blocking nuclear

XX factor kappaB activation, and for treating asthma, lung inflammation,

XX psoriasis

XX PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWEWL 6

Db 2 LDWEWL 7

RESULT 12

AAM48612

ID AAM48612 standard; Peptide; 10 AA.

XX AC AAM48612;

XX DT 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 115.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

XX autoimmune disorder; multiple sclerosis; transplant rejection;

XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX WO200183554-A2.

XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US14346.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYVA) UNIV YALE.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX DR WPI; 2002-121889/16.
 XX PS Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 41; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 2 LDWEWL 7
 RESULT 13
 AAM48615
 ID AAM48615 standard; Peptide; 10 AA.
 XX AC AAM48615;
 XX 20-MAR-2002 (first entry)
 DT Anti-inflammatory peptide SEQ ID NO 118.
 DE Anti-inflammatory peptide SEQ ID NO 118.
 XX Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX WO200183554-A2.
 PN 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 41; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 3 LDWEWL 8
 RESULT 14
 AAM48609
 ID AAM48609 standard; Peptide; 11 AA.
 XX AC AAM48609;
 XX 20-MAR-2002 (first entry)
 DT Anti-inflammatory peptide SEQ ID NO 112.
 DE Anti-inflammatory peptide SEQ ID NO 112.
 XX Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14346.
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
XX (UYUA) UNIV YALE.
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX Claim 6; Page 62; 88pp; English.
XX The invention relates to an antiinflammatory compound (especially
XX AAM48628-AAM48645), comprising a membrane translocation domain
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
XX cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NFkappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IKKbeta kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g. asthma,
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
XX bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
XX telangiectasia. The compounds are also useful for treating
XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and
XX arthritis.
XX Sequence 11 AA;
XX Query Match 100.0%; Score 41; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 4.1;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
Db 3 LDWEWL 8
RESULT 15
ABB77307
ID ABB77307 standard; protein; 756 AA.
XX ABB77307;
AC ABB77307;

14-JUN-2002 (first entry)
Human IKKbeta mutant S740E.
IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-KB;
kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
autoimmune disease; transplant rejection; osteoporosis; cancer;
Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
antiarteriosclerotic; virucide; antiasthmatic; anti-allergic;
dermatological; antibacterial; antipsoriatic; antirheumatic;
antiarthritic; osteopathic; antiulcer; mutant; muten.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
FT Misc-difference 740 /note= "Wildtype Ser substituted by Glu"
FT (UYUA) UNIV YALE.
PN WO200183547-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US40654.
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX (UYUA) UNIV YALE.
XX May MJ, Ghosh S;
XX WPI; 2002-179350/23.
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
XX inflammatory disorders, osteoporosis and cancer, comprises contacting a
XX cell with an anti-inflammatory compound comprising at least one NEMO
XX binding domain -
XX Example 11; Page -; 82pp; English.
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
XX comprises contacting a cell with an anti-inflammatory compound
XX (ABB08725-ABB08742) comprising at least one NEMO binding domain
XX (ABB77313). The compound has acts through selective inhibition of
XX cytokine-mediated NF-kB activation by blocking the interaction of NEMO
XX with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
XX interaction results in inhibition of IKKbeta kinase activation and
XX subsequent decreased phosphorylation of IkappaB. The compound may also
XX act (directly or indirectly) by blocking the recruitment of leukocytes
XX into sites of acute and chronic inflammation, by down-regulating the
XX expression of E-selectin on leukocytes or by blocking osteoclast
XX differentiation. The compound is useful in treating NF-kB mediated
XX conditions, where the condition is an inflammatory disorder, an
XX autoimmune disease, transplant rejection, osteoporosis, cancer,
XX Alzheimer's disease, atherosclerosis, a viral infection or ataxia
XX telangiectasia. The inflammatory disorder is asthma, allergies,
XX urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
XX rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
XX bowel disease, chronic obstructive pulmonary disease, vasculitis and
XX bursitis. The inflammatory disorder may also be dermatitis, eczema,
XX psoriasis, osteoarthritis, psoriatic arthritis, lupus and
XX spondylarthritis. Also for Crohn's disease, ulcerative colitis,
XX polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
XX cryoglobulinemia or multiple sclerosis. For chronic viral infections
XX caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
XX diseases include HIV and influenza. The compound may also be useful for
XX treating anaphylaxis, drug and food sensitivity, contact dermatitis,
XX sunburn or aging. The compound may be used to replace corticosteroids in

CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. O14920 (ABB77294).

XX
 SQ Sequence 756 AA;

Query Match 100.0%; Score 41; DB 23; Length 756;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6

|||||

Db 737 LDWEWL 742

Search completed: May 30, 2003, 14:50:02
 Job time : 20.7529 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred..No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	87.8	439	4	US-09-172-952-14
2	36	87.8	745	2	US-08-887-518-3
3	36	87.8	745	2	US-09-023-321-3
4	36	87.8	745	2	US-08-890-853-4
5	36	87.8	745	2	US-09-032-475-3
6	36	87.8	745	2	US-09-099-125A-4
7	36	87.8	745	2	US-09-099-124A-4
8	36	87.8	745	4	US-09-032-476-4
9	36	87.8	745	4	US-08-850-854-4
10	36	87.8	745	4	US-09-023-324-4
11	36	87.8	745	4	US-09-168-629-2
12	36	87.8	745	4	US-08-910-820-10
13	36	87.8	745	4	US-08-810-131A-2
14	36	87.8	756	2	US-08-887-518-4
15	36	87.8	756	2	US-09-023-321-4
16	36	87.8	756	2	US-08-890-853-2
17	36	87.8	756	2	US-09-032-475-4
18	36	87.8	756	2	US-09-099-125A-2
19	36	87.8	756	2	US-09-099-124A-2
20	36	87.8	756	4	US-09-032-476-2
21	36	87.8	756	4	US-08-890-854-2
22	36	87.8	756	4	US-09-023-324-2
23	36	87.8	756	4	US-09-168-629-15
24	36	87.8	756	4	US-08-910-820-9
25	34	82.9	38	2	US-08-488-161-55
26	34	82.9	38	3	US-09-273-685-55
27	34	82.9	38	5	PCT-US95-11934-55

28	34	82.9	138	1	US-08-686-878A-33	Sequence 33, Appl
29	34	82.9	138	4	US-09-175-928-33	Sequence 33, Appl
30	33	80.5	25	4	US-09-082-279B-1275	Sequence 1275, Ap
31	33	80.5	25	4	US-09-315-304B-1275	Sequence 1275, Ap
32	33	80.5	162	4	US-09-199-637A-161	Sequence 161, App
33	33	80.5	162	4	US-09-199-637A-162	Sequence 162, App
34	33	80.5	437	4	US-09-199-637A-116	Sequence 116, App
35	33	80.5	566	1	US-08-419-078-2	Sequence 2, Appl
36	33	80.5	566	1	US-08-726-883-2	Sequence 2, Appl
37	33	80.5	853	3	US-09-254-325-2	Sequence 2, Appl
38	33	80.5	866	3	US-09-079-415-6	Sequence 6, Appl
39	33	80.5	866	3	US-08-750-458A-2	Sequence 2, Appl
40	32	78.0	23	6	5368712-2	Patent No. 5368712
41	32	78.0	23	6	5516890-2	Patent No. 5516890
42	32	78.0	100	1	US-08-241-853-28	Sequence 28, Appl
43	32	78.0	100	1	US-08-241-853-29	Sequence 29, Appl
44	32	78.0	100	2	US-08-850-917-28	Sequence 28, Appl
45	32	78.0	100	2	US-08-850-917-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-172-952-14
; Sequence 14, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172.952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 439
; TYPE: PRT
; ORGANISM: YiaX2
US-09-172-952-14

Query Match 87.8%; Score 36; DB 4; Length 439;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qv 1 LDWEWL 6
Db 171 LDWEWL 176

RESULT 2
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 738 LDWSWL 743

RESULT 3
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 87.8%; Score 36; DB 2; Length 745;

Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 738 LDWSWL 743

RESULT 4
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 738 LDWSWL 743

RESULT 5
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA

;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/032,475
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/887,518
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-032-475-3

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 6
US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-099-125A-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 7
US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 8
US-09-032-476-4

; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-032-476-4

Query Match 87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 9
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-032-476-4

; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-854-4

Query Match 87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 10
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-023-324-4

Query Match 87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 11

US-09-168-629-2
Sequence 2, Application US/09168629

Patent No. 6242253

GENERAL INFORMATION:

APPLICANT: Karin, Michael

APPLICANT: DiDonato, Joseph A.

APPLICANT: Rothwarf, David M.

APPLICANT: Hayakawa, Makio

APPLICANT: Zandi, Ebrahim

TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same

FILE REFERENCE: P-UD 3295

CURRENT APPLICATION NUMBER: US/09/168,629

CURRENT FILING DATE: 1998-10-08

EARLIER APPLICATION NUMBER: 60/061,470

EARLIER FILING DATE: 1997-10-09

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 745

TYPE: PRT

ORGANISM: Homo sapiens

US-09-168-629-2

Query Match 87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 12

US-08-910-820-10

Sequence 10, Application US/08910820

Patent No. 6258579

GENERAL INFORMATION:

APPLICANT: Mercurio, Frank

APPLICANT: Zhu, Hengyi

APPLICANT: Barbosa, Miguel

APPLICANT: Li, Gian

APPLICANT: Murray, Brian W.

TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE

TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,820

FILING DATE: 12-AUG-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 860098.413C1

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-910-820-10

Query Match 87.8%; Score 36; DB 4; Length 745;

Best Local Similarity 83.3%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 13

US-08-810-131A-2

Sequence 2, Application US/08810131A

Patent No. 6268194

GENERAL INFORMATION:

APPLICANT: Karin, Michael

APPLICANT: DiDonato, Joseph A.

APPLICANT: Rothwarf, David M.

APPLICANT: Hayakawa, Makio

APPLICANT: Zandi, Ebrahim

TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,131A

FILING DATE: 25-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2408

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-810-131A-2

Query Match 87.8%; Score 36; DB 4; Length 745;

Best Local Similarity 83.3%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6

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Db      738 LDWSWL 743
|||||
RESULT 14
US-08-887-518-4
; Sequence 4, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-887-518-4

Query Match      87.8%; Score 36; DB 2; Length 756;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDWEWL 6
Db      737 LDWSWL 742

RESULT 15
US-09-023-321-4
; Sequence 4, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-023-321-4

Query Match      87.8%; Score 36; DB 2; Length 756;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDWEWL 6
Db      737 LDWSWL 742

Search completed: May 30, 2003, 14:41:32
Job time : 6.03947 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	95.1	501	2 S45914	probable glucan 1,
2	37	90.2	210	2 T41553	thymidylate kinase
3	37	90.2	210	2 S28955	trmp kinase (EC 2.
4	37	90.2	242	2 T27590	hypothetical prote
5	37	90.2	277	1 JC5900	bo-type ubiquinol
6	37	90.2	281	2 S73617	MG373 homolog G12
7	37	90.2	296	2 A84985	cytochrome o ubiq
8	37	90.2	307	1 A36885	bo-type ubiquinol
9	37	90.2	318	2 AD0384	cytochrome o ubiq
10	37	90.2	331	2 D83480	cytochrome o ubiq
11	37	90.2	344	2 AG3489	cytochrome o ubiq
12	37	90.2	353	2 A87459	ubiquinol oxidase
13	37	90.2	377	2 B71184	probable sarcosine
14	37	90.2	379	2 F75144	sarcosine oxidase,
15	37	90.2	386	2 C96006	alanine-trna ligas
16	37	90.2	404	2 A71213	alanyl-trna synthe
17	37	90.2	405	2 G75027	hypothetical prote
18	37	90.2	488	2 S40706	o-antigen biosynth
19	37	90.2	1275	2 T18556	hypothetical prote
20	36	87.8	82	2 C69013	hypothetical prote
21	36	87.8	162	2 C70829	hypothetical prote
22	36	87.8	270	2 I40724	hypothetical prote
23	36	87.8	322	2 A13395	NADH2 dehydrogenas
24	36	87.8	348	2 C97514	NADH dehydrogenase
25	36	87.8	348	2 AE2733	NADH ubiquinone ox
26	36	87.8	414	2 B82408	hypothetical prote
27	36	87.8	443	2 AE0309	probable sugar tra
28	36	87.8	745	1 I49101	conserved helix-lo
29	36	87.8	764	2 H98143	cbbc protein (U60

30 36 87.8 764 2 AD3144
31 36 87.8 1120 2 AI0561
32 35 85.4 332 2 AH2593
33 35 85.4 377 2 B97376
34 35 85.4 378 2 T12895
35 35 85.4 385 2 F69941
36 35 85.4 420 2 A54759
37 35 85.4 451 2 G82218
38 35 85.4 480 2 T24087
39 35 85.4 660 2 S66708
40 35 85.4 700 2 T24092
41 35 85.4 723 2 T32136
42 35 85.4 765 2 T35719
43 35 85.4 783 2 F88808
44 35 85.4 854 2 C83905
45 35 85.4 903 2 T20804

ALIGNMENTS

RESULT 1

S45914

Probable glucan 1,3-beta-glucosidase (EC 3.2.1.58) YBR056w - yeast (Saccharomyces cer
N:Alternate names: hypothetical protein YBR0510

C:Species: Saccharomyces cerevisiae

C>Date: 26-Aug-1994 #sequence-revision 09-Sep-1994 #text_change 19-Apr-2002

C:Accession: S45914; S49511; S55855

R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45906

A:Accession: S45914

A:Molecule type: DNA

A:Residues: 1-501 <ALJ>

A:Cross-references: EMBL:Z35925; NID:G536292; PID:G536293; MIPS:YBR056w

A:Experimental source: strain S288C

R:Aljinovic, G.

submitted to the EMBL Data Library, October 1994

A:Description: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerev

A:Reference number: S49503

A:Accession: S49511

A:Molecule type: DNA

A:Residues: 1-501 <ALJ>

A:Cross-references: EMBL:Z46260; NID:G559942; PID:G559952

A:Experimental source: strain S288C

R:Aljinovic, G.; Pohl, T.M.

Yeast 11, 475-479, 1995

A:Title: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae.

A:Reference number: S55846; MUID:95321020; PMID:7597852

A:Accession: S55855

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-501 <ALJ>

A:Cross-references: EMBL:Z46260; NID:G559942; PID:CAA86399.1; PID:G559952

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

C:Genetics:

A:Cross-references: SGD:S0000260

A:Map position: 2R

C:Keywords: glycosidase; hydrolase

Query Match 95.1%; Score 39; DB 2; Length 501;

Best Local Similarity 83.3%; Pred. No. 63;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEWL 6

Db 109 IDWEWL 114

RESULT 2

T41553

thymidylate kinase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C:Accession: T41553
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z22001
 A:Accession: T41553
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-210 <MOO>
 A:Cross-references: EMBL:AL023794; PIDN:CAA19357.1; GSPDB:GN00068; SPDB:SPCC70.07C
 A:Experimental source: strain 972h-; cosmid c70
 C:Genetics:
 A:Gene: SPDB:SPCC70.07C
 A:Map position: 3
 A:Introns: 45/1; 110/3
 C:Superfamily: dtmP kinase

Query Match 90.2%; Score 37; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 |||||

Db 112 LDWEW 116

RESULT 3

S28955

dtmP Kinase (EC 2.7.4.9) - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jan-2001

C:Accession: S28955

R:Abalgar, L.T.; Yeh, Y.I.S.; Jong, A.Y.

Biochim. Biophys. Acta 1132, 222-224, 1992

A:Title: Functional and structural conservation of Schizosaccharomyces pombe dtmP kinase

A:Reference number: S28955; MUID:93003330; PMID:1327149

A:Accession: S28955

A:Molecule type: mRNA

A:Residues: 1-210 <ABA>

A:Cross-references: EMBL:X65068; NID:94973; PIDN:CAA46698.1; PID:94974

C:Superfamily: dtmP kinase

C:Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase

F.14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 90.2%; Score 37; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 |||||

Db 111 LDWEW 115

RESULT 4

T27590

hypothetical protein ZC47.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T27590

R:McMurray, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z20391

A:Accession: T27590

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-242 <WIL>

A:Cross-references: EMBL:Z81141; PIDN:CA803488.1; CESP:ZC47.13

C:Genetics:

A:Gene: CESP:ZC47.13

A:Introns: 172/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 90.2%; Score 37; DB 2; Length 242;
 Best Local Similarity 83.3%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |:|||||

Db 226 LDWEWL 231

RESULT 5

JC5900

bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum

C:Species: Bradyrhizobium japonicum

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JC5900

R:Surpin, M.A.; Luebben, M.; Maier, R.J.

Gene 183, 201-206, 1996

A:Title: The Bradyrhizobium japonicum coxXYZ gene cluster encodes a bb3-type ubiquinol

A:Reference number: JC5900; MUID:97149299; PMID:8996107

A:Accession: JC5900

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-277 <SUR>

C:Genetics:

A:Gene: coxW

C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha

C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; r

Query Match 90.2%; Score 37; DB 1; Length 277;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||

Db 108 LDWKWL 113

RESULT 6

S73617

MG373 homolog G12_orf281 - Mycoplasma pneumoniae (strain ATCC 29342)

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C:Accession: S73617

R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A:Reference number: S73327; MUID:97105885; PMID:8948633

A:Accession: S73617

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-281 <HIM>

A:Cross-references: EMBL:AE000027; GB:U00089; NID:g1673941; PIDN:AAB95939.1; PID:g167

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Genetic code: SGC3

Query Match 90.2%; Score 37; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
 |||||

Db 271 DWEWL 275

RESULT 7

A84985

cytochrome o ubiquinol oxidase subunit II [Imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001

C:Accession: A84985

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: AB4930; MUID:20445173; PMID:10993077
A:Accession: A84985
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: cyoA; BU472
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 296;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:||
Db 125 LDWKWL 130

RESULT 8
A36885
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter acetii
N:Alternate names: cytochrome al chain II
C:Species: Acetobacter acetii
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A36885
R:Fukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horinouchi
J. Bacteriol. 175, 4307-4314, 1993
A:Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A
A:Reference number: A36885; MUID:93322308; PMID:8392509
A:Accession: A36885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <FUK>
A:Cross-references: GB:D13185; NID:g409064; PIDN:BAA02480.1; PID:g433186
A:Experimental source: isolate 1023
C:Genetics:
A:Gene: cyaB
C:Complex: heterotetramer; chains I, II, III and IV
C:Function:
A:Description: terminal oxidase for ethanol oxidation
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C:Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>
F:48-64/Domain: transmembrane #status predicted <TM1>
F:89-105/Domain: transmembrane #status predicted <TM2>

Query Match 90.2%; Score 37; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:||
Db 135 LDWKWL 140

RESULT 9
AD0384
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [Imported] - Yersinia pestis (stra
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD0384
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC923399.1; PID:g15981102; GSPDB:GN00175
C:Genetics:
A:Gene: cyoA
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; r

Query Match 90.2%; Score 37; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:||
Db 135 LDWKWL 140

RESULT 10
D83480
cytochrome o ubiquinol oxidase subunit II PA1317 [Imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83480
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <STO>
A:Cross-references: GB:AE004561; GB:AE004091; NID:g9947253; PIDN:AAG04706.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: cyoA; PA1317
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 331;
Best Local Similarity 83.3%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:||
Db 133 LDWKWL 138

RESULT 11
AG3489
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [Imported] - Brucella melitensi
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002
C:Accession: AG3489
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AG3489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53082.1; PID:g17983945; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1901
A:Map position: I
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; r

Query Match 90.2%; Score 37; DB 2; Length 344;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 DB 141 LDWKWL 146

RESULT 12
 A87469
 ubiquinol oxidase subunit II [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
 C:Accession: A87469
 R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87469
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-353 <STO>
 A:Cross-references: GB:AE005673; NID:gi3423199; PIDN:AAK23749.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC1773
 C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 353;
 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 DB 146 LDWKWL 151

RESULT 13
 B71184
 Probable sarcosine oxidase - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
 C:Accession: B71184
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: B71184
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-377 <KAW>
 A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30865.1; PID:g3258182
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1751
 C:Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 5
 DB 354 LDWEWL 358

F75144

sarcosine oxidase, chain beta (soxb) PAB0214 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: F75144
 R:Anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
 A:Reference number: A75001
 A:Accession: F75144
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-379 <KAW>
 A:Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49237.1; PID:g545
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: soxb; PAB0214
 C:Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 5
 DB 356 LDWEWL 360

RESULT 15

C96006

Probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] - S
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C96006
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C96006
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-386 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:gl5141202; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 658-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: cyoA; Smb21487
 A:Genome: plasmid
 C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase cha
 C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; r

Query Match 90.2%; Score 37; DB 2; Length 386;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 DB 141 LDWKWL 146

Search completed: May 30, 2003, 14:52:59
 Job time : 6.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	501	1 YB06_YEAST	P38081 saccharomyc
2	37	90.2	210	1 KTHY_SCHPO	P36590 schizosacch
3	37	90.2	281	1 Y373_MYCPN	P75227 mycoplasma
4	37	90.2	296	1 CY0A_BUCAI	P57344 buchnera ap
5	37	90.2	307	1 Q0X2_ACEAC	P50853 acetobacter
6	37	90.2	314	1 CY0A_PSEPU	Q9wwr1 pseudomonas
7	37	90.2	488	1 YKT1_CAEEL	P34312 caenorhabdi
8	37	90.2	1275	1 RFPC_MYXXA	Q50864 myxococcus
9	36	87.8	289	1 Y250_CORGL	P42459 corynebacte
10	36	87.8	745	1 IKKA_HUMAN	O15111 h inhibitor
11	36	87.8	745	1 IKKA_MOUSE	Q60680 m inhibitor
12	36	87.8	756	1 IKKB_HUMAN	O14920 homo sapien
13	36	87.8	757	1 IKKB_MOUSE	O88351 mus musculu
14	36	87.8	757	1 IKKB_RAT	Q9qy78 rattus norv
15	35	85.4	385	1 YPSC_BACSU	P50840 bacillus su
16	34	82.9	191	1 GD1R_CAEEL	Q20496 caenorhabdi
17	34	82.9	470	1 NOS2_ONCMY	Q92091 oncorhynchu
18	34	82.9	473	1 LACG_LACAC	P50977 lactobacill
19	34	82.9	844	1 AMPN_LACHE	Q10730 lactobacill
20	34	82.9	1113	1 Y140_MYCCE	P47386 mycoplasma
21	34	82.9	1113	1 Y140_MYCPN	P75033 mycoplasma
22	34	82.9	1120	1 KEFA_ECOLI	P77338 escherichia
23	33	80.5	94	1 FIXX_AZOVI	P53658 azotobacter
24	33	80.5	125	1 YG61_BPMO2	O64253 mycobacteri
25	33	80.5	162	1 PHZB_PSEFL	Q51788 pseudomonas
26	33	80.5	223	1 WNT1_STRPU	P28094 strongyloc
27	33	80.5	387	1 INTD_ECOLI	P24218 escherichia
28	33	80.5	418	1 HLT_VIBPA	Q99289 vibrio para
29	33	80.5	468	1 WNTG_DROME	P09615 drosophila
30	33	80.5	547	1 SPAK_HUMAN	Q9uew8 homo sapien
31	33	80.5	553	1 SPAK_RAT	O88506 rattus norv
32	33	80.5	556	1 SPAK_MOUSE	Q921w9 mus musculu
33	33	80.5	725	1 AREA_PENCH	Q01582 penicillium

34	33	80.5	807	1 PHK_RHILO	Q989v7 rhizobium 1
35	33	80.5	860	1 AREA_PENRO	O13508 penicillium
36	33	80.5	865	1 NRFA_PENUR	Q92269 penicillium
37	33	80.5	866	1 AREA_ASPOR	O13415 aspergillus
38	33	80.5	876	1 AREA_EMENI	P17429 emericella
39	33	80.5	878	1 SYV_MERJA	Q58413 methanococc
40	33	80.5	882	1 AREA_ASPNG	O13412 aspergillus
41	33	80.5	891	1 SYV_PYRAB	Q9uy55 pyrococcus
42	33	80.5	891	1 SYV_PYRHO	O58052 pyrococcus
43	33	80.5	971	1 AREA_GIBFU	P78688 gibberella
44	33	80.5	1036	1 NIT2_NEUCR	P19212 neurospora
45	32	78.0	254	1 CBYP_ALCEU	Q04541 alcaligenes

ALIGNMENTS

RESULT 1
YB06_YEAST STANDARD; PRT; 501 AA.
ID P38081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 57.8 kDa protein in PRP6-MOM2 intergenic region.
GN YBR056W OR YBR0510.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95321020; PubMed=7597852;
RA Aljinovic G., Pohl T.M.;
RT "Sequence and analysis of 24 kb on chromosome II of Saccharomyces
cerevisiae";
RL Yeast 11:475-479(1995).
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
HYDROLASES).
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CC
DR EMBL; Z35925; CAA84999.1; -;
DR EMBL; Z46260; CAA86399.1; -;
DR PIR; S45914; S45914.
DR SGD; S0000260; YBR056W.
DR InterPro; IPR001547; GH_5.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; FALSE_NEG.
KW Hypothetical protein; Hydrolase; Glycosidase.
FT ACT_SITE 236 236 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 333 333 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 501 AA; 57822 MW; 5133A161736ADD3 CRC64;
Query Match 95.1%; Score 39; DB 1; Length 501;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 109 IDWEWL 114

RESULT 2
KTHY_SCHPO STANDARD; PRT; 210 AA.
ID P36590; O74528;

DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thymidylate kinase (EC 2.7.4.9) (dTMP kinase).
 GN TMP OR SPCC70.07C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93003330; Pubmed=1327149;
 RA Abaigar L.F., Yeh Y.I., Jong A.Y.;
 RT "Functional and structural conservation of Schizosaccharomycetes pombe
 dTMP kinase gene.";
 RL Biochim. Biophys. Acta 1132:222-224(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; Pubmed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gencies S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weijens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jinenz J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE CONVERSION OF dTMP TO dTDP.
 CC -1- CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate -> ADP + thymidine
 CC 5'-diphosphate
 CC -1- PATHWAY: SYNTHESIS OF dTTP FROM dTMP.
 CC -1- SIMILARITY: BELONGS TO THE THYMIDYLATE KINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: X65868; CAA46698.1; -;
 CC EMBL: AL023794; CAA19357.1; -;
 CC PIR: S28955; S28955.
 CC HSP: P00572; ITMK.
 CC InterPro: IPR000062; Thymidylate_kin.
 CC Pfam: PF02223; Thymidylate_kin; 1.
 CC TIGRfam: TIGR00041; dTMP_kinase; 1.
 CC PROSITE: PS01331; THYMIDYLATE_KINASE; 1.
 CC Transferase; Kinase; Nucleotide biosynthesis; ATP-binding.
 CC NP_BIND 14 21 ATP (POTENTIAL).
 CC CONFLICT 33 39 SQUEAK -> LNMKRLK (IN REF. 1).
 CC CONFLICT 59 59 K -> T (IN REF. 1).
 CC FT

FT FT TIQYIEQINKGV -> PSYIRANQQRN (IN REF. 1).
 FT P -> T (IN REF. 1).
 FT CONFLICT 125 125
 FT CONFLICT 164 164
 FT CONFLICT 186 186
 FT CONFLICT 191 191
 FT CONFLICT 191 191
 FT H -> D (IN REF. 1).
 SQ SEQUENCE 210 AA; 24249 MW; 4266144AEDAB68C0 CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEW 5
 DB 112 LDWEW 116
 RESULT 3
 Y373_MYCPN STANDARD; PRT; 281 AA.
 AC P75227;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG373 homolog (G12_Orf281).
 GN MPN551 OR MP291.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; Pubmed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
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 CC -----
 CC EMBL: AE000027; AAB95939.1; -;
 CC Hypothetical protein; Complete proteome.
 KW SEQUENCE 281 AA; 32569 MW; FC70957510D7BEF3 CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWEWL 6
 DB 271 DWEWL 275
 RESULT 4
 CYOA_BUCAI STANDARD; PRT; 296 AA.
 ID CYOA_BUCAI
 AC P57544;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome o
 subunit 2) (oxidase BO(3) subunit 2) (Cytochrome o ubiquinol oxidase
 subunit 2).
 DE CYOA OR BU472.
 GN Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OS

OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RA MEDLINE=20445173; PubMed=10993077;
 RX Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
 CC GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) -> Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AP001119; BAB13169.1; -
 DR HSP; P18400; ICYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR Pfam; PF001116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
 DR KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 KW Signal; Lipoprotein; Complete proteome.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 54 POTENTIAL.
 FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 79 99 POTENTIAL.
 FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
 FT SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FFBAC CRC64;
 SQ
 Query Match 90.2%; Score 37; DB 1; Length 296;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 125 LDWKWL 130
 RESULT 5
 OOX2_ACEAC STANDARD; PRT; 307 AA.
 ID OOX2_ACEAC
 AC P50653;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
 DE A1 subunit 2) (Oxidase BA(3) subunit 2).
 GN CYAB.
 OS Acetobacter aceti.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Acetobacter.
 OX NCBI_TaxID=435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1023;
 RA MEDLINE=93322308; PubMed=8392509;

RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
 RA Kawamura Y., Horinouchi S., Beppu T.;
 RT "Characterization of a cytochrome a1 that functions as a ubiquinol
 RT oxidase in Acetobacter aceti.";
 RL J. Bacteriol. 175:4307-4314(1993).
 CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
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 CC -----
 CC EMBL; D13185; BAA02480.1; -
 DR HSP; P18400; ICYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR Pfam; PF001116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 DR KW Oxidoreductase; Transmembrane; Respiratory chain; Signal;
 KW Lipoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 SQ SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 307;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 135 LDWKWL 140
 RESULT 6
 CYOA_PSEPU STANDARD; PRT; 314 AA.
 ID CYOA_PSEPU
 AC Q9WRL1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).
 GN CYOA.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IH-2000;
 RX MEDLINE=99085656; PubMed=9868765;
 RA Hirayama H., Takami H., Inoue A., Horikoshi K.;
 RT "Isolation and characterization of toluene-sensitive mutants from
 RT FEMS Microbiol. Lett. 169:219-225(1998).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
 CC GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) -> Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.

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CC CC or send an email to license@isb-sib.ch).
CC CC
DR EMBL; AB016787; BAA76356.1; -
DR HSSP; F18400; ICIW.
DR InterPro; IPR001505; Copper_CUA.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Inner membrane; Signal; Lipoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 POTENTIAL.
FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 314 AA; 34702 MW; 96EE04FC3AA77F07 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 314;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKL 138

RESULT 7
YKTL_CAEEL
ID YKTL_CAEEL STANDARD; PRT; 488 AA.
AC P34312;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C07A9.1 in chromosome III.
GN C07A9.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Crawford M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohlman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
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CC CC
DR EMBL; Z29094; CAA82340.1; -
DR PIR; S40706; S40706.
DR HSSP; P23807; IIXX.
DR WormPep; C07A9.1; C500502.
DR InterPro; IPR002619; CX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 54717 MW; 9022691E47078814 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
DB 287 DWEWL 291

RESULT 8
RFBC_MYXXA
ID RFBC_MYXXA STANDARD; PRT; 1275 AA.
AC Q50864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE O-antigen biosynthesis protein rfbc.
GN RFBC.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=DK6640;
RX MEDLINE=96198166; PubMed=8626291;
RA Guo D., Bowden M.G., Pershad R., Kaplan H.B.;
RT "The Myxococcus xanthus rfABC operon encodes an ATP-binding cassette
RT transporter homolog required for O-antigen biosynthesis and
RT multicellular development.";
RL J. Bacteriol. 178:1631-1639(1996).
CC CC
CC CC -1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
CC CC
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CC CC
DR EMBL; U36795; AAB05019.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00535; Glycos_transf_2; 2.
KW Lipopolysaccharide biosynthesis.
SQ SEQUENCE 1275 AA; 139596 MW; 3AF9662A10A140F1 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
DB 349 DWEWL 353

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RESULT 9
ID Y250_CORGL STANDARD; PRT; 289 AA.
AC P42459;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein Cgl0250 (ORF).
GS CGL0250.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A., DSM 20300 / NCIB 10025;
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=94161495; PubMed=8117072;
RA Patek M., Krumbach K., Eggeling L., Sahn H.;
RT "Leucine synthesis in Corynebacterium glutamicum: enzyme activities,
RT structure of leuA, and effect of leuA inactivation on lysine
RT synthesis."
RL Appl. Environ. Microbiol. 60:133-140(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 59.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70959; CNA50297.1; ALT_FRAME.
DR EMBL; AP005274; BAB97642.1;
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 230 250 POTENTIAL.
FT TRANSMEM 258 278 POTENTIAL.
SQ SEQUENCE 289 AA; 31381 MW; 5C7A38DC6BFF078A CRC64;

Query Match 87.88; Score 36; DB 1; Length 289;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 256 VDWEWI 261
:||||:

RESULT 10
ID IKKA_HUMAN STANDARD; PRT; 745 AA.
AC O15111; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

```

DE DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)
DE DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikappab kinase)
DE DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN IKKA OR CHUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an Ikappab kinase."
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive Ikappab kinase that activates the transcription
RT factor NF-kappaB."
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for
RT NF-kappaB activation."
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes."
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connolly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain."
RL Cell. Mol. Biol. Res. 41:537-549(1995).
RN [6]
RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND
RP S-180.
RX MEDLINE=98188283; PubMed=9520446;
RA Ling L., Cao Z., Goeddel D.V.;
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
RT Ser-176."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
RN [7]
RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE=99413720; PubMed=10485710;
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
RA Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt
RT serine-threonine kinase."
RL Nature 401:82-85(1999).
RN [8]
RP IKKA-IKKB BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of Ikappab kinase activity through
RT IKKbeta subunit phosphorylation."
RL Science 284:309-313(1999).

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[9]
 IKK PHOSPHORYLATION.
 MEDLINE-99038238; PubMed-9819420;
 Nemoto S., DiDonato J.A., Lin A.;
 "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 Mol. Cell. Biol. 18:7336-7343(1998).
 [10]
 REVIEW.
 MEDLINE-20178139; PubMed-10712233;
 Jobin C., Sartor R.B.;
 "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -!- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 WHEN DEPHOSPHORYLATED.
 CC -!- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -!- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
 MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPA-B KINASE SUBFAMILY.

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 DR EMBL; AF012890; AAC51662.1; -;
 DR EMBL; AF009225; AAC51671.1; -;
 DR EMBL; AF080157; AAD08996.1; -;
 DR EMBL; U22512; AAC50713.1; -;
 DR HSP; Q63450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
 ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).

FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS -> DE (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 738 LDMSWL 743
 RESULT 11
 IKKA_MOUSE
 ID IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.1-)
 DE (I kappa-B kinase alpha) (IKKalpha) (IKK-alpha) (ikappab kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase)
 DE Nuclear factor NF-kappaB inhibitor kinase alpha (NFKBIA).
 GN IKKA OR CHUK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALE/C;
 RX MEDLINE-9604444; PubMed-7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALE/C;
 RX MEDLINE-96258427; PubMed-8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 families of interacting proteins, contains a serine-threonine kinase
 catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guncich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]

RP ALTERNATIVE SPLICING.
RX MEDLINE-20198447; PubMed-10733566;
RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
RA Gelezianas R., Marcu K.B.;
RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
RT IKKbeta have different activation requirements.";
RL Mol. Cell. Biol. 20:2635-2649(2000).
RN [5]
RP PHOSPHORYLATION BY MAP3K14/NIK.
RX MEDLINE-9818238; PubMed-9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [6]
RP IKKA-IKKB BINDING.
RX MEDLINE-99212141; PubMed-10195894;
RA Dehaise M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
RT IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [7]
RP IKK PHOSPHORYLATION.
RX MEDLINE-99038238; PubMed-9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [8]
RP REVIEW.
RX MEDLINE-20178139; PubMed-10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of
RT mucosal inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
CC WHEN DEPHOSPHORYLATED.
CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/DELTA LH AND
CC 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS ONLY FOR ISOFORM 1, ISOFORMS 2 AND
CC 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.
CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY
CC E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION
CC PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.
CC -1- FTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
CC MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC EMBL; U12473; AAC52589.1;
CC EMBL; AK018671; BAB31335.1;
CC HSSP; Q63450; 1A06.
CC MGD; MGI:99484; Chuk.

DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD00001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 738 743 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1) (BY
FT SIMILARITY).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14) (BY
FT SIMILARITY).
FT VARSPLIC 452 471 MSLRLRYNALTMMKNLTLS -> IFRKNVKSMEGRKKGH
FT VARSPLIC 472 472 MISSING (IN ISOFORM 2).
FT VARSPLIC 577 584 DLYSDST -> GKTLSQV (IN ISOFORM 3).
FT VARSPLIC 585 745 MISSING (IN ISOFORM 3).
FT CONFLICT 236 236 K -> E (IN REF. 3).
FT CONFLICT 400 400 S -> Y (IN REF. 3).
SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AFF92233 CRC64;
Query Match 87.8%; Score 36; DB 1; Length 745;
Best Local Similarity 83.3%; Pred No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDWEWL 6
Db 738 LDWSWL 743
RESULT 12
IKKB_HUMAN
ID IKKB_HUMAN STANDARD; PRT; 756 AA.
AC Q14920; O75327;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE Cervical carcinoma;
RX MEDLINE-98008813; PubMed-9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:866-869(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE-98008814; PubMed-9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RX MEDLINE-99032998; PubMed-9813230;
RA Hu M.C.-T., Wang Y.-P.;

RT *Ikkapab kinase-alpha and -beta genes are coexpressed in adult and
 RL embryonic tissues but localized to different human chromosomes.";
 RN Gene 22:31-40(1998).
 RP [4]
 RX SEQUENCE FROM N.A., AND GENE MAPPING.
 RA MEDLINE-98438415; Pubmed-9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 RA "Assignment of Ikkapab kinase beta (IKKB) to human chromosome band
 RT 8p12->p11 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE-Lung;
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; Pubmed-9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RA "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [7]
 RP REVIEW.
 RX MEDLINE-20178139; Pubmed-10712233;
 RA Jobin C., Sartor R.B.;
 RL "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND
 CC PERIPHERAL BLOOD.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC
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 CC
 CC EMBL; AF029684; AAC51860.1; -
 CC EMBL; AF030158; AAD08997.1; -
 CC EMBL; AF031416; AAC84675.1; -
 CC EMBL; BC006231; AAH06231.1; -
 CC HSSP; Q63450; 1A06.
 CC Genew; HGNC:5960; IKKB.
 CC MIM; 603258; -
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00240; ubiquitin; 1.
 CC PRINTS; PR00109; TYRKINASE
 CC PROSITE; PD000001; Euk_pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE-ATP; FALSE_NEG.
 CC PROSITE; PS00108; PROTEIN_KINASE-ST; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW

KW Phosphorylation. 300
 FT DOMAIN 15
 FT FT LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 458
 FT FT NEMO-BINDING.
 FT NP_BIND 737
 FT FT ATP (BY SIMILARITY).
 FT BINDING 21
 FT FT ATP (BY SIMILARITY).
 FT ACT_SITE 44
 FT FT BY SIMILARITY.
 FT MOD_RES 145
 FT FT PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 23
 FT FT PHOSPHORYLATION.
 FT MOD_RES 177
 FT FT PHOSPHORYLATION.
 FT MUTAGEN 181
 FT FT K->A: LOSS OF KINASE ACTIVITY AND NO
 FT FT EFFECT ON BINDING TO NIK.
 FT MUTAGEN 44
 FT FT S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 177
 FT FT S->E: FULL ACTIVATION.
 FT MUTAGEN 177
 FT FT S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181
 FT FT S->E: FULL ACTIVATION.
 FT CONFLICT 231
 FT FT WSKVRQKSEVDIVVSEDLNGTVKF -> CYRMMWPTVAHS
 FT FT CNPSTLGGGRGHWI (IN REF. 5).
 FT CONFLICT 425
 FT FT Q -> H (IN REF. 1).
 SQ SEQUENCE 756 AA; 86363 MW; F9CADF671AE9E14E CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 756;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 737 LDWSWL 742
 RESULT 13
 IKKB_MOUSE
 ID IKKB_MOUSE STANDARD; PRT: 757 AA.
 AC O88351; Q9R1J6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 GN IKKB OR IKKBK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE-9818238; Pubmed-9520401;
 RA Nakano H., Shindo M., Sakon S., Mishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RA "Differential regulation of Ikkapab kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1".
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RA "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RA "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates Ikkapab kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; Pubmed-9819420;
 RA Nemoto S., Didonato J.A., Lin A.;

RT *Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RL kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RN Mol. Cell. Biol. 18:7336-7343(1998).
 RP [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RA "The IkappaB/NF-kappaB system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEKK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBIQUITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEKK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF026524; AAC23557.1; -;
 CC EMBL; AF088910; AAD52095.1; -;
 CC HSSP; Q63450; 1A06.
 CC MGD; MGI:1338071; Ikbb.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 CC DOMAIN 15 300 PROTEIN KINASE.
 CC DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC DOMAIN 737 742 NEMO-BINDING.
 CC NP_BIND 21 29 ATP (BY SIMILARITY).
 CC BINDING 44 44 ATP (BY SIMILARITY).
 CC ACT_SITE 145 145 BY SIMILARITY.
 CC MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 CC MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 CC MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 CC CONFLICT 56 56 N -> D (IN REF. 2).
 CC CONFLICT 343 343 N -> D (IN REF. 2).
 CC CONFLICT 356 356 K -> E (IN REF. 2).
 CC CONFLICT 390 390 L -> F (IN REF. 2).
 CC CONFLICT 406 406 P -> Q (IN REF. 2).
 CC CONFLICT 573 573 K -> R (IN REF. 2).
 CC CONFLICT 736 757 TLDSWQLQMEDEKCSLEQACD -> VTA (IN REF. 2).
 CC SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 III II
 Db 737 LDWSWL 742
 RESULT 14
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (1-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKBK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IkB beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RL kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RL mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEKK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED BY MEKK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF115282; AAF21978.1; -;
 CC HSSP; Q63450; 1A06.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PD00109; TYRKINASE.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
FT Phosphorylation.
KW DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT NP_BIND 21 29 NEMO-BINDING.
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 757 AA; 86866 MW; 3AFPE46A7DF91FC CRC64;

Query Match 87.8%; Score 36; DB 1; Length 757;

Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6

Db 737 LDWSWL 742

RESULT 15

YFSC_BACSU

ID YFSC_BACSU STANDARD; PRT; 385 AA.

AC P50840;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein ypsc precursor.

GN YPSC.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168 / Marburg;

RA MEDLINE=96349105; PubMed=8760912;

RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,

RA Serron P.;

RT "Sequence analysis of the Bacillus subtilis chromosome region between

the serA and kds loci cloned in a yeast artificial chromosome.";

RL Microbiology 142:2005-2016(1996).

RN [2]

RP SEQUENCE OF 1-124 FROM N.A.

RA MEDLINE=86224088; PubMed=2423526;

RA Reich C., Gardiner K.J., Olsen G.J., Pace B., Marsh T.L., Pace N.R.;

RT "The RNA component of the Bacillus subtilis RNase P. Sequence,

activity, and partial secondary structure.";

RL J. Biol. Chem. 261:7888-7893(1986).

CC -1- SIMILARITY: BELONGS TO THE UPF0020 FAMILY.

CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO

CC FRAMESHIFTS.

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CC EMBL; L47838; AAB38473.1; -

DR EMBL; M13175; -; NOT ANNOTATED_CDS.

DR EMBL; Z99115; CAB14134.1; -

DR Subtilist; BG11455; ypsc.

DR InterPro; IPR002052; N6_Mtase.

DR InterPro; IPR000241; RNA_methylase.

DR InterPro; IPR000051; SAM_bind.

DR InterPro; IPR004114; THUMP_dom.

DR Pfam; PF01170; UPF0020; 1.

DR Pfam; PF02926; THUMP; 1.
DR PROSITE; PS01261; UPF0020; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 385 HYPOTHETICAL PROTEIN YPSC.
SQ SEQUENCE 385 AA; 43507 MW; 587792F17E82B3B6 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 385;

Best Local Similarity 80.0%; Pred. No. 95;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6

Db 228 DWEWI 232

Search completed: May 30, 2003, 15:49:09

Job time : 6.11842 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTEMBL21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rv.*
- 17: sp_bacteriophage.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	95.1	513	2 Q8VPV8	Q8VPV8 synechococc
2	37	90.2	107	9 Q9FZX5	Q9FZX5 bacterioph
3	37	90.2	288	2 Q8VTT4	Q8VTT4 pseudomonas
4	37	90.2	311	5 Q94380	Q94380 caenorhabdl
5	37	90.2	313	2 Q8VUQ6	Q8VUQ6 pseudomonas
6	37	90.2	318	16 Q8ZC58	Q8ZC58 yersinia pe
7	37	90.2	329	16 Q8XVB4	Q8XVB4 raietonia s
8	37	90.2	331	16 Q9IA27	Q9IA27 pseudomonas
9	37	90.2	344	16 Q8VEH7	Q8VEH7 brucella me
10	37	90.2	353	16 Q9A7F0	Q9A7F0 caulobacter
11	37	90.2	377	17 Q59445	Q59445 pyrococcus
12	37	90.2	378	17 Q8U022	Q8U022 pyrococcus
13	37	90.2	379	17 Q9V1W1	Q9V1W1 pyrococcus
14	37	90.2	386	16 Q92027	Q92027 rhizobium m
15	37	90.2	393	16 Q987Z1	Q987Z1 rhizobium l
16	37	90.2	404	17 Q57734	Q57734 pyrococcus

17	37	90.2	405	17 Q9UXV2	Q9UXV2 pyrococcus
18	37	90.2	1291	5 Q9VP46	Q9VP46 drosophila
19	36	87.8	82	17 Q26213	Q26213 methanobact
20	36	87.8	162	16 Q53756	Q53756 mycobacteri
21	36	87.8	322	16 Q8YK7	Q8YK7 brucella me
22	36	87.8	347	16 Q98KR3	Q98KR3 rhizobium l
23	36	87.8	347	16 Q92QP5	Q92QP5 rhizobium m
24	36	87.8	348	16 Q8UFX0	Q8UFX0 agrobacteri
25	36	87.8	414	16 Q9K194	Q9K194 vibrio chol
26	36	87.8	439	2 Q93Q61	Q93Q61 klebsiella
27	36	87.8	443	16 Q8ZDM7	Q8ZDM7 yersinia pe
28	36	87.8	618	15 Q88284	Q88284 snakehead r
29	36	87.8	740	6 Q95KV1	Q95KV1 bos taurus
30	36	87.8	756	6 Q95KV0	Q95KV0 bos taurus
31	36	87.8	764	16 Q8U6N1	Q8U6N1 agrobacteri
32	36	87.8	1120	16 Q8ZRA5	Q8ZRA5 salmonella
33	36	87.8	1120	16 Q8ZRT6	Q8ZRT6 salmonella
34	36	87.8	2017	15 Q88285	Q88285 snakehead r
35	35	85.4	135	2 Q8VQ17	Q8VQ17 uncultured
36	35	85.4	136	2 Q8VQ16	Q8VQ16 uncultured
37	35	85.4	136	2 Q8VQ15	Q8VQ15 uncultured
38	35	85.4	136	2 Q8VQ17	Q8VQ17 uncultured
39	35	85.4	136	2 Q8RNB0	Q8RNB0 uncultured
40	35	85.4	139	2 Q8VQ09	Q8VQ09 uncultured
41	35	85.4	139	2 Q8VLE8	Q8VLE8 uncultured
42	35	85.4	139	2 Q8VQ19	Q8VQ19 uncultured
43	35	85.4	139	2 Q8RNA3	Q8RNA3 uncultured
44	35	85.4	139	2 Q8RJD9	Q8RJD9 uncultured
45	35	85.4	140	2 Q8VQ18	Q8VQ18 uncultured

ALIGNMENTS

RESULT 1

Q8VPV8
ID Q8VPV8 PRELIMINARY; PRT; 513 AA.
AC Q8VPV8; 2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE NADPH dehydrogenase subunit 4.
GN NDH3.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC 7942;
RA Maeda S., Badger M.R., Price G.D.;
RT "Identification of Chp and ChpV, catalyzing light-dependent CO2
hydration involved in CO2 uptake in Cyanobacteria."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY029338; AAK37764.1;
DR InterPro: IPR003918; NADHoxred4.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; Oxidored_q1; 1.
DR PRINTS: PR01437; NUOXDRDTASE4.
SQ SEQUENCE 513 AA; 54237 MW; 2732576525224AB CRC64;

Query Match 95.1%; Score 39; DB 2; Length 513;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 59 IDWEWL 64

RESULT 2

Q9FZX5
ID Q9FZX5 PRELIMINARY; PRT; 107 AA.
AC Q9FZX5;

DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical 12.6 kDa protein.
OS Bacteriophage GA-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=12345;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094855; PubMed=8940089;
RA Freire R., Serrano M., Salas M., Hermoso J.;
RT "Activation of replication origins in phi29-related phages requires
the recognition of initiation proteins to specific nucleoprotein
complexes.";
RN J. Biol. Chem. 271:31000-31007(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97123975; PubMed=8969297;
RA Illana B., Blanco L., Salas M.;
RT "Functional characterization of the genes coding for the terminal
protein and DNA polymerase from bacteriophage GA-1. Evidence for a
sliding-back mechanism during protein-primed GA-1 DNA replication.";
RN J. Mol. Biol. 264:453-464(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99370049; PubMed=10438592;
RA Horcajadas J.A., Monsalve M., Rojo F., Salas M.;
RT "The switch from early to late transcription in phage GA-1:
characterization of the regulatory protein p4G.";
RN J. Mol. Biol. 290:917-928(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20280072; PubMed=10773070;
RA Gascon I., Lazaro J.M., Salas M.;
RT "Differential functional behavior of viral phi29, Nf and GA-1 SSB
proteins.";
RN Nucleic Acids Res. 28:2034-2042(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA Meijer W.J.J., Horcajadas J.A., Salas M.;
RT "The phi29 family of phages.";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Horcajadas J.A., Meijer W.J.J., Rojo F., Salas M.;
RT "Transcriptional map of the Bacillus bacteriophage GA-1. Analysis of
the viral C2 promoter.";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; X96987; CAC21518.1; -
KW Hypothetical protein.
SQ SEQUENCE 107 AA; 12636 MW; A8EF24E69A255E02 CRC64;
Query Match 90.2%; Score 37; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWEWL 6
Db 100 DWEWL 104
RESULT 3
ID Q8VTT4 PRELIMINARY; PRT; 288 AA.
AC Q8VTT4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Cytochrome o ubiquinol oxidase A (Fragment).
GN CytoA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PML1;
RA Syn C.K.C., Liew C.F., Swarup S.;
RT "Pseudomonas putida cytochrome o ubiquinol oxidase A, B, C, and D
genes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321090; AAL37192.1; -
DR InterPro; IPR001505; Copper_CuA.
DR ProDom; PD000131; Copper_CuA; 1.
FT NON_TER 1
SQ SEQUENCE 288 AA; 31882 MW; 60E40B3A36516BFC CRC64;
Query Match 90.2%; Score 37; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWEWL 6
Db 108 LDWKWL 113
RESULT 4
ID Q94380 PRELIMINARY; PRT; 311 AA.
AC Q94380;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ZC47.13 protein.
GN ZC47.13.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RN Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81141; CAB03488.2; -
DR InterPro; IPR002900; DUF38.
DR InterPro; IPR001810; F-box.
DR Pfam; PF01827; DUF38; 1.
DR Pfam; PF00646; F-box; 1.
SQ SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;
Query Match 90.2%; Score 37; DB 5; Length 311;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWEWL 6
Db 295 LEWEWL 300
RESULT 5
ID Q8VUQ6 PRELIMINARY; PRT; 313 AA.
AC Q8VUQ6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Cytochrome o oxidase A.
GN CytoA.

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OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KT2442;
RA Fukumori F., Kishii M.;
RT "Characterization of the toluene-sensitive mutants of Pseudomonas putida KT2442TOL.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB066295; BAB83593.1; -
DR InterPro: IPR001505; Copper_Cua.
DR InterPro: IPR002429; Cyt_c_ox_2.
DR Pfam: PF001116; COX2; 1.
DR ProDom: PD000131; Copper_Cua; 1.
SQ SEQUENCE 313 AA; 34557 MW; 193BE3F7F8EBDA42B CRC64;

Query Match 90.2%; Score 37; DB 2; Length 313;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKWL 138

RESULT 6
Q8ZC58
ID Q8ZC58 PRELIMINARY; PRT; 318 AA.
AC Q8ZC58
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome o ubiquinol oxidase subunit II (EC 1.10.3.-).
GN CYOA OR YPO3164.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Felwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL: AJ414155; CAC92399.1; -
DR InterPro: IPR001505; Copper_Cua.
DR ProDom: PD000131; Copper_Cua; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 318 AA; 35049 MW; E2947941923016D3 CRC64;

Query Match 90.2%; Score 37; DB 16; Length 318;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 135 LDWKWL 140

RESULT 7
Q8XVB4
ID Q8XVB4 PRELIMINARY; PRT; 329 AA.
AC Q8XVB4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)
DE Oxidoreductase protein (EC 1.10.3.-).
GN CYOA OR RSC2917 OR RS00308.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GMI1000.
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646072; CAD16624.1; -
DR InterPro: IPR001505; Copper_Cua.
DR InterPro: IPR002429; Cyt_c_ox_2.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF001116; COX2; 1.
DR ProDom: PD000131; Copper_Cua; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;

Query Match 90.2%; Score 37; DB 16; Length 329;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKWL 138

RESULT 8
Q9I427
ID Q9I427 PRELIMINARY; PRT; 331 AA.
AC Q9I427
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome o ubiquinol oxidase subunit II.
GN CYOA OR PA1317.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Miziochuchi S.D., Warrenner P.,
RA Hackey R.J., Ginkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004561; AAC04706.1; -
DR HSP; F18400; ICIW.
DR InterPro: IPR001505; Copper_Cua.
DR InterPro: IPR002429; Cyt_c_ox_2.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF001116; COX2; 1.
DR ProDom: PD000131; Copper_Cua; 1.

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DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 331 AA; 36623 MW; DC4449ED0FF0BB66 CRC64;

Query Match 90.2%; Score 37; DB 16; Length 331;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||:|
 Db 133 LDWKWL 138

RESULT 9

Q8YEH7 PRELIMINARY; PRT; 344 AA.
 AC Q8YEH7;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-).
 GN BMEI1901.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Muler C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis";
 FT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RL EMBL; AE009623; AAL53082.1; -;
 DR InterPro; IPR001505; Copper_CuA.
 DR ProDom; PD000131; Copper_CuA; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 344 AA; 38948 MW; B643C91321B600EC CRC64;

Query Match 90.2%; Score 37; DB 16; Length 344;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||:|
 Db 141 LDWKWL 146

RESULT 10

Q9A7F0 PRELIMINARY; PRT; 353 AA.
 AC Q9A7F0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ubiquinol oxidase subunit II.
 GN CCI1773.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 CC Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CBI15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Uitterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005851; AAC23749.1; -;
 DR HSSP; P18400; 1CYW.
 DR TIGR; CC1773; -;
 DR InterPro; IPR001505; Copper_CuA.
 DR ProDom; PD000131; Copper_CuA; 1.
 KW Complete proteome.
 SQ SEQUENCE 353 AA; 38817 MW; 607AF178B2AD184D CRC64;

Query Match 90.2%; Score 37; DB 16; Length 353;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||:|
 Db 146 LDWKWL 151

RESULT 11

O59445 PRELIMINARY; PRT; 377 AA.
 AC O59445;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 377AA long hypothetical sarcosine oxidase.
 GN PHI751.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 CC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kwarabavasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya N., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3";
 RL DNA Res. 5:55-76(1998).
 DR EMBL; AP000007; BAA30865.1; -;
 DR InterPro; IPR000927; D_aa_Oxidase.
 DR InterPro; IPR000205; NAD_Binding.
 DR Pfam; PF01266; DAO; 1.
 KW Complete proteome.
 SQ SEQUENCE 377 AA; 42421 MW; FA9B0966328EA097 CRC64;

Query Match 90.2%; Score 37; DB 17; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 5
 |||||
 Db 354 LDWEWL 358

RESULT 12

Q8U022 PRELIMINARY; PRT; 378 AA.
 AC Q8U022;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Sarcosine oxidase, subunit beta.

GN Pfl198.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE010277; AAL81922.1;
 KW Complete proteome.
 SQ SEQUENCE 378 AA; 42388 MW; 42547893DD702FD3 CRC64;
 Query Match 90.2%; Score 37; DB 17; Length 378;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEW 5
 Db 355 LDWEW 359
 RESULT 13
 Q9V1W1 PRELIMINARY; PRT; 379 AA.
 AC Q9V1W1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Sarcosine oxidase, subunit beta (SOXB).
 GN SOXB OR PAB0214.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ORSAY;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ248284; CAB49237.1;
 DR InterPro: IPR000927; D_aa_oxidase.
 DR Pfam: PF01266; NAD_binding.
 DR Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 379 AA; 42628 MW; EAF67AF20C0F695 CRC64;
 Query Match 90.2%; Score 37; DB 17; Length 379;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEW 5
 Db 356 LDWEW 360
 RESULT 14
 Q92U27 PRELIMINARY; PRT; 386 AA.
 AC Q92U27;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.).
 GN CYOA OR RB1315 OR SMB21487.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021;
 RX MEDLINE-21396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
 DR EMBL; AL603646; CAC49715.1;
 DR InterPro: IPR001505; Copper_CuA; 1.
 DR ProDom: PD000131; Copper_CuA;
 KW Oxidoreductase; Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 386 AA; 42869 MW; 215550C43C141A62 CRC64;
 Query Match 90.2%; Score 37; DB 16; Length 386;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEW 6
 Db 141 LDWKWL 146
 RESULT 15
 Q987Z1 PRELIMINARY; PRT; 393 AA.
 AC Q987Z1;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cytochrome o ubiquinol oxidase subunit II.
 GN MLE6846.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MAFF303099;
 RX MEDLINE-21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003010; BAB53059.1;
 DR InterPro: IPR001505; Copper_CuA.
 DR ProDom: PD000131; Copper_CuA; 1.
 KW Complete proteome.
 SQ SEQUENCE 393 AA; 42748 MW; 6656C220867AF9D0 CRC64;
 Query Match 90.2%; Score 37; DB 16; Length 393;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEW 6
 Db 137 LDWKWL 142
 Search completed: May 30, 2003, 14:39:07
 Job time : 15.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDNAWL 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	40	100.0	6	9	US-09-847-946A-16
3	40	100.0	6	9	US-09-847-946A-44
4	40	100.0	6	9	US-09-847-946A-106
5	40	100.0	7	9	US-09-847-946A-110
6	40	100.0	8	9	US-09-847-946A-103
7	40	100.0	8	9	US-09-847-946A-111
8	40	100.0	9	9	US-09-847-946A-102
9	40	100.0	9	9	US-09-847-946A-105
10	40	100.0	9	9	US-09-847-946A-108
11	40	100.0	9	9	US-09-847-946A-109
12	40	100.0	10	9	US-09-847-946A-104
13	40	100.0	10	9	US-09-847-946A-107
14	40	100.0	11	9	US-09-847-946A-101
15	37	92.5	6	9	US-09-847-940B-2
16	37	92.5	6	9	US-09-847-946A-2
17	37	92.5	6	9	US-09-847-946A-33
18	37	92.5	7	9	US-09-847-946A-37
19	37	92.5	8	9	US-09-847-946A-30

Sequence 38, Appl
Sequence 29, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 31, Appl
Sequence 34, Appl
Sequence 28, Appl
Sequence 132, App
Sequence 140, App
Sequence 143, App
Sequence 144, App
Sequence 145, App
Sequence 148, App
Sequence 141, App
Sequence 142, App
Sequence 146, App
Sequence 147, App
Sequence 131, App
Sequence 135, App
Sequence 136, App
Sequence 133, App
Sequence 134, App
Sequence 137, App
Sequence 138, App
Sequence 139, App

US-09-847-940B-16
US-09-847-946A-29
US-09-847-946A-32
US-09-847-946A-35
US-09-847-946A-36
US-09-847-946A-31
US-09-847-946A-34
US-09-847-946A-28
US-09-847-946A-132
US-09-847-946A-140
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US-09-847-946A-142
US-09-847-946A-146
US-09-847-946A-147
US-09-847-946A-131
US-09-847-946A-135
US-09-847-946A-136
US-09-847-946A-133
US-09-847-946A-134
US-09-847-946A-137
US-09-847-946A-138
US-09-847-946A-139

ALIGNMENTS

RESULT 1

US-09-847-940B-16
Sequence 16, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-16

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAWL 6
DB 1 LDNAWL 6

RESULT 2

US-09-847-946A-16
Sequence 16, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 16
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-16

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 1 LDRAWL 6

RESULT 3

US-09-847-946A-44

;; Sequence 44, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J
;; APPLICANT: Ghosh, Sankar
;; APPLICANT: Findeis, Mark A
;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Hannig, Gerhard
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 44
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-44

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 1 LDRAWL 6

RESULT 4

US-09-847-946A-106

;; Sequence 106, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J
;; APPLICANT: Ghosh, Sankar
;; APPLICANT: Findeis, Mark A

;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Hannig, Gerhard
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 106
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-106

Query Match 100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 1 LDRAWL 6

RESULT 5

US-09-847-946A-110

;; Sequence 110, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J
;; APPLICANT: Ghosh, Sankar
;; APPLICANT: Findeis, Mark A
;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Hannig, Gerhard
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 110
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-110

Query Match 100.0%; Score 40; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 1 LDRAWL 6

RESULT 6

US-09-847-946A-103

;; Sequence 103, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-103

Query Match 100.0%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 3 LDRAWL 8

RESULT 7

US-09-847-946A-111

; Sequence 111, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-111

Query Match 100.0%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 1 LDRAWL 6

RESULT 8

US-09-847-946A-102

; Sequence 102, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-102

Query Match 100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 1 LDRAWL 6

RESULT 9

US-09-847-946A-105

; Sequence 105, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-105

Query Match 100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 1 LDRAWL 6

RESULT 10
US-09-847-946A-108
; Sequence 108, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-108

Query Match 100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
111111
Db 3 LDRAWL 8

RESULT 11
US-09-847-946A-109
; Sequence 109, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-109

Query Match 100.0%; Score 40; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6

111111
Db 2 LDRAWL 7

RESULT 12
US-09-847-946A-104
; Sequence 104, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-104

Query Match 100.0%; Score 40; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
111111
Db 2 LDRAWL 7

RESULT 13
US-09-847-946A-107
; Sequence 107, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 107
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-107

Query Match 100.0%; Score 40; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 3 LDRAWL 8

Db | | | | |
1 LDRAWL 6

Search completed: May 30, 2003, 15:53:21
Job time : 10.4605 secs

RESULT 14

US-09-847-946A-101
; Sequence 101, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-101

Query Match 100.0%; Score 40; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 3 LDRAWL 8

RESULT 15

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 92.5%; Score 37; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	745	1 IKKA_HUMAN	O15111 h inhibitor
2	37	92.5	745	1 IKKA_MOUSE	O60680 m inhibitor
3	37	92.5	756	1 IKKB_HUMAN	O14920 homo sapien
4	37	92.5	757	1 IKKB_MOUSE	O88351 mus musculus
5	37	92.5	757	1 IKKB_RAT	O9qy78 rattus norv
6	36	90.0	524	1 CP72_CATRO	Q05047 catharanthu
7	36	90.0	656	1 VEXE_SALTI	P43112 salmonella
8	36	90.0	840	1 VPH1_YEAST	P32563 saccharomyc
9	35	87.5	296	1 CYOA_BUCAI	P57544 buchnera ap
10	35	87.5	307	1 OOX2_ACEAC	P50653 acetobacter
11	35	87.5	314	1 CYOA_PSEPU	Q9wrr1 pseudomonas
12	34	85.0	99	1 NOS3_SHEEP	P79209 ovis aries
13	34	85.0	262	1 LY4A_MOUSE	P20937 mus musculus
14	34	85.0	263	1 KLR4_MOUSE	O60651 mus musculus
15	34	85.0	914	1 GUX2_CLOSR	P50900 clostridium
16	34	85.0	1167	1 ITAE_MOUSE	O60677 mus musculus
17	34	85.0	1201	1 NOS3_MOUSE	P70313 mus musculus
18	34	85.0	1202	1 NOS3_HUMAN	P29474 homo sapien
19	34	85.0	1204	1 NOS3_BOVIN	P29473 bos taurus
20	34	85.0	1204	1 NOS3_PIG	Q28969 sus scrofa
21	33	82.5	220	1 Y132_METJA	O57596 methanococc
22	33	82.5	300	1 Y223_HAEIN	P44579 haemophilus
23	33	82.5	362	1 DCUP_YEAST	P32347 saccharomyc
24	33	82.5	411	1 CYB_CHRVI	O31215 chromatiu
25	33	82.5	501	1 YBQ6_YEAST	P38081 saccharomyc
26	33	82.5	578	1 YC20_METJA	O58617 methanococc
27	33	82.5	983	1 EPA3_CHICK	P29318 gallus gall
28	33	82.5	983	1 EPA3_HUMAN	P29320 homo sapien
29	33	82.5	983	1 EPA3_MOUSE	P29319 mus musculus
30	33	82.5	984	1 EPA3_RAT	O08680 rattus norv
31	33	82.5	1002	1 EPB5_CHICK	Q07497 gallus gall
32	33	82.5	1039	1 GUNB_CALSA	P10474 c endogluc
33	32	80.0	83	1 VG41_BPML5	Q05252 mycobacteri

RESULT 1

ID	IKKA_HUMAN	STANDARD;	PRT;	745 AA.
AC	O15111; O14666; Q13132; Q92467;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.1.-)			
DE	(I kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (Ikappab kinase)			
DE	(I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous			
DE	kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KA).			
GN	IKKA OR CHUK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.			
RC	TISSUE=T-cell;			
RC	MEDLINE-97386461; PubMed-9244310;			
RA	Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;			
RT	"Identification and characterization of an Ikappab kinase."			
RL	Cell 90:373-383(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RP	MEDLINE-97394468; PubMed-9252186;			
RA	Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;			
RT	"A cytokine-responsive Ikappab kinase that activates the transcription			
RT	factor NF-kappaB."			
RL	Nature 388:548-554(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND			
RP	SER-176.			
RC	TISSUE=Cervical carcinoma;			
RC	MEDLINE-98008813; PubMed-9346484;			
RA	Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,			
RA	Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;			
RT	"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for			
RT	NF-kappaB activation."			
RL	Science 278:860-866(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RC	MEDLINE-99032998; PubMed-9813230;			
RA	Hu M.C.-T., Wang Y.-P.;			
RT	"IkappaB kinase-alpha and -beta genes are coexpressed in adult and			
RT	embryonic tissues but localized to different human chromosomes.";			
RL	Gene 222:31-40(1998).			
RN	[5]			
RP	SEQUENCE OF 32-745 FROM N.A.			
RC	TISSUE=Cervical carcinoma;			
RC	MEDLINE-96258427; PubMed-8777433;			
RA	Connelly M.A., Marcu K.B.;			
RT	"CHUK, a new member of the helix-loop-helix and leucine zipper			
RT	families of interacting proteins, contains a serine-threonine kinase			
RT	catalytic domain."			

ALIGNMENTS

34	32	80.0	94	1	VG41_BPMD2
35	32	80.0	269	1	BASI_HUMAN
36	32	80.0	315	1	T2S1_STRAL
37	32	80.0	336	1	NOSO_BACSU
38	32	80.0	339	1	RFAI_ECOLI
39	32	80.0	380	1	APJ_MACMU
40	32	80.0	387	1	MANA_RHIME
41	32	80.0	397	1	Y303_ARCFU
42	32	80.0	499	1	TMOA_PSEME
43	32	80.0	500	1	PROP_ECOLI
44	32	80.0	541	1	Y537_SYNY3
45	32	80.0	552	1	NU5M_RHISA

O64231 mycobacteri
P35613 h basigin p
Q33608 streptomyce
Q34453 bacillus su
P27128 escherichia
O97666 macaca mula
P29954 rhizobium m
O29939 archaeoglob
Q00456 pseudomonas
P30848 escherichia
P54148 synechocyst
Q9zym7 rhipicephal

Cell. Mol. Biol. Res. 41:537-549(1995).
 [6] PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND S-180.
 RX MEDLINE-9818283; PubMed-9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 [7] PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE-99413720; PubMed-10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M., Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 [8] IKK- α BINDING. PubMed-10195894;
 RX MEDLINE-99212141;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 [9] IKK PHOSPHORYLATION.
 RX MEDLINE-99038238; PubMed-9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 [10] REVIEW.
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO. HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.

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 DR EMBL; AF012890; AAC51662.1;
 DR EMBL; AF009225; AAC51671.1;
 DR EMBL; AF080157; AAC08996.1;
 DR EMBL; U22512; AAC50713.1;
 DR HSSP; Q63450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT NP_BIND 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS -> DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDRAWL 6
 DB 738 LDWSWL 743
 RESULT 2
 IKKA_MOUSE STANDARD; PRT; 745 AA.
 ID IKKA_MOUSE
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IKK α) (IKK-alpha) (Ikappab kinase)
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
 GN IKKA OR CHUK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE-96044444; PubMed-7558004;
 RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 [2] SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE-96258427; PubMed-8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 [3]

SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli R., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
 RA Gelezianus R., Marcu K.B.,
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.,
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.,
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.,
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.,
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL An. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 CC WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2/DELTA LH AND
 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.
 -1- TISSUE SPECIFICITY: UBIQUITOUS ONLY FOR ISOFORM 1, ISOFORMS 2 AND
 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.
 -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY
 E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION
 PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.
 -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
 MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 IKAPAB KINASE SUBFAMILY.

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 or send an email to license@isb-sib.ch.

 EMBL; U12473; AAC52589.1; -
 DR EMBL; AK018671; BAB31335.1; -
 DR HSSP; O63450; 1A06.
 DR MGD; MGI:99484; Chuk.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Alternative splicing.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1) (BY
 FT MOD_RES 176 176 SIMILARITY).
 FT MOD_RES 452 471 PHOSPHORYLATION (BY MAP3K14) (BY
 FT VARSPLIC 472 471 SIMILARITY).
 FT VARSPLIC 472 745 MISSING (IN ISOFORM 2).
 FT VARSPLIC 577 584 DLHYSST -> GRTLOSQV (IN ISOFORM 3).
 FT VARSPLIC 585 745 MISSING (IN ISOFORM 3).
 FT CONFLICT 236 236 K -> E (IN REF. 3).
 FT CONFLICT 400 400 S -> Y (IN REF. 3).
 SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AFF92233 CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 738 LDWAWL 743
 RESULT 3
 IKKB_HUMAN STANDARD; PRT; 756 AA.
 ID IKKB_HUMAN
 AC O14920; O75327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC [1]
 CC NCBI_TaxID=9606;
 CC [1]
 CC SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 CC [1]
 CC TISSUE=Cervical carcinoma;
 CC MEDLINE=98008813; PubMed=9346484;
 CC RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 CC Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 CC [1]
 CC *IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 CC NF-kappaB activation.*;
 CC Science 278:860-866(1997).
 CC [2]
 CC SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 CC MEDLINE=98008814; PubMed=9346485;
 CC RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 CC [1]
 CC *IkappaB kinase-beta: NF-kappaB activation and complex formation with
 CC IkappaB kinase-alpha and NIK.*;
 CC Science 278:866-869(1997).
 CC [3]
 CC SEQUENCE FROM N.A., AND GENE MAPPING.
 CC TISSUE=Heart;
 CC MEDLINE=99032998; PubMed=9813230;
 CC RA Hu M.C.-T., Wang Y.-P.;
 CC [1]
 CC *IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 CC embryonic tissues but localized to different human chromosomes.*;
 CC Gene 222:31-40(1998).
 CC [4]
 CC SEQUENCE FROM N.A., AND GENE MAPPING.
 CC MEDLINE=98438415; PubMed=9763654;
 CC RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 CC [1]
 CC *Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 CC 8p12->p11 by in situ hybridization.*;
 CC Cytogenet. Cell Genet. 82:32-33(1998).
 CC [5]
 CC SEQUENCE OF 1-256 FROM N.A.
 CC TISSUE=Lung;
 CC Strausberg R.;
 CC Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC [6]
 CC IKK PHOSPHORYLATION.
 CC MEDLINE=99038238; PubMed=9819420;
 CC RA Nemoto S., Didonato J.A., Lin A.;
 CC [1]
 CC *Coordinate regulation of IkappaB kinases by mitogen-activated protein
 CC kinase kinase 1 and NF-kappaB-inducing kinase.*;
 CC Mol. Cell. Biol. 18:7336-7343(1998).
 CC [7]
 CC REVIEW.
 CC MEDLINE=20178139; PubMed=10712233;
 CC RA Jobin C., Sartor R.B.;
 CC [1]
 CC *The I kappa B/NF-kappa B system: a key determinant of
 CC mucosal inflammation and protection.*;
 CC Am. J. Physiol. 278:C451-C462(2000).
 CC [1]
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND
 CC PERIPHERAL BLOOD.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPA-B KINASE SUBFAMILY.
 CC [1]

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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AF029684; AAC31860.1; -;
 CC DR EMBL; AF080158; AAD08997.1; -;
 CC DR EMBL; AF031416; AAC64675.1; -;
 CC DR EMBL; BC006231; AAH06231.1; -;
 CC DR HSP; Q63450; IAO6;
 CC DR Genew; HGNC:5960; IKKB.
 CC DR MIM; 603258; -;
 CC DR InterPro; IPR000719; Euk_pkinase.
 CC DR InterPro; IPR002290; Ser_thr_pkinase.
 CC DR InterPro; IPR001245; Tyr_pkinase.
 CC DR Pfam; PF00069; pkinase; 1.
 CC DR Pfam; PF00240; ubiquitin; 1.
 CC DR PRINTS; PR00109; TYRKINASE.
 CC DR ProDom; PD000001; Euk_pkinase; 1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 CC FT DOMAIN 15 300 PROTEIN KINASE.
 CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC FT NP_BIND 21 29 NEMO-BINDING.
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 145 145 BY SIMILARITY.
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 177 177 PHOSPHORYLATION.
 CC FT MOD_RES 181 181 PHOSPHORYLATION.
 CC FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
 CC EFFECT ON BINDING TO NIK.
 CC FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
 CC FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
 CC FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
 CC FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
 CC FT CONFLICT 231 255 WSKVRQKSEVDIVVSEDLNGTVKF -> CYRMPGTVVHNS
 CC CNPSTLGGGRHWI (IN REF. 5).
 CC FT CONFLICT 425 425 Q -> H (IN REF. 1).
 CC SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
 CC Query Match 92.5%; Score 37; DB 1; Length 756;
 CC Best Local Similarity 83.3%; Pred. No. 75;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 LDNAWL 6
 CC Db 737 LDNSWL 742
 CC RESULT 4
 CC IKKB_MOUSE STANDARD; PRT; 757 AA.
 CC AC O88351; O9R136;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 CC (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
 CC 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 CC GN IKKB OR IKKBK.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
 CC RC STRAIN=C57BL/6; TISSUE=Spleen;
 CC RX MEDLINE=98188238; PubMed=9520401;

RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of Ikappab kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates Ikappab kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein
 RT kinase kinase kinase-1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The Ikappab/NF-kappaB system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEKK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBIQUITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEKK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF026524; AAC23557.1;
 DR EMBL; AF088910; AAD52095.1;
 DR HSSP; Q63450; IAO6.
 DR MGD; MGI:1338071; Ikbkb.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 BY SIMILARITY.
 FT ACT_SITE 145 145 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 N -> D (IN REF. 2).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDSWLQMEDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 75;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 DB 737 LDWSWL 742
 RESULT 5
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 GN IKKB OR IKKBK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein
 RT kinase kinase kinase-1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEKK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.

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CC CC COMPLEX.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
CC CC WEAKLY AUTOPHOSPHORYLATED.
CC CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CC IKAPPAB KINASE SUBFAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL; AF115282; AAF21978.1; -.
DR DR HSSP; O63450; 1A06.
DR DR InterPro; IPR000719; Euk_pkinase.
DR DR InterPro; IPR002290; Ser_thr_pkinase.
DR DR InterPro; IPR001245; Tyr_pkinase.
DR DR Pfam; PF00069; pkinase; 1.
DR DR PRINTS; PR00109; TYRKINASE.
DR DR PRODOM; PD000001; Euk_pkinase; 1.
DR DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 757 AA; 86866 MW; 3AFFE46A7DF91F9C CRC64;

Query Match 92.5%; Score 37; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 737 LDWSWL 742

RESULT 6
CP72_CATRO
ID CP72_CATRO STANDARD; PRT; 524 AA.
AC Q05047;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome P450 72A1 (EC 1.14.14.1) (CYPLXXII) (Secologanin synthase)
DE (SLS).
DE GN CYP72A1 OR CYP72 OR P450CR3.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
OC Viscaceae; Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. CP3A;
RA Vetter H.-P., Mangold U., Schroeder G., Marner F.-J.,
RA Werck-Reichhart D., Schroeder J.;
RT "Molecular analysis and heterologous expression of an inducible
RT cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
RL Plant Physiol. 100:998-1007(1992).
RN [2]

```

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RP SEQUENCE OF 469-524 FROM N.A.
RC STRAIN=cv. G. Don;
RX MEDLINE=93283641; PubMed=8507838;
RA Meijer A.H., Souer E., Verpoorte R., Hoge J.H.C.;
RT "Isolation of cytochrome P-450 cDNA clones from the higher plant
RT Catharanthus roseus by a PCR strategy.";
RL Plant Mol. Biol. 22:379-383(1993).
RN [3]
RP FUNCTION.
RC STRAIN=cv. CP3A;
RX MEDLINE=20575722; PubMed=11135113;
RA Irmier S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
RA Schmidt J., Strack D., Matern U., Schroeder J.;
RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme
RT activities and identification of cytochrome P450 CYP72A1 as
RT secologanin synthase.";
RL Plant J. 24:797-804(2000).
RP FUNCTION.
RC STRAIN=cv. CP3A;
RX MEDLINE=20575722; PubMed=11135113;
RA Irmier S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
RA Schmidt J., Strack D., Matern U., Schroeder J.;
RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme
RT activities and identification of cytochrome P450 CYP72A1 as
RT secologanin synthase.";
RL Plant J. 24:797-804(2000).
CC -1- FUNCTION: Converts loganin into secologanin.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) -> ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- PATHWAY: INDOLE ALKALOID SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
CC -1- TISSUE SPECIFICITY: Upper and lower leaf epidermis.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC CC -----
DR DR EMBL; L10081; AAA33106.1; -.
DR DR EMBL; X69775; CAA49430.1; -.
DR DR HSSP; P14779; IJPZ.
DR DR InterPro; IPR001128; Cytochrome_P450.
DR DR Pfam; PF00067; P450; 1.
DR DR PRINTS; PR00385; P450.
DR DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR DR Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
KW Heme; Alkaloid metabolism.
FT TRANSMEM 12 32 POTENTIAL.
FT BINDING 470 470 HEME (BY SIMILARITY).
FT VARIANT 190 190 I -> L.
FT VARIANT 194 194 Q -> E.
FT VARIANT 223 223 E -> D.
FT VARIANT 312 312 K -> R.
FT VARIANT 318 318 S -> T.
FT VARIANT 403 403 V -> I.
FT VARIANT 405 405 K -> E.
FT VARIANT 411 411 S -> P.
SQ SEQUENCE 524 AA; 60557 MW; EF5D864E43C751E8 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5
DB 28 LDRAW 32

RESULT 7
VEXE_SALTI
ID VEXE_SALTI STANDARD; PRT; 656 AA.
AC P43112;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE VI polysaccharide export protein vexe.
DE VEXE OR STY4551.
OS Salmonella typhi.

```

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GIFU 10007;
 RX MEDLINE=93322324; PubMed=8331073;
 RA Hashimoto Y., Li N., Yokoyama H., Ezaki T.;
 RT "Complete nucleotide sequence and molecular characterization of Viab
 RL region encoding Vi antigen in Salmonella typhi.";
 RN J. Bacteriol. 175:4456-4465(1993).
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RL enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSLOCATION OF THE VI ANTIGEN.
 CC -----
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 CC -----
 DR EMBL; D14156; BAA03200.1; -;
 DR EMBL; AL627283; CAD06771.1; -;
 DR InterPro; IPR001440; TPR.
 KW Polysaccharide transport; Transport; Complete proteome.
 SQ SEQUENCE 656 AA; 73652 MW; 26097F9D6F51ECD CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 656;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDNAW 5
 Db 411 LDNAW 415
 RESULT 8
 ID VP1_YEAST STANDARD; PRT; 840 AA.
 AC P32563;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Vacuolar ATP synthase 95 kDa subunit (Vacuolar ATPase 95 kDa subunit).
 GN VP1 OR YOR270C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92332542; PubMed=1385813;
 RA Manolson M.F., Proteau D., Preston R.A., Stenbit A., Roberts B.T.,
 RA Hoyt M.A., Preus D., Mulholland J., Botstein D., Jones E.W.;
 RT "The VP1 gene encodes a 95-kDa integral membrane polypeptide
 RT required for in vivo assembly and activity of the yeast vacuolar
 RT H(+)-ATPase.";
 RL J. Biol. Chem. 267:14294-14303(1992).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93147685; PubMed=1491220;
 RA Manolson M.F., Proteau D., Jones E.W.;
 RT "Evidence for a conserved 95-120 kDa subunit associated with and
 RL essential for activity of V-ATPases.";
 RN J. Exp. Biol. 172:105-112(1992).
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=97051594; PubMed=8896271;
 RA Cheret G., Bernardi A., Sor F.J.;
 RT "DNA sequence analysis of the VP1-SNF2 region on chromosome XV of
 RL Saccharomyces cerevisiae.";
 RL Yeast 12:1059-1064(1996).
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=97298311; PubMed=9153759;
 RA Polrey R., Jauniaux J.C.;
 RT "Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV
 RL reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1,
 RL RBL2, PNT1, PAC1 and VP1.";
 RL Yeast 13:483-487(1997).
 CC -1- FUNCTION: REQUIRED FOR ASSEMBLY AND ACTIVITY OF THE VACUOLAR
 CC ATPASE. POTENTIAL ROLE IN DIFFERENTIAL TARGETING AND REGULATION OF
 CC THE ENZYME FOR A SPECIFIC ORGANELLE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
 CC -1- SIMILARITY: BELONGS TO THE V-ATPASE 116 kDa SUBUNIT FAMILY.
 CC -----
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 CC -----
 DR EMBL; M89778; AAA3211.1; -;
 DR EMBL; X89633; CAA61776.1; -;
 DR EMBL; Z75178; CAA99494.1; -;
 DR EMBL; Z75179; CAA99496.1; -;
 DR PIR; A42970; A42970.
 DR SGD; S0005796; VP1.
 DR InterPro; IPR002490; V_ATPase_sub116.
 DR Pfam; PF01496; V_ATPase_sub_a; 1.
 KW Hydrogen ion transport; Transmembrane; Glycoprotein.
 FT DOMAIN 1 411
 FT TRANSMEM 412 432
 FT DOMAIN 433 462
 FT TRANSMEM 463 483
 FT DOMAIN 484 540
 FT TRANSMEM 541 561
 FT DOMAIN 562 571
 FT TRANSMEM 572 592
 FT DOMAIN 593 635
 FT TRANSMEM 636 656
 FT DOMAIN 657 760
 FT TRANSMEM 761 787
 FT DOMAIN 788 840
 FT CARBOHYD 113 113
 FT CARBOHYD 280 280
 FT CARBOHYD 324 324
 SQ SEQUENCE 840 AA; 95528 MW; 77709A914410CD4D CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDNAW 5
 Db 518 LDNAW 522


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RESULT 9
CYOA_BUCAI
ID CYOA_BUCAI STANDARD; PRT; 296 AA.
AC P57544;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA OR B0472.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS."
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC
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CC
CC -----
CC EMBL; D13185; BAA02480.1; -
CC HSP; P18400; LCYW.
CC InterPro; IPR001505; Copper_CuA.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF00116; COX2; 1.
CC ProDom; PD000131; Copper_CuA; 1.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.
CC Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
CC Signal; Lipoprotein; Complete proteome.
CC SIGNAL
CC CHAIN 1 15 POTENTIAL.
CC FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 34 54 POTENTIAL.
CC FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 79 99 POTENTIAL.
CC FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
CC SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FFBAC CRC64;

Query Match 87.5%; Score 35; DB 1; Length 296;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDNAWL 6
Db 125 LDWKWL 130

RESULT 10
QOX2_ACEAC
ID QOX2_ACEAC STANDARD; PRT; 307 AA.
AC P50653;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
DE A1 subunit 2) (Oxidase BA(3) subunit 2).
GN CYAB.
OS Acetobacter acetii.
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OC Acetobacter.
OX NCBI_TaxID=435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1023;
RX MEDLINE=93322308; PubMed=83925209;
RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
RA Kawamura Y., Horinouchi S., Beppu T.;
RT "Characterization of a cytochrome a1 that functions as a ubiquinol
RT oxidase in Acetobacter acetii."
RL J. Bacteriol. 175:4307-4314(1993).
CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC
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CC
CC -----
CC EMBL; D13185; BAA02480.1; -
CC HSP; P18400; LCYW.
CC InterPro; IPR001505; Copper_CuA.
CC InterPro; IPR002429; Cyt_c_ox_2.
CC Pfam; PF00116; COX2; 1.
CC ProDom; PD000131; Copper_CuA; 1.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC Oxidoreductase; Transmembrane; Respiratory chain; Signal;
CC Lipoprotein.
CC SIGNAL 1 23 POTENTIAL.
CC FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT TRANSMEM 46 66 POTENTIAL.
CC FT TRANSMEM 87 107 POTENTIAL.
CC SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;

Query Match 87.5%; Score 35; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDNAWL 6
Db 135 LDWKWL 140

RESULT 11
CYOA_PSEPU
ID CYOA_PSEPU STANDARD; PRT; 314 AA.
AC Q9WWR1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;

```


RN SEQUENCE FROM N.A.
 RP STRAIN=IH-2000;
 RC MEDLINE=99085656; PubMed=9868765;
 RA Hirayama H., Takami H., Inoue A., Horikoshi K.;
 RT "Isolation and characterization of toluene-sensitive mutants from
 RL Pseudomonas putida IH-2000.";
 CC FEMS Microbiol. Lett. 169:219-225(1998).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
 CC GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) - Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AB016787; BAA76356.1; -;
 DR HSSP; P18400; ICYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR Pfam; PF002429; Cyt_c_ox_2.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 KW Inner membrane; Signal; Lipoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 43 63 POTENTIAL.
 FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
 SQ SEQUENCE 314 AA; 34702 MW; 96E04FC3AA77F07 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 314;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDRAWL 6
 DB 133 LDRAWL 138

RESULT 12
 NOS3_SHEEP
 ID NOS3_SHEEP STANDARD; PRT; 99 AA.
 AC P79209;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
 DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS)
 DE (fragment).
 GN NOS3 OR ENOS.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endothelial cells;
 RA Aguan K., Weiner C.P.;
 RT "Effect of hypoxia on the microvasculature of developing fetal

RT brain of sheep: a studies on the expression pattern of
 RT constitutive forms of nitric oxide synthase.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
 CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL
 CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
 CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
 CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) - citrulline +
 CC nitric oxide + N NADP(+).
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
 CC THE ENZYME (BY SIMILARITY).
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
 CC -----
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 CC -----
 DR EMBL; U76738; AAB40705.1; -;
 DR HSSP; P29473; IDOC.
 DR InterPro; IPR004030; NO_synthase.
 DR Pfam; PF02898; NO_synthase; 1.
 DR PROSITE; PS00001; NOS; PARTIAL.
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
 KW Heme; Multigene family.
 FT NON_TER 99 99
 FT NON_TER 1 1
 SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 99;
 Best Local Similarity 80.0%; Pred. No. 33;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DRAWL 6
 DB 66 DRAWI 70

RESULT 13
 LY4A_MOUSE
 ID LY4A_MOUSE STANDARD; PRT; 262 AA.
 AC P20937;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE T-cell surface glycoprotein YEL/48 (T lymphocyte antigen A1) (LY49-A
 DE antigen).
 GN KLRA1 OR LY49A OR LY-49A OR LY49 OR LY-49.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89140367; PubMed=2783949;
 RA Chan P.-Y., Takei F.;
 RT "Molecular cloning and characterization of a novel murine T cell
 RT surface antigen, YEL/48.";
 RL J. Immunol. 142:1727-1736(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89309828; PubMed=2787364;
 RA Yokoyama W.M., Jacobs L., Kanagawa O., Shevach E.M., Cohen D.I.;
 RT "A murine T lymphocyte antigen belongs to a supergene family of type

II integral membrane proteins.";
 RL Smith H.R.C., Karhofer F.M., Yokoyama W.M.;
 CC "Ly-49 multigene family expressed by IL-2-activated NK cells.";
 CC J. Immunol. 153:1068-1079(1994).
 CC [2]
 CC SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 CC STRAIN=C57BL/6;
 CC MEDLINE=96421544; PubMed=8824161;
 CC Silver E.T., Elliott J.F., Kane K.P.;
 CC "Alternately spliced Ly-49D and H transcripts are found in IL-2-
 CC activated NK cells.";
 CC Immunogenetics 44:478-482(1996).
 CC [3]
 CC SEQUENCE FROM N.A. (ISOFORM D1).
 CC STRAIN=NOD, and NOR;
 CC MEDLINE=20384764; PubMed=10925254;
 CC Silver E.T., Gong D.-E., Chang C.S., Amrani A., Santamaria P.,
 CC Kane K.P.;
 CC "Ly-49p activates NK-mediated lysis by recognizing H-2Dd.";
 CC J. Immunol. 165:1771-1781(2000).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; D1 (shown here) and D2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 CC EMBL; M25775; AAA40578.1; ALT_SEQ.
 CC EMBL; M25812; AAA37242.1; -
 CC PIR; A30573; A30573.
 CC MGI; MGI:101907; Klr4l.
 CC InterPro: IPR001304; Lectin_C.
 CC Pfam; PF00059; lectin_c; 1.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
 CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 CC T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
 CC Signal-anchor; Lectin; Receptor; Multigene family.
 CC DOMAIN 1 44 CYTOPLASMIC (PROBABLE).
 CC TRANSMEM 45 66 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 67 262 EXTRACELLULAR (PROBABLE).
 CC DISULFID 138 257 C-TYPE LECTIN (LONG FORM).
 CC DISULFID 167 253 BY SIMILARITY.
 CC SITE 232 245 BY SIMILARITY.
 CC SITE 137 139 CELL ATTACHMENT SITE.
 CC CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 76 78 NCE -> KIQ (IN REF. 2).
 CC CONFLICT 106 106 I -> M (IN REF. 2).
 CC CONFLICT 166 166 A -> T (IN REF. 2).
 CC CONFLICT 223 223 G -> R (IN REF. 2).
 CC SEQUENCE 262 AA; 30498 MW; 3C3328D265F71B5E CRC64;
 CC -----
 CC Query Match 85.0%; Score 34; DB 1; Length 262;
 CC Best Local Similarity 80.0%; Pred. No. 81;
 CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 2 DWAWL 6
 CC | | | |
 CC Db 207 DWAMI 211
 CC -----
 CC RESULT 14
 CC KLR4_MOUSE STANDARD; PRT; 263 AA.
 CC AC Q60651; O78026; Q9EPA5;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Killer cell lectin-like receptor 4 (T-cell surface glycoprotein
 CC LY-49D) (LY49-D antigen).
 CC GN KLR4 OR LY49D OR LY-49D OR LY49-D.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC OC NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A. (ISOFORM D2).
 CC RC STRAIN=C57BL/6; TISSUE=Spleen;

RX MEDLINE=94300068; PubMed=8027540;
 RA Smith H.R.C., Karhofer F.M., Yokoyama W.M.;
 RT "Ly-49 multigene family expressed by IL-2-activated NK cells.";
 RL J. Immunol. 153:1068-1079(1994).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96421544; PubMed=8824161;
 RA Silver E.T., Elliott J.F., Kane K.P.;
 RT "Alternately spliced Ly-49D and H transcripts are found in IL-2-
 RT activated NK cells.";
 RL Immunogenetics 44:478-482(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM D1).
 RC STRAIN=NOD, and NOR;
 RX MEDLINE=20384764; PubMed=10925254;
 RA Silver E.T., Gong D.-E., Chang C.S., Amrani A., Santamaria P.,
 RA Kane K.P.;
 RT "Ly-49p activates NK-mediated lysis by recognizing H-2Dd.";
 RL J. Immunol. 165:1771-1781(2000).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; D1 (shown here) and D2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 CC EMBL; U10090; AAA50218.1; -
 CC EMBL; L78247; AAC32667.1; -
 CC EMBL; AF218079; AAF99592.1; -
 CC EMBL; AF218078; AAF99591.1; -
 CC MGI; MGI:101904; Klr4l.
 CC InterPro: IPR001304; Lectin_C.
 CC Pfam; PF00059; lectin_c; 1.
 CC SMART; SM00034; CLECT; 1.
 CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
 CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 CC T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
 CC Signal-anchor; Lectin; Receptor; Multigene family;
 CC Alternative splicing; Polymorphism.
 CC DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 45 65 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 66 263 EXTRACELLULAR (POTENTIAL).
 CC DISULFID 139 258 C-TYPE LECTIN (LONG FORM).
 CC DISULFID 168 254 BY SIMILARITY.
 CC SITE 233 246 BY SIMILARITY.
 CC CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC VARSPLIC 39 41 MISSING (IN ISOFORM D2).
 CC VARIANT 5 5 E -> K (IN STRAINS NOD AND NOR).
 CC VARIANT 29 29 R -> W (IN STRAINS NOD AND NOR).
 CC VARIANT 32 32 E -> Q (IN STRAINS NOD AND NOR).
 CC VARIANT 35 35 R -> G (IN STRAINS NOD AND NOR).
 CC VARIANT 45 45 L -> F (IN STRAINS NOD AND NOR).
 CC VARIANT 60 60 T -> I (IN STRAINS NOD AND NOR).
 CC VARIANT 79 79 K -> Q (IN STRAINS NOD AND NOR).
 CC VARIANT 132 132 Y -> S (IN STRAINS NOD AND NOR).
 CC VARIANT 189 189 L -> F (IN STRAINS NOD AND NOR).
 CC SEQUENCE 263 AA; 30872 MW; D0A940A089A9F42D CRC64;
 CC -----
 CC Query Match 85.0%; Score 34; DB 1; Length 263;
 CC Best Local Similarity 80.0%; Pred. No. 81;

Search completed: May 30, 2003, 15:49:06
Job time : 8.11842 secs

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWAWL 6
||||
Db 208 DAWI 212

RESULT 15

GUX2_CLOS
ID GUX2_CLOS STANDARD; PRT; 914 AA.
AC P50900;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Exoglucanase II precursor (EC 3.2.1.91) (Exocellobiohydrolase II)
DE (1,4-beta-cellobiohydrolase II) (Avicelase II).
GN CELY.
OS Clostridium stercorarium.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NCIB 11754;
RA Bronnenmeier K., Riedel K., Staudenbauer W.H.,
RA Staudenbauer W.L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP CHARACTERIZATION.
RC STRAIN-NCIB 11754;
RX MEDLINE-91364686; PubMed-1909625;
RA Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;
RT "Purification and properties of a novel type of
RT exo-1,4-beta-glucanase (avicelase II) from the cellulolytic
RT thermophile Clostridium stercorarium";
RL Eur. J. Biochem. 200:379-385(1991).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellotetraose, releasing cellobiose from the non-
CC reducing ends of the chains.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY L (FAMILY 48 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Z69359; CAA93280.1; -
DR HSP; Q06851; INBC.
DR InterPro; IPR001956; CBD_3.
DR InterPro; IPR005102; DUF291.
DR InterPro; IPR000556; Glyco_hydro_48.
DR Pfam; PF00942; CBM_3; 1.
DR Pfam; PF02011; Glyco_hydro_48; 1.
DR Pfam; PF03442; DUF291; 1.
DR PRINTS; PR00844; GLHYDRLASE48.
DR ProDom; PD001947; CBD_3; 1.
DR ProDom; PD011903; Glyco_hydro_48; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 914 EXOGLUCANASE II.
SQ SEQUENCE 914 AA; 103020 MW; D0DB6017D6DF82C CRC64;

Query Match 85.08; Score 34; DB 1; Length 914;
Best Local Similarity 80.08; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWAWL 6
||||
Db 339 DAWI 343

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDNAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	92.5	745	1 I49101	conserved helix-loop-helix
2	36	90.0	215	2 D75215	probable phosphoribosyltransferase
3	36	90.0	251	2 E70521	probable phosphoribosyltransferase
4	36	90.0	304	2 F83632	probable cytochrome
5	36	90.0	316	2 D98351	probable cytochrome
6	36	90.0	316	2 AB2931	probable cytochrome
7	36	90.0	516	2 T10000	probable cytochrome
8	36	90.0	524	2 T09999	probable cytochrome
9	36	90.0	524	2 T09944	probable cytochrome
10	36	90.0	656	2 A56975	Vi polysaccharide
11	36	90.0	656	2 AF1040	Vi polysaccharide
12	36	90.0	840	1 A42970	H ⁺ -exporting ATPase
13	36	90.0	1212	2 F83153	probable two-component
14	36	90.0	1575	2 T18545	lysobactin synthetase
15	35	87.5	162	2 C70829	hypothetical protein
16	35	87.5	204	2 C83748	hypothetical protein
17	35	87.5	277	1 JC5900	bo-type ubiquinol
18	35	87.5	226	2 A84985	cytochrome o ubiquinol
19	35	87.5	299	2 B83443	cytochrome o ubiquinol
20	35	87.5	307	1 A36885	bo-type ubiquinol
21	35	87.5	318	2 AD0384	cytochrome o ubiquinol
22	35	87.5	331	2 D83480	cytochrome o ubiquinol
23	35	87.5	337	2 C98336	probable integral protein
24	35	87.5	337	2 AG2946	hypothetical protein
25	35	87.5	344	2 AG3489	cytochrome o ubiquinol
26	35	87.5	353	2 A87469	ubiquinol oxidase
27	35	87.5	386	2 C96006	probable cytochrome
28	35	87.5	394	2 C85064	hypothetical protein
29	35	87.5	418	2 D85064	hypothetical protein

30	35	87.5	443	2 AE0309	probable sugar transporter
31	35	87.5	1139	2 AI0379	probable potassium
32	34	85.0	260	2 I49049	Ly-49D-GE antigen
33	34	85.0	262	2 I49361	natural killer cell
34	34	85.0	262	2 A30573	T-cell surface glycoprotein
35	34	85.0	262	2 A45813	T-cell surface glycoprotein
36	34	85.0	267	2 I55886	LDL-1 - mouse
37	34	85.0	322	2 AI3395	NADH2 dehydrogenase
38	34	85.0	348	2 G97514	NADH dehydrogenase
39	34	85.0	348	2 AE2733	NADH ubiquinone oxidoreductase
40	34	85.0	395	2 E90438	hypothetical protein
41	34	85.0	395	2 B96610	hypothetical protein
42	34	85.0	616	2 C69226	type I restriction endonuclease
43	34	85.0	1202	2 S71424	nitric-oxide synthase
44	34	85.0	1203	1 A47501	nitric-oxide synthase
45	34	85.0	1205	1 A38943	nitric-oxide synthase

ALIGNMENTS

RESULT 1

I49101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1) CHUK - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: I49101

R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

Genomics 27, 348-351, 1995

A>Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 12p11.2

A:Reference number: I49101; MUID:9604444; PMID:7538004

A:Accession: I49101

A:Molecule type: mRNA

A:Residues: 1-745 <RES>

A:Cross-references: EMBL:U12473; NID:gl079492; PIDN:ARC52589.1; PID:gl079493

C:Genetics:

A:Gene: CHUK

C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homology

C:Keywords: ATP; phosphotransferase

F:13-283/Domain: protein kinase homology <KIN>

Query Match 92.5%; Score 37; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAWL 6
DB 738 LDNAWL 743

RESULT 2

D75215

purine phosphoribosyltransferase PAB2405 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: D75215

R:anonymous, Genoscope

A:Submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosomes

A:Reference number: A75001

A:Accession: D75215

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-215 <KAW>

A:Cross-references: GB:AJ248283; GB:AL096836; NID:q5457433; PIDN:CAB49171.1; PID:el51

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: gptA; PAB2405

Query Match 90.0%; Score 36; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAWL 6
:|||||
Db 141 IDWAWI 146

RESULT 3
E70521
probable phosphotransferase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: E70521
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70521
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-251 <COL>
A:Cross-references: GB:Z97188; GB:AL123456; NID:g3261805; PIDN:CAB10016.1; PID:g2224828
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Kv3817
C:Superfamily: kanamycin kinase

Query Match 90.0%; Score 36; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
:|||||
Db 86 DWAWL 90

RESULT 4
F83632
probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83632
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83632
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <STO>
A:Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03503.1; GSPDB:GN001187
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0113
C:Superfamily: heme O synthase

Query Match 90.0%; Score 36; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAW 5
:|||||
Db 259 LDNAW 263

RESULT 5
D98351
dipeptide ABC transporter, dipeptide-binding protein PAB0092 [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: D98351
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: D98351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90334.1; PID:gl5160371; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_3514
A:Map position: linear chromosome

Query Match 90.0%; Score 36; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAW 5
:|||||
Db 67 LDNAW 71

RESULT 6
AB2931
hypothetical protein Atu3048 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AB2931
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Rao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL43864.1; PID:gl7741409; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3048
A:Map position: linear chromosome

Query Match 90.0%; Score 36; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAW 5
:|||||
Db 67 LDNAW 71

RESULT 7
T10000
cytochrome P450 (CYP72C) - Madagascar periwinkle (fragment)
C:Species: Catharanthus roseus (Madagascar periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C:Accession: T10000
R:Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Wer Plant Sci. 96, 129-136, 1994
A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Cathara
A:Reference number: Z16915
A:Accession: T10000
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-516 <MAN>
A:Cross-references: EMBL:L19075; NID:g404689; PID:g404690

A;Experimental source: cv. cp3
C;Genetics:

A;Gene: CYP72C

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein

F;318-481/Domain: cytochrome P450 homology <P45>

F;459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5

Db 17 LDRAW 21

RESULT 8

T09599

cytochrome P450 - Madagascar periwinkle

C;Species: Catharanthus roseus (Madagascar periwinkle)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001

C;Accession: T09599

R;Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-

Plant Sci 96, 129-136, 1994

A;Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharan-

A;Reference number: Z16915

A;Accession: T09599

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-524 <MAN>

A;Cross-references: EMBL:L19074; NID:g404687; PID:g404688

A;Experimental source: cv. cp3

C;Genetics:

A;Gene: CYP72B

A;Introns: 96/1; 170/3; 252/2; 381/3

C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;329-492/Domain: cytochrome P450 homology <P45>

F;470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 524;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5

Db 28 LDRAW 32

RESULT 9

T09944

probable cytochrome P450 protein - Madagascar periwinkle

N;Alternate names: CYP72 protein

C;Species: Catharanthus roseus (Madagascar periwinkle)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001

C;Accession: T09944

R;Vetter, H.P.; Mangold, U.; Schroeder, U.; Marner, F.J.; Werck-Reichhart, D.; Schroeder

Plant Physiol. 100, 998-1007, 1992

A;Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450

A;Reference number: Z16902

A;Accession: T09944

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-524 <VET>

A;Cross-references: EMBL:L10081; NID:g167483; PID:g167484

C;Genetics:

A;Gene: CYP72

C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;329-492/Domain: cytochrome P450 homology <P45>

F;470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5

Db 28 LDRAW 32

RESULT 10

A56975

Vi polysaccharide capsule transporter vexE - Salmonella typhi

C;Species: Salmonella typhi

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 11-Jan-2000

C;Accession: A56975

R;Hashimoto, Y.; Li, N.; Yokoyama, H.; Ezaki, T.

J. Bacteriol. 175, 4456-4465, 1993

A;Title: Complete nucleotide sequence and molecular characterization of viab region e

A;Reference number: A36892; MUID:93322324; PMID:8331073

A;Accession: A56975

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-656 <HAS>

A;Cross-references: GB:DL4156; NID:g426443; PIDN:BAA03200.1; PID:dl003709; PID:g42645

C;Genetics:

A;Gene: vexE

C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat

F;284-317/Domain: tetratricopeptide repeat homology <TP1>

F;318-351/Domain: tetratricopeptide repeat homology <TP2>

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 656;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5

Db 411 LDRAW 415

RESULT 11

AF1040

Vi polysaccharide export protein [imported] - Salmonella enterica subsp. enterica ser

C;Species: Salmonella enterica subsp. enterica serovar typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C;Accession: AF1040

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A;Reference number: AB0502; PMID:11677608

A;Accession: AF1040

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-656 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06771.1; PID:g16505421; GSPDB:GN00176

C;Genetics:

A;Gene: vexE

C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 656;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5

Db 411 LDRAW 415

RESULT 12

A42970

Hi-exporting ATPase (EC 3.6.3.6) 95K chain, vacuolar - yeast (Saccharomyces cerevisiae)
 H:Alternate names: protein O3430c; protein YOR270c
 C:Species: Saccharomyces cerevisiae
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 C:Accession: A42970; S67167; S67172; S72041
 R:Manolson, M.F.; Proteau, D.; Preston, R.A.; Stenbit, A.; Roberts, B.T.; Hoyt, M.A.; P
 J. Biol. Chem. 267, 14294-14303, 1992
 A:Title: The VPH1 gene encodes a 95-kDa integral membrane polypeptide required for in vi
 A:Reference number: A42970; MUID:92332542; PMID:1385813
 A:Accession: A42970
 A:Molecule type: DNA
 A:Residues: 1-840 <MAN>
 A:Cross-references: GB:M89778; NID:g173172; PIDN:AAA35211.1; PID:g173173
 A:Experimental source: strain X2180-1b; vacuolar acidification-defective mutants
 A:Note: sequence extracted from NCBI backbone (NCBI:108529, NCBI:108530)
 R:Jauniaux, J.C.; Poirey, R.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67143
 A:Accession: S67167
 A:Molecule type: DNA
 A:Residues: 1-840 <MAN>
 A:Cross-references: EMBL:Z75178; NID:g1420605; PIDN:CAA99494.1; PID:g1420606; GSPDB:GN00
 A:Experimental source: strain S288C
 R:Cheret, G.; Sor, F.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67169
 A:Accession: S67172
 A:Molecule type: DNA
 A:Residues: 1-840 <CH>
 A:Cross-references: EMBL:Z75178; NID:g1420605; PIDN:CAA99494.1; PID:g1420606; GSPDB:GN00
 A:Experimental source: strain S288C
 R:Cheret, G.; Bernardi, A.; Sor, F.
 Yeast 12, 1059-1064, 1996
 A:Title: DNA sequence analysis of the VPH1-SNF2 region on chromosome XV of Saccharomyces
 A:Reference number: S72039; MUID:97051594; PMID:8896271
 A:Accession: S72041
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-840 <CH>
 A:Cross-references: EMBL:X89633; NID:g1279694; PIDN:CAA61776.1; PID:g1279697
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
 C:Genetics:
 A:Gene: SGD:VPH1; MIPS:YOR270c
 A:Cross-references: MIPS:YOR270c; SGD:S0005796
 A:Map position: 13R
 C:Function:
 A:Description: hydrogen ion transport; hydrolase; required for assembly and activity of
 C:Superfamily: vacuolar ATP synthase 95K chain
 C:Keywords: ATP; glycoprotein; hydrogen ion transport; hydrolase; membrane-associated co
 F:407-441/Domain: transmembrane #status predicted <TM1>
 F:457-478/Domain: transmembrane #status predicted <TM2>
 F:539-538/Domain: transmembrane #status predicted <TM3>
 F:565-591/Domain: transmembrane #status predicted <TM4>
 F:635-656/Domain: transmembrane #status predicted <TM5>
 F:733-795/Domain: transmembrane #status predicted <TM6>

Query Match 90.0%; Score 36; DB 1; Length 840;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNAW 5

Db 518 LDNAW 522

RESULT 13

F83153

probable two-component sensor PA3946 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83153

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim

.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83153

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-1212 <STO>

A:Cross-references: GB:AE004812; GB:AE004091; NID:g9950125; PIDN:AAG07333.1; GSPDB:GN
 A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA3946

C:Superfamily: evgs protein; response regulator homology

Query Match 90.0%; Score 36; DB 2; Length 1212;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWAWL 6

Db 47 DWAWL 51

RESULT 14

T18545

Lysobactin synthetase - Lysobacter sp. (ATCC 53042) (fragment)

C:Species: Lysobacter sp.

A:Variety: ATCC 53042

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000

C:Accession: T18545

R:Bernhard, F.

submitted to the EMBL Data Library, March 1996

A:Description: Identification of genes encoding for peptide synthetases from Gram-neg

A:Reference number: Z18962

A:Accession: T18545

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1575 <BER>

A:Cross-references: EMBL:X96558; NID:e991096; PID:e236566; PIDN:CAA65394.1

A:Experimental source: ATCC 53042

C:Superfamily: acyl carrier protein homology; acetate-CoA ligase homology

C:Keywords: carrier protein; phosphopantetheine; phosphoprotein

F:468-924/Domain: acetate-CoA ligase homology <ACL>

F:942-1010/Domain: acyl carrier protein homology <ACP>

F:974/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 1575;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNAW 5

Db 601 LDNAW 605

RESULT 15

C70829

hypothetical protein Rv0471c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000

C:Accession: C70829

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feitwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70829

A:Status: preliminary;

A:Molecule type: DNA

A:Residues: 1-162 <COL>

A:Cross-references: GB:AL021933; GB:AL123456; NID:g3261529; PIDN:CAA17426.1; PID:el25

A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: Rv0471c
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0471c
 Query Match: 87.5%; Score 35; DB 2; Length 162;
 Best Local Similarity 83.3%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDRAWL 6
 ||| ||
 Db 63 LDWRWL 68

Search completed: May 30, 2003, 14:52:59
 Job time : 7.5921 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	745	2	US-08-887-518-3
2	37	92.5	745	2	US-09-023-321-3
3	37	92.5	745	2	US-08-890-853-4
4	37	92.5	745	2	US-09-032-475-3
5	37	92.5	745	2	US-09-099-125A-4
6	37	92.5	745	2	US-09-099-124A-4
7	37	92.5	745	4	US-09-032-476-4
8	37	92.5	745	4	US-08-890-854-4
9	37	92.5	745	4	US-09-023-324-4
10	37	92.5	745	4	US-09-168-629-2
11	37	92.5	745	4	US-08-910-820-10
12	37	92.5	745	4	US-08-810-131A-2
13	37	92.5	756	2	US-08-887-518-4
14	37	92.5	756	2	US-09-023-321-4
15	37	92.5	756	2	US-08-890-853-2
16	37	92.5	756	2	US-09-032-475-4
17	37	92.5	756	2	US-09-099-125A-2
18	37	92.5	756	2	US-09-099-124A-2
19	37	92.5	756	4	US-09-032-476-2
20	37	92.5	756	4	US-08-890-854-2
21	37	92.5	756	4	US-09-023-324-2
22	37	92.5	756	4	US-09-168-629-15
23	37	92.5	756	4	US-08-910-820-9
24	35	87.5	439	4	US-09-172-952-14
25	34	85.0	1205	1	US-07-908-245-2
26	34	85.0	1205	2	US-08-319-866-10
27	34	85.0	1205	4	US-09-123-708-6

Sequence 6, Appli
Sequence 2, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 47, Appli
Sequence 4, Appli
Sequence 16, Appli
Sequence 10, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 10, Appli
Sequence 21, Appli
Sequence 43, Appli
Sequence 44, Appli
Sequence 1187, Ap
Sequence 1188, Ap

ALIGNMENTS

RESULT 1
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 RUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 92.5% Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
Db 738 LDRAWL 743

RESULT 2
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6
DB 738 LDMSWL 743

RESULT 3
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6
DB 738 LDMSWL 743

RESULT 4
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6

Db 738 LDMSWL 743

RESULT 5

US-09-099-125A-4

; Sequence 4, Application US/09099125A

; Patent No. 5916760

; GENERAL INFORMATION:

; APPLICANT: Goeddel, David V.

; APPLICANT: Woronicz, John

; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/099,125A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/890,853

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: T97-006-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 745 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-099-125A-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6

Db 738 LDMSWL 743

RESULT 6

US-09-099-124A-4

; Sequence 4, Application US/09099124A

; Patent No. 5939302

; GENERAL INFORMATION:

; APPLICANT: Goeddel, David V.

; APPLICANT: Woronicz, John

; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/099,124A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/890,853

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: T97-006-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 745 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-099-124A-4

Query Match

92.5%; Score 37; DB 2; Length 745;

Best Local Similarity 83.3%; Pred. No. 2.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6

Db 738 LDMSWL 743

RESULT 7

US-09-032-476-4

; Sequence 4, Application US/09032476

; Patent No. 6235492

; GENERAL INFORMATION:

; APPLICANT: Rothe, Mike

; APPLICANT: Cao, Zhaodan

; APPLICANT: R gnier, Catherine

; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/032,476

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/890,854

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNAWL 6
Db 738 LDWSWL 743

RESULT 8
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNAWL 6
Db 738 LDWSWL 743

RESULT 9
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNAWL 6
Db 738 LDWSWL 743

RESULT 10
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2

Query Match          92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWAWL 6
Db      738 LDWSWL 743

RESULT 11
US-08-910-820-10
; Sequence 10, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-910-820-10

Query Match          92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWAWL 6
Db      738 LDWSWL 743

RESULT 12
US-08-810-131A-2
; Sequence 2, Application US/08810131A
; Patent No. 6268194

; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: DiDonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,131A
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-131A-2

Query Match          92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWAWL 6
Db      738 LDWSWL 743

RESULT 13
US-08-887-518-4
; Sequence 4, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-4

Query Match 92.5%; Score 37; DB 2; Length 756;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||:|
DB 737 LDWSWL 742

RESULT 14
US-09-023-321-4
Sequence 4, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-4

Query Match 92.5%; Score 37; DB 2; Length 756;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||:|
DB 737 LDWSWL 742
RESULT 15
US-08-890-853-2
Sequence 2, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-2

Query Match 92.5%; Score 37; DB 2; Length 756;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||:|
DB 737 LDWSWL 742

Search completed: May 30, 2003, 14:41:32
Job time : 7.03947 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds
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Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	40	100.0	6	ABB08738	Mutated IKKbeta NE
2	40	100.0	6	AA48521	NBD mutant peptide
3	40	100.0	6	AA48541	Anti-inflammatory
4	40	100.0	6	AA48603	Anti-inflammatory
5	40	100.0	7	AA48607	Anti-inflammatory
6	40	100.0	8	AA48600	Anti-inflammatory
7	40	100.0	8	AA48608	Anti-inflammatory
8	40	100.0	9	AA48599	Anti-inflammatory
9	40	100.0	9	AA48602	Anti-inflammatory
10	40	100.0	9	AA48605	Anti-inflammatory

11	40	100.0	9	23	AA48606	Anti-inflammatory
12	40	100.0	10	23	AA48601	Anti-inflammatory
13	40	100.0	10	23	AA48604	Anti-inflammatory
14	40	100.0	11	23	AA48598	Anti-inflammatory
15	40	100.0	173	23	ABP30297	Streptococcus poly
16	40	100.0	186	23	ABP27565	Streptococcus poly
17	40	100.0	756	23	ABP77306	Human IKKbeta muta
18	38	95.0	342	22	AA40149	Human polypeptide
19	38	95.0	358	22	AA41935	Human polypeptide
20	37	92.5	6	23	IKB08725	IKKbeta NEMO bindi
21	37	92.5	6	23	AA48530	Anti-inflammatory
22	37	92.5	6	23	AA48535	NBD mutant peptide
23	37	92.5	7	23	AA48534	Anti-inflammatory
24	37	92.5	8	23	AA48527	Anti-inflammatory
25	37	92.5	8	23	AA48535	Anti-inflammatory
26	37	92.5	9	20	AAW96182	IKK-alpha polypept
27	37	92.5	9	23	AA48526	Anti-inflammatory
28	37	92.5	9	23	AA48529	Anti-inflammatory
29	37	92.5	9	23	AA48532	Anti-inflammatory
30	37	92.5	9	23	AA48533	Anti-inflammatory
31	37	92.5	10	23	ABB77313	IKKbeta NEMO bindi
32	37	92.5	10	23	AA48528	Anti-inflammatory
33	37	92.5	10	23	AA48531	Anti-inflammatory
34	37	92.5	11	23	ABP77311	Human NBD peptide
35	37	92.5	11	23	AA48506	Human IKKbeta pept
36	37	92.5	11	23	AA48525	Anti-inflammatory
37	37	92.5	11	23	AA48653	NBD peptide. Synt
38	37	92.5	13	23	AA48640	Anti-inflammatory
39	37	92.5	13	23	AA48641	Anti-inflammatory
40	37	92.5	13	23	AA48642	Anti-inflammatory
41	37	92.5	13	23	AA48645	Anti-inflammatory
42	37	92.5	17	23	AA48638	Anti-inflammatory
43	37	92.5	17	23	AA48639	Anti-inflammatory
44	37	92.5	17	23	AA48643	Anti-inflammatory
45	37	92.5	17	23	AA48644	Anti-inflammatory

ALIGNMENTS

RESULT 1

ABB08738

ID ABB08738 standard; peptide; 6 AA.

XX ABB08738;

XX ABB08738;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 16.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX autoimmune disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; antineoplastic; immunosuppressive;
XX osteopathic; cyclostatic; nontropic; neuroprotective; anti-HIV; human;
XX antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
XX dermatological; antibacterial; antipsoriatic; antirheumatic;
XX antiarthritic; osteopathic; antiulcer; mutant; mutelin.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 4 /note= "Wildtype Ser substituted by Ala"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYVA) UNIV YALE.
 XX May MJ, Ghosh S;
 PI WPI; 2002-179350/23.
 DR
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia,
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDNAWL 6
 Db 1 LDNAWL 6
 RESULT 2
 AAM48521
 ID AAM48521 standard; Peptide; 6 AA.
 XX
 AC AAM48521;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 16.
 XX

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO2000183554-A2.
 PN
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 XX factor kappaB activation, and for treating asthma, lung inflammation,
 XX psoriasis -
 XX
 XX Example 6; Page 48; 88pp; English.
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, The
 CC compounds act as selective inhibitors of cytokine-mediated activity. The
 CC compounds act as selective inhibitors of cytokine-mediated activity. The
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyomyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDNAWL 6
 Db 1 LDNAWL 6
 RESULT 3
 AAM48541
 ID AAM48541 standard; Peptide; 6 AA.
 XX

RESULT 4	
AA48603	
ID	AA48603 standard; Peptide; 6 AA.
XX	
AC	AA48603;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 106.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
XX	
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
XX	
PA	(UYIA) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AA48628-AA48645), comprising a membrane translocation domain
CC	(AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AA48625-AA48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappa
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikbapab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	burstis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 6 AA;

CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	eczema, dermatitis, sunburn, aging and
CC	arthritis.
xx	
xx	
SQ	Sequence 6 AA;
	Query Match 100.0%; Score 40; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |
Db 1 LDRAWL 6

RESULT 5

AA48607
ID AA48607 standard; Peptide; 7 AA.

XX
AC AA48607;

XX
DT 20-MAR-2002 (first entry)

XX
DE Anti-inflammatory peptide SEQ ID NO 110.

XX
KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
OS Synthetic.

XX
PN WO200183554-A2.

XX
PD 08-NOV-2001.

XX
PF 02-MAY-2001; 2001WO-US14346.

XX
PR 02-MAY-2000; 2000US-201261P.

XX
PR 22-AUG-2000; 2000US-0643260.

XX
PA (PRAE-) PRAECIS PHARM INC.

XX
PA (UYVA) UNIV YALE.

XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX
DR WPI; 2002-121889/16.

XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis

XX
PS Claim 6; Page 62; 88pp; English.

XX
CC The invention relates to an antiinflammatory compound (especially
CC AA48628-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence

XX
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC antibacterial, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC cytostatic, immunosuppressive, dermatological, neuroprotective,
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IkappaB kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
| | | | |

Db 1 LDRAWL 6

RESULT 6

AA48600

ID AA48600 standard; Peptide; 8 AA.

XX
AC AA48600;

XX
DT 20-MAR-2002 (first entry)

XX
DE Anti-inflammatory peptide SEQ ID NO 103.

XX
KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX
PN WO200183554-A2.

XX
PD 08-NOV-2001.

XX
PF 02-MAY-2001; 2001WO-US14346.

XX
PR 02-MAY-2000; 2000US-201261P.

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PR 22-AUG-2000; 2000US-0643260.

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DR WPI; 2002-121889/16.

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PT psoriasis

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PS Claim 6; Page 62; 88pp; English.

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CC The invention relates to an antiinflammatory compound (especially
CC AA48628-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IkappaB kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDRAWL 6
 Db 3 LDRAWL 8
 RESULT 7
 AAM48608
 ID AAM48608 standard; Peptide; 8 AA.
 XX
 AC AAM48608;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 111.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PS Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 Claim 6; Page 62; 88pp; English.
 XX
 PS The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDRAWL 6
 Db 1 LDRAWL 6
 RESULT 8
 AAM48599
 ID AAM48599 standard; Peptide; 9 AA.
 XX
 AC AAM48599;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 102.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PS Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 Claim 6; Page 62; 88pp; English.
 XX
 PS The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 CC antibacterial, immunosuppressive, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
 Db 1 LDWAWL 6
 |||||

RESULT 9
 AAM48602
 ID AAM48602 standard; Peptide; 9 AA.
 AC AAM48602;
 XX 20-MAR-2002 (first entry)
 DT Anti-inflammatory peptide SEQ ID NO 105.
 DE
 DE
 KW Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis
 XX Claim 6; Page 62; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48525-AAM48619) fused to a NEMO binding sequence from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 CC antibacterial, immunosuppressive, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
 Db 1 LDWAWL 6
 |||||

RESULT 10
 AAM48605
 ID AAM48605 standard; Peptide; 9 AA.
 AC AAM48605;
 XX 20-MAR-2002 (first entry)
 DT Anti-inflammatory peptide SEQ ID NO 108.
 DE
 DE
 KW Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.
 XX PA Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX PS Claim 6; Page 62; 88pp; English.
 XX CC The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 LDWAWL 6
 Db 3 LDWAWL 8
 RESULT 11
 AA48606
 ID AA48606 standard; Peptide; 9 AA.
 XX AC AA48606;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 109.
 XX KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX OS Synthetic.
 XX PN WO200183554-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US14346.
 XX PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.
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 PA (UYA) UNIV YALE.
 XX May MT, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 LDWAWL 6
 Db 2 LDWAWL 7
 RESULT 12
 AA48601
 ID AA48601 standard; Peptide; 10 AA.
 XX AC AA48601;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 104.
 XX KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX OS Synthetic.
 XX PN WO200183554-A2.

XX 08-NOV-2001.
 PD
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 PF 02-MAY-2001; 2001WO-US14346.
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 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PR
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 PA (UYVA) UNIV YALE.
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 PT psoriasis
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 FS Claim 6; Page 62; 88pp; English.
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 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
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 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDNAWL 6
 Db 2 LDNAWL 7
 RESULT 13
 AAM48604
 ID AAM48604 standard; Peptide; 10 AA.
 XX
 AC AAM48604;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 107.
 DE
 XX
 XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PW
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
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 PA (UYVA) UNIV YALE.
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDNAWL 6
 Db 3 LDNAWL 8
 RESULT 14
 AAM48598
 ID AAM48598 standard; Peptide; 11 AA.
 XX
 AC AAM48598;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 101.
 DE
 XX
 XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; neurotropic;

KW anti-rheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX OS
XX PN W0200183554-A2.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US14346.
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX PR (PRAE-) PRAECIS PHARM INC.
XX PA (UYA) UNIV YALE.
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX DR Novel anti-inflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis
XX Claim 6; Page 62; 88pp; English.
XX PS The invention relates to an anti-inflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48523-AAM48619). The anti-inflammatory compounds have antiasthmatic,
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neutropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX SQ Sequence 11 AA;
Query Match 100.0%; Score 40; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDNAWL 6
| | | | |
Db 3 LDNAWL 8
RESULT 15
ID ABP30297
XX ABP30297 standard; protein; 173 AA.
AC ABP30297;

XX 02-JUL-2002 (first entry)
XX Streptococcus polypeptide SEQ ID NO 9770.
XX DE Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX group A streptococcus; Streptococcus pyogenes; antibacterial;
XX anti-inflammatory; infection; vaccine; meningitis; gene therapy.
XX OS Streptococcus agalactiae.
XX PN W0200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026333.
XX PR 24-NOV-2000; 2000GB-0028727.
XX PR 07-MAR-2001; 2001GB-0005640.
XX (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
XX Tettelin H;
XX WPI; 2002-352536/38.
XX DR N-PSDB; ABN70928.
XX PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX Claim 1; Page 4104; 4525pp; English.
XX PS The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX SQ Sequence 173 AA;
Query Match 100.0%; Score 40; DB 23; Length 173;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDNAWL 6
| | | | |
Db 125 LDNAWL 130
Search completed: May 30, 2003, 14:50:01
Job time : 19.7529 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.4	98	1 YDAS_ECOLI	P7063 escherichia
2	33	91.7	330	1 YETK_BACSU	O31540 bacillus su
3	32	88.9	265	1 FADI_SCHPO	O74841 schizosacch
4	32	88.9	445	1 YKAB_BACFI	P30268 bacillus fi
5	32	88.9	476	1 CLS_CLOPE	Q92nc6 clostridium
6	32	88.9	517	1 SEST_CAEEL	Q9n4d6 caenorhabdi
7	32	88.9	707	1 ORC1_SCHPO	P54789 schizosacch
8	32	88.9	734	1 GYSL_RABIT	P13834 oryctolagus
9	32	88.9	737	1 GYSL_HUMAN	P13807 homo sapien
10	32	88.9	737	1 GYSL_MOUSE	P54859 mus musculus
11	32	88.9	738	1 GYSL_MOUSE	Q92ie4 mus musculus
12	32	88.9	2245	1 MYSU_DICDI	P54697 dictyostelli
13	31	86.1	223	1 RM49_CAEEL	Q21939 caenorhabdi
14	31	86.1	385	1 O46A_DROME	P81919 drosophila
15	31	86.1	506	1 PORB_SCHPO	Q09855 schizosacch
16	31	86.1	703	1 GYS2_HUMAN	P54840 homo sapien
17	31	86.1	703	1 GYS2_RAT	P17625 rattus norv
18	31	86.1	745	1 IKKA_HUMAN	O15111 h inhibitor
19	31	86.1	745	1 IKKA_MOUSE	Q60680 m inhibitor
20	31	86.1	756	1 IKKB_HUMAN	O14920 homo sapien
21	31	86.1	757	1 IKKB_MOUSE	O88351 mus musculus
22	31	86.1	757	1 IKKB_RAT	Q9q78 rattus norv
23	31	86.1	758	1 VKGC_BOVIN	Q07175 bos taurus
24	31	86.1	758	1 VKGC_HUMAN	P38435 homo sapien
25	31	86.1	758	1 VKGC_RAT	O88496 rattus norv
26	30	83.3	97	1 FIXX_RHISN	O53207 rhizobium s
27	30	83.3	121	1 YCF2_VICFA	P15821 vicia faba
28	30	83.3	266	1 UPK_FUSNN	Q8ria6 fusobacteri
29	30	83.3	364	1 KITH_ILTVT	P23983 infectious
30	30	83.3	366	1 ALF_NEUCR	P53444 neurospora
31	30	83.3	417	1 CPB2_HUMAN	P48052 homo sapien
32	30	83.3	419	1 CBPA_BOVIN	P00730 bos taurus
33	30	83.3	446	1 PIV2_ADE40	P48752 human adeno

34	30	83.3	452	1	PIV2_ADE12	P12540 human adeno
35	30	83.3	488	1	ARI2_CAEEL	Q22431 caenorhabdi
36	30	83.3	492	1	ARI2_MOUSE	Q921k6 mus musculu
37	30	83.3	493	1	ARI2_HUMAN	O95376 homo sapien
38	30	83.3	509	1	ARI2_DROME	O76924 drosophila
39	30	83.3	528	1	YC79_MYCTU	Q11038 mycobacteri
40	30	83.3	675	1	CPAA_BACTJ	O87906 bacillus th
41	30	83.3	691	1	TOK1_YEAST	P40310 saccharomyc
42	30	83.3	1179	1	ATX1_ARATH	Q91t02 arabidopsis
43	29	80.6	103	1	Y131_METJA	Q57595 methanococc
44	29	80.6	116	1	CAN3_BOVIN	P51186 bos taurus
45	29	80.6	309	1	CBPC_RAT	P21961 rattus norv

ALIGNMENTS

RESULT 1
YDAS_ECOLI STANDARD; PRT; 98 AA.
AC P76063;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydaS precursor.
GN YDAS OR B1357.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).

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CC EMBL; AE000233; AAC74439.1; -
DR EcoGene; EG13361; ydaS.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 98 HYPOTHETICAL PROTEIN YDAS.
SQ SEQUENCE 98 AA; 10975 MW; 397F00BA459F3BC4 CRC64;

Query Match 94.4%; Score 34; DB 1; Length 98;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
Db 67 IDMSYL 72

RESULT 2
YETK_BACSU STANDARD; PRT; 330 AA.
AC O31540;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical transport protein yetK.


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RESULT 4
ID YKAB_BACFI STANDARD; PRT; 445 AA.
AC P30268;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE Probable aminotransferase in kata 3'/region (EC 2.6.-.-) (ORF B).
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1399;
RN [1]
SEQUENCE FROM N.A.
RA Quirk P.G., Krulwich T.A.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; L02548; AAA22560.1; -
CC DR PIR; S27492; S27492.
CC DR HSSP; P12995; 1QJ3.
CC DR InterPro; IPR000954; Aminotran_3.
CC DR Pfam; PF00202; aminotran_3; 1.
CC DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
CC DR Hypothetical protein; Amino transferase; Transferase;
CC KW Pyridoxal phosphate.
CC FT BINDING 280 280 PYRIDOXAL PHOSPHATE (POTENTIAL).
CC SQ SEQUENCE 445 AA; 48849 MW; 5C921199BC3E24BC CRC64;

Query Match 88.9%; Score 32; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
Db [1111]
4 DWSYL 8

RESULT 5
CLS_CLOPE
ID CLS_CLOPE STANDARD; PRT; 476 AA.
AC Q9ZNC6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardiolipin synthetase (EC 2.7.8.-) (Cardiolipin synthase) (CL
DE synthase).
GN CLS OR CLSD OR CPE1430.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN-NCTC 8237;
RX MEDLINE=20049836; PubMed=10585141;
RA Koyama M., Katayama S., Kaji M., Taniguchi Y., Matsushita O.,
RA Minami J., Morita S., Okabe A.;
RT "A Clostridium perfringens hem gene cluster contains a cysg(B)
RL homologue that is involved in cobalamin biosynthesis.";
RL Microbiol. Immunol. 43:947-957(1999).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN-13 / Type A;
RX PubMed=11792842;
RA Shiba T., Ogasawara N., Hattori M., Kubara S., Hayashi H.;
RA Shiba T., Ogasawara N., Hattori M., Kubara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
CC from one phosphatidylglycerol molecule to another to form
CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol -
CC diphosphatidylglycerol + glycerol.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY. CARDIOLIPIN
CC SYNTHASE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 PLD PHOSPHODIESTERASE DOMAINS.
CC -----
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CC -----
CC EMBL; AB017186; BAA74786.1; -
CC DR EMBL; AP003190; BAB81136.1; -
CC DR InterPro; IPR001736; PLD.
CC DR Pfam; PF00614; PLDC; 2.
CC DR SMART; SM00155; PLDC; 2.
CC DR PROSITE; PSS0035; PLD; 2.
CC KW Transferase; Phospholipid biosynthesis; Transmembrane;
CC FT Repeat; Complete proteome.
CC FT TRANSMEM 2 22 POTENTIAL.
CC FT TRANSMEM 31 51 POTENTIAL.
CC FT DOMAIN 207 234 PLD PHOSPHODIESTERASE 1.
CC FT DOMAIN 389 416 PLD PHOSPHODIESTERASE 2.
CC FT ACT_SITE 212 212 POTENTIAL.
CC FT ACT_SITE 394 394 POTENTIAL.
CC FT CONFLICT 469 469 T -> I. (IN REF. 1).
CC SQ SEQUENCE 476 AA; 55040 MW; 8EC32FC113F0A9CB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
Db [1111]
265 LDWSY 269

RESULT 6
SEST_CAEL
ID SEST_CAEL STANDARD; PRT; 517 AA.
AC Q9N4D6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative sestrin.
GN Y74C9A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN-Bristol N2;
RA Du H., Wohlmann P., Ames M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
CONCEPTUAL TRANSLATION.

```

RA Axelsen K., Balroch A.;
 RL Unpublished observations (MAR-2001).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SESTRIN FAMILY.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS AT SEVERAL POSITIONS FROM THAT
 CC SHOWN DUE TO DIFFERENCES IN THE PREDICTION OF SPLICE SITES.
 CC
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 CC -----

DR EMBL; AC024206; AAF36051.1; ALT_SEQ.
 DR WormPep; Y74C9A.5; CE24563.
 KW Hypothetical protein; Nuclear protein.
 SQ SEQUENCE 517 AA; 60881 MW; D7BC041916D0E205 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 517;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 DB 156 IDWSYM 161

RESULT 7

ORCL1_SCHPO STANDARD; PRT; 707 AA.
 ID ORCL1_SCHPO
 AC P54789;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Origin recognition complex subunit 1.
 GN ORCL1 OR ORP1 OR SPBC29A10.15.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCBI TaxID:4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96099401; PubMed-7502077;
 RA Gavin K.A., Hidak M., Stillman B.D.;
 RT "Conserved initiator proteins in eukaryotes.";
 RL Science 270:1667-1671(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-96109289; PubMed-8618924;
 RA Muzi-Falconi M., Kelly T.J.;
 RT "Orp1, a member of the Cdc18/Cdc6 family of S-phase regulators, is
 RT homologous to a component of the origin recognition complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:12475-12479(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT The genome sequence of Schizosaccharomyces pombe.;
 RL Nature 415:871-880(2002).
 RN [4]
 RP SUBUNIT.
 RX MEDLINE-20006240; PubMed-10535928;
 RA Moon K.Y., Kong D., Lee J.K., Raychaudhuri S., Hurwitz J.;
 RT "Identification and reconstitution of the origin recognition complex
 RT from Schizosaccharomyces pombe.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:12367-12372(1999).
 CC -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
 CC BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
 CC REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
 CC THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.
 CC -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY DURING THE CELL
 CC CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ORC1/CDC6/CDC18 FAMILY.
 CC -1- SIMILARITY: SOME, TO YEAST SIR3.

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DR EMBL; U40378; AAC49141.1;
 DR EMBL; U43392; AAB38247.1;
 DR EMBL; U38522; AAC49129.1;
 DR EMBL; AL034463; CAA22443.1;
 DR InterPro; IPR003593; AAA_ATPase;
 DR InterPro; IPR003959; AAA_ATPase_cent.
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR001025; BAH.
 DR Pfam; PF00004; AAA; 1.
 DR Pfam; PF01426; BAH; 1.
 DR Pfam; PF02178; AT_hook; 1.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00384; AT_hook; 1.
 DR SMART; SM00439; BAH; 1.
 KW DNA replication; Nuclear protein; DNA-binding; ATP-binding.
 FT NP_BIND 368 375 ATP (POTENTIAL).
 SQ SEQUENCE 707 AA; 80514 MW; D056018159A40A44 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSY 5
 DB 193 LDWSY 197

RESULT 8

GYS1_RABIT STANDARD; PRT; 734 AA.
 ID GYS1_RABIT
 AC P13834; O18817;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)


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CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
CC -!- PATHWAY: Glycogen biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04501; AA88046.1; -
DR EMBL; J33622; CA83916.1; -
DR EMBL; J33623; CA83916.1; JOINED.
DR EMBL; J33609; CA83916.1; JOINED.
DR EMBL; J33624; CA83916.1; JOINED.
DR EMBL; J33625; CA83916.1; JOINED.
DR EMBL; J33626; CA83916.1; JOINED.
DR EMBL; J33610; CA83916.1; JOINED.
DR EMBL; J33627; CA83916.1; JOINED.
DR EMBL; J33628; CA83916.1; JOINED.
DR EMBL; J33629; CA83916.1; JOINED.
DR EMBL; J33630; CA83916.1; JOINED.
DR EMBL; J33631; CA83916.1; JOINED.
DR EMBL; J33633; CA83916.1; JOINED.
DR EMBL; U32573; AA860385.1; -
DR PIR; A32156; A32156.
DR GENE; HGNC:4706; GYS1.
DR MIM; 138570; -
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Allosteric enzyme; Phosphorylation; Disease mutation;
KW Diabetes mellitus.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD_RES 8 8 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 464 464 /FTID=VAR_007859.
FT CONFLICT 136 136 T -> I (IN REF. 1 AND 3).
FT CONFLICT 462 462 MISSING (IN REF. 3).
FT CONFLICT 608 608 A -> D (IN REF. 3).
FT CONFLICT 706 706 S -> R (IN REF. 1 AND 3).
SQ SEQUENCE 737 AA; 83785 MW; 0E321BBFDEB0BD7F CRC64;

Query Match 88.9%; Score 32; DB 1; Length 737;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 596 LDWKYL 601

RESULT 10
GYS3_MOUSE STANDARD; PRT; 737 AA.
AC P54859;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogen [starch] synthase, brain (EC 2.4.1.11).
GN GYS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
CC -!- PATHWAY: Glycogen biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; J04501; AA88046.1; -
DR EMBL; J33622; CA83916.1; -
DR EMBL; J33623; CA83916.1; JOINED.
DR EMBL; J33609; CA83916.1; JOINED.
DR EMBL; J33624; CA83916.1; JOINED.
DR EMBL; J33625; CA83916.1; JOINED.
DR EMBL; J33626; CA83916.1; JOINED.
DR EMBL; J33610; CA83916.1; JOINED.
DR EMBL; J33627; CA83916.1; JOINED.
DR EMBL; J33628; CA83916.1; JOINED.
DR EMBL; J33629; CA83916.1; JOINED.
DR EMBL; J33630; CA83916.1; JOINED.
DR EMBL; J33631; CA83916.1; JOINED.
DR EMBL; J33633; CA83916.1; JOINED.
DR EMBL; U32573; AA860385.1; -
DR PIR; A32156; A32156.
DR GENE; HGNC:4706; GYS1.
DR MIM; 138570; -
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Allosteric enzyme; Phosphorylation; Disease mutation;
KW Diabetes mellitus.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD_RES 8 8 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 464 464 /FTID=VAR_007859.
FT CONFLICT 136 136 T -> I (IN REF. 1 AND 3).
FT CONFLICT 462 462 MISSING (IN REF. 3).
FT CONFLICT 608 608 A -> D (IN REF. 3).
FT CONFLICT 706 706 S -> R (IN REF. 1 AND 3).
SQ SEQUENCE 737 AA; 83785 MW; 0E321BBFDEB0BD7F CRC64;

Query Match 88.9%; Score 32; DB 1; Length 737;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 596 LDWKYL 601

RESULT 10
GYS3_MOUSE STANDARD; PRT; 737 AA.
AC P54859;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogen [starch] synthase, brain (EC 2.4.1.11).
GN GYS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ofl Albino; TISSUE=Brain;
RA MEDLINE=96385248; PubMed=8793107;
RT Pellegri G., Rossier C., Magistretti P.J., Martin J.L.;
RT "Cloning, localization and induction of mouse brain glycogen
RT synthase.";
RL Brain Res. Mol. Brain Res. 38:191-199 (1996).
CC -!- FUNCTION: TRANSFERS THE GLYCOSYL RESIDUE FROM UDPG TO THE
CC NONREDUCING END OF ALPHA-1,4-GLUCAN.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) -
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE.
CC -!- PATHWAY: Glycogen biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X94616; CAA64322.1; -
DR MGI; MGI:107378; Gys3.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Allosteric enzyme; Phosphorylation.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD_RES 8 8 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 640 640 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 644 644 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 648 648 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 652 652 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 656 656 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 697 697 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 737 AA; 83824 MW; 891A0614C8F6C085 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 737;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 595 LDWKYL 600

RESULT 11
GYS1_MOUSE STANDARD; PRT; 738 AA.
AC Q9Z1E4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogen [starch] synthase, muscle (EC 2.4.1.11).
GN GYS1 OR GYS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Seidlin M.F., Xue Z., Rochelle J.M., DeBry R., Surwit R.;
RT "Mouse glycogen synthase gene.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSFERS THE GLYCOSYL RESIDUE FROM UDP-GLC TO THE
CC NONREDUCING END OF ALPHA-1,4-GLUCAN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) -

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CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE (BY SIMILARITY).
 CC -1- PATHWAY: Glycogen biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; U53218; AAD09457.1; -;
 CC MGD; MGI:101805; Gys1.
 CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
 CC KW Allosteric enzyme; Phosphorylation.
 CC FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
 CC FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 738 AA; 62C8B5D5004F1D1 CRC64;
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 CC Query Match 88.9%; Score 32; DB 1; Length 738;
 CC Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 CC Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 LDWSYL 6
 CC III I
 CC DB 596 LDWKYL 601
 CC
 CC RESULT 12
 CC MYSJ_DICDI
 CC ID MYSJ_DICDI STANDARD; PRT; 2245 AA.
 CC AC P54697;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Myosin IJ heavy chain.
 CC GN MYOJ.
 CC OS Dictyostellium discoideum (Slime mold).
 CC OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostellium.
 CC OX NCBI_TaxID=44689;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=AX3;
 CC RX MEDLINE=96215148; PubMed=8636147;
 CC RA Hammer J.A. III, Jung G.;
 CC RT "The sequence of the dictyostellium myo J heavy chain gene predicts a
 CC RT novel, dimeric, unconventional myosin with a heavy chain molecular
 CC RT mass of 258 kDa."
 CC RL J. Biol. Chem. 271:7120-7127(1996).
 CC RN [2]
 CC RP SEQUENCE OF 1-1021 FROM N.A.
 CC RX MEDLINE=97039016; PubMed=8884597;
 CC RA Peterson M.D., Urtoe A.S., Titus M.A.;
 CC RT "Dictyostellium discoideum myoJ: a member of a broadly defined myosin
 CC RT V class or a class XI unconventional myosin?";
 CC RL J. Muscle Res. Cell Motil. 17:411-424(1996).
 CC RN [3]
 CC RP SEQUENCE OF 182-298 FROM N.A.
 CC RX MEDLINE=95023928; PubMed=7937787;
 CC RA Titus M.A., Kuspa A., Loomis W.F.;
 CC RT "Discovery of myosin genes by physical mapping in Dictyostellium.";
 CC RT Proc. Natl. Acad. Sci. U.S.A. 91:9446-9450(1994).
 CC RL

CC -1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE
 CC ACTIVITY THAT IS ACTIVATED BY ACTIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 IQ DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.
 CC -----
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 CC -----
 CC EMBL; U42409; AAA85186.1; -;
 CC EMBL; L35322; AAA79858.1; -;
 CC HSP; P08799; LMND.
 CC Dictydb; DD01095; myoJ.
 CC InterPro; IPR002710; DIL.
 CC InterPro; IPR000048; IQ_region.
 CC InterPro; IPR004009; Myosin_N.
 CC InterPro; IPR001609; myosin_head.
 CC Pfam; PF00063; myosin_head; 2.
 CC Pfam; PF00612; IQ; 6.
 CC Pfam; PF01843; DIL; 1.
 CC Pfam; PF02736; Myosin_N; 1.
 CC PRINTS; PD000355; myosin_head; 2.
 CC PRODOM; PD003376; DIL; 1.
 CC SMART; SM00015; IQ; 3.
 CC SMART; SM00242; MYSc; 1.
 CC PROSITE; PSS0096; IQ; 3.
 CC KW Myosin; ATP-binding; Actin-binding; Calmodulin-binding; Repeat;
 CC KW Coiled coil.
 CC FT DOMAIN 1 809 MYOSIN HEAD-LIKE.
 CC FT DOMAIN 824 851 IQ 1.
 CC FT DOMAIN 872 901 IQ 2.
 CC FT DOMAIN 943 972 IQ 3.
 CC FT DOMAIN 973 1812 COILED COIL (POTENTIAL).
 CC FT DOMAIN 1813 2245 TAIL.
 CC FT NP_BIND 174 181 ATP (POTENTIAL).
 CC FT DOMAIN 669 749 ACTIN-BINDING.
 CC FT CONFLICT 191 191 L -> F (IN REF. 2).
 CC FT CONFLICT 284 284 A -> T (IN REF. 2).
 CC FT CONFLICT 291 291 G -> R (IN REF. 2).
 CC FT CONFLICT 332 347 NKSGCFIEGVSDEEH -> IENMFELKVVYRMKS (IN
 CC REF. 2).
 CC FT CONFLICT 550 550 N -> K (IN REF. 2).
 CC FT CONFLICT 865 866 HH -> QQ (IN REF. 2).
 CC SQ SEQUENCE 2245 AA; 258478 MW; 615E5EFID1AB45BE CRC64;
 CC
 CC Query Match 88.9%; Score 32; DB 1; Length 2245;
 CC Best Local Similarity 66.7%; Pred. No. 4.3e+02;
 CC Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 LDWSYL 6
 CC III I
 CC DB 530 IDWSYI 535
 CC
 CC RESULT 13
 CC RM49_CAEEL
 CC ID RM49_CAEEL STANDARD; PRT; 223 AA.
 CC AC Q21939;
 CC DT 15-JUL-1999 (Rel. 38, Created)
 CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Potential mitochondrial 60s ribosomal protein L49 (MRP-L49).
 CC GN R11D1.9.
 CC OS Caenorhabditis elegans.
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodirinae; Caenorhabditis.

OX NCBI_TaxID=6239;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Steward C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MRP-L49 FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 CC EMBL; 275547; CAA99906.1;
 DR WormPep; R1D1.9; CR06314.
 KW Hypothetical protein; Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 223 AA; 25862 MW; 2ABDC95C813CBA3F CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 223;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 DB 90 IDMSYV 95
 RESULT 14
 O46A_DROME STANDARD; PRT; 385 AA.
 ID P81919; Q9V5H3; Q9UGX9;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Odorant receptor 46A.
 GN OR46A OR OR46F.1 OR DOR46F.1 OR AN9 OR CG17849.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99389723; PubMed-10458908;
 RA Gao Q., Chess A.;
 RT "Identification of candidate Drosophila olfactory receptors from
 RT genomic DNA sequence."
 RL Genomics 60:31-39(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.A., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.F., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon S., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reineert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Rhue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS.
 RC STRAIN=Berkley;
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradscky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celnik S.E.,
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Rubin G.M.,
 RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP IDENTIFICATION AND TISSUE SPECIFICITY.
 RX MEDLINE-9916866; PubMed-10069338;
 CC Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
 RT "A novel family of divergent seven-transmembrane proteins: candidate
 RT odorant receptors in Drosophila.";
 RL Neuron 22:327-338(1999).
 CC
 CC -1- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
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 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF 17 OLFACTORY RECEPTOR
 CC NEURONS IN THE MAXILLARY PALP.
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 CC RECEPTORS.
 CC
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 CC
 CC EMBL; AE003830; AAF58834.2;
 CC FlyBase; FBgn0026388; Or46a.
 CC InterPro; IPR004117; 7tm_6.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF02949; 7tm_6; 1.
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 CC TRANSMEM 171 191 4 (POTENTIAL).
 CC DOMAIN 192 255 EXTRACELLULAR (POTENTIAL).

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FT DOMAIN 277 287 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 288 308 6 (POTENTIAL).
FT DOMAIN 309 354 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 355 375 7 (POTENTIAL).
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QY 1 LDWSYL 6
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AC 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
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GN POF11 OR SPAC29B6.01 OR SPAC30.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA Harrison C.L., Toda T.;
RT "Systematic genome-wide analysis of F-box protein-encoding genes in fission yeast."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgoutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC
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DR EMBL; AB061694; BAB55543.1; -
DR EMBL; AL136538; CAB66464.1; -
DR EMBL; Z66525; CAA91423.1; -
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
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DR PRODOM; PD000018; WD40; 3.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 8.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00082; WD_REPEATS_2; 6.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
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FT REPEAT 219 256 WD 1.
FT REPEAT 259 298 WD 2.
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FT REPEAT 388 426 WD 5.
FT REPEAT 427 464 WD 6.
FT REPEAT 468 505 WD 7.
SQ SEQUENCE 506 AA; 58257 MW; CEF34D4EFFBC2E10 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 178 LDWSYL 183
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Search completed: May 30, 2003, 15:49:01
Job time : 4.11842 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

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Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
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 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	36	100.0	6	9	US-09-847-946A-15
3	32	88.9	6	9	US-09-847-940B-14
4	32	88.9	6	9	US-09-847-946A-14
5	32	88.9	27	9	US-09-847-879-385
6	32	88.9	27	9	US-09-305-736-385
7	32	88.9	561	10	US-09-815-242-12101
8	32	88.9	1024	9	US-10-213-990-30
9	32	88.9	1689	9	US-10-080-943-2
10	31	86.1	6	9	US-09-847-940B-2
11	31	86.1	6	9	US-09-847-946A-2
12	31	86.1	6	9	US-09-847-946A-33
13	31	86.1	7	9	US-09-847-946A-37
14	31	86.1	8	9	US-09-847-946A-30
15	31	86.1	8	9	US-09-847-946A-38
16	31	86.1	9	9	US-09-847-946A-29
17	31	86.1	9	9	US-09-847-946A-32
18	31	86.1	9	9	US-09-847-946A-35
19	31	86.1	9	9	US-09-847-946A-36

20	31	86.1	10	9	US-09-847-946A-31	Sequence 31, Appl
21	31	86.1	10	9	US-09-847-946A-34	Sequence 34, Appl
22	31	86.1	11	9	US-09-847-946A-28	Sequence 28, Appl
23	31	86.1	11	9	US-09-847-946A-132	Sequence 132, App
24	31	86.1	11	9	US-09-847-946A-140	Sequence 140, App
25	31	86.1	13	9	US-09-847-946A-143	Sequence 143, App
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31	31	86.1	17	9	US-09-847-946A-146	Sequence 146, App
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34	31	86.1	18	9	US-09-847-946A-136	Sequence 136, App
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36	31	86.1	22	9	US-09-847-946A-134	Sequence 134, App
37	31	86.1	22	9	US-09-847-946A-137	Sequence 137, App
38	31	86.1	22	9	US-09-847-946A-138	Sequence 138, App
39	31	86.1	22	9	US-09-847-946A-139	Sequence 139, App
40	31	86.1	28	9	US-09-847-940B-18	Sequence 18, Appl
41	31	86.1	28	9	US-09-847-946A-18	Sequence 18, Appl
42	31	86.1	54	10	US-09-864-761-46492	Sequence 46492, A
43	31	86.1	222	10	US-09-771-161A-141	Sequence 141, App
44	31	86.1	745	9	US-09-844-988-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-15
; Sequence 15, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: NBD mutants

US-09-847-940B-15

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DB 1 LDWSYL 6

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; Sequence 15, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119

;; CURRENT APPLICATION NUMBER: US/09/847,946A

;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 60/201,261

;; PRIOR FILING DATE: 2000-05-02

;; PRIOR APPLICATION NUMBER: 09/643,260

;; PRIOR FILING DATE: 2000-08-22

;; NUMBER OF SEQ ID NOS: 160

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 15

;; LENGTH: 6

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

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;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15

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Best Local Similarity 100.0%; Pred. No. 3.4e+05;

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Db 1 LDWSYL 6

RESULT 3

US-09-847-940B-14

;; Sequence 14, Application US/09847940B

;; Patent No. US2002015600A1

;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J.

;; APPLICANT: Ghosh, Sankar

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;; FILE REFERENCE: PPI-117CP

;; CURRENT APPLICATION NUMBER: US/09/847,940B

;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 09/643,260

;; PRIOR FILING DATE: 2000-08-22

;; NUMBER OF SEQ ID NOS: 27

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 14

;; LENGTH: 6

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

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;; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
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Db 1 LDWSFL 6

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US-09-847-946A-14

;; Sequence 14, Application US/09847946A

;; Publication No. US2003005499A1

;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J

;; APPLICANT: Ghosh, Sankar

;; APPLICANT: Flindels, Mark A

;; APPLICANT: Phillips, Kathryn

;; APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;; FILE REFERENCE: PPI-119

;; CURRENT APPLICATION NUMBER: US/09/847,946A

;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 60/201,261

;; PRIOR FILING DATE: 2000-05-02

;; PRIOR APPLICATION NUMBER: 09/643,260

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US-09-974-879-385

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;; Publication No. US20030028003A1

;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: 125 Human Secreted Proteins

;; FILE REFERENCE: P2020P2

;; CURRENT APPLICATION NUMBER: US/09/974,879

;; CURRENT FILING DATE: 2001-10-12

;; PRIOR APPLICATION NUMBER: US 60/239,893

;; PRIOR FILING DATE: 2000-10-13

;; PRIOR APPLICATION NUMBER: US 09/818,683

;; PRIOR FILING DATE: 2001-03-28

;; PRIOR APPLICATION NUMBER: US 09/305,736

;; PRIOR FILING DATE: 1999-05-05

;; PRIOR APPLICATION NUMBER: PCT/US98/23435

;; PRIOR FILING DATE: 1998-11-04

;; PRIOR APPLICATION NUMBER: US 60/064,911

;; PRIOR FILING DATE: 1997-11-07

;; PRIOR APPLICATION NUMBER: US 60/064,912

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;; PRIOR FILING DATE: 1997-11-07

;; PRIOR APPLICATION NUMBER: US 60/064,988

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;; PRIOR FILING DATE: 1997-11-07

;; PRIOR APPLICATION NUMBER: US 60/064,908

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;; PRIOR APPLICATION NUMBER: US 60/064,984

;; PRIOR FILING DATE: 1997-11-07

;; PRIOR APPLICATION NUMBER: US 60/064,985

;; PRIOR FILING DATE: 1997-11-07

;; PRIOR APPLICATION NUMBER: US 60/066,094

;; PRIOR FILING DATE: 1997-11-17

;; PRIOR APPLICATION NUMBER: US 60/066,100

;; PRIOR FILING DATE: 1997-11-17

;; PRIOR APPLICATION NUMBER: US 60/066,089

;; PRIOR FILING DATE: 1997-11-17

;; PRIOR APPLICATION NUMBER: US 60/066,095

;; PRIOR FILING DATE: 1997-11-17

;; PRIOR APPLICATION NUMBER: US 60/066,090

;; PRIOR FILING DATE: 1997-11-17

;; NUMBER OF SEQ ID NOS: 611

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 385

;; LENGTH: 27

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-385

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Db      8 LDWSY 12

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; Sequence 385, Application US/09305736
; Publication No. US20030088078A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
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; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12101
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12101

Query Match      88.9%; Score 32; DB 10; Length 561;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSYL 6
Db      117 DWSYL 121

RESULT 8
US-10-213-990-30
; Sequence 30, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-30

Query Match      88.9%; Score 32; DB 9; Length 1024;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDWSYL 6
```

DB 693 LDWXYL 698
||| ||

RESULT 9

US-10-080-943-2
; Sequence 2, Application US/10080943
; Publication No. US20030073236A1
; GENERAL INFORMATION:
; APPLICANT: Tsai, Shih-Chong
; APPLICANT: Field, Loren J.
; TITLE OF INVENTION: P193 PROTEINS AND NUCLEIC ACIDS, AND USES THEREOF
; FILE REFERENCE: IU99-PCT
; CURRENT APPLICATION NUMBER: US/10/080,943
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/150,266
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1689
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-080-943-2

Query Match 88.9%; Score 32; DB 9; Length 1689;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
||| ||
DB 1105 DWSYL 1109

RESULT 10

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 86.1%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
||| ||
DB 1 LDWSYL 6

RESULT 11

US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar

; APPLICANT: Findels, Mark A.
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2

Query Match 86.1%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
||| ||
DB 1 LDWSYL 6

RESULT 12

US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-33

Query Match 86.1%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
||| ||
DB 1 LDWSYL 6

RESULT 13

US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathrynn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-37

Query Match 86.1%; Score 31; DB 9; Length 7;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 1 LDWSWL 6

RESULT 14

US-09-847-946A-30
Sequence 30, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathrynn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-30

Query Match 86.1%; Score 31; DB 9; Length 8;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 3 LDWSWL 8

RESULT 15

US-09-847-946A-38

Sequence 38, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathrynn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-38

Query Match 86.1%; Score 31; DB 9; Length 8;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 1 LDWSWL 6

Search completed: May 30, 2003, 15:53:21
Job time: 11.4605 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	88.9	462	4	US-09-134-001C-4300
2	32	88.9	706	1	Sequence 4300, Ap
3	32	88.9	706	1	Sequence 16, Appl
4	32	88.9	911	1	Sequence 16, Appl
5	31	86.1	745	2	Sequence 2, Appli
6	31	86.1	745	2	Sequence 3, Appli
7	31	86.1	745	2	Sequence 4, Appli
8	31	86.1	745	2	Sequence 4, Appli
9	31	86.1	745	2	Sequence 4, Appli
10	31	86.1	745	2	Sequence 4, Appli
11	31	86.1	745	4	US-09-032-476-4
12	31	86.1	745	4	US-08-890-854-4
13	31	86.1	745	4	US-09-023-324-4
14	31	86.1	745	4	US-09-168-629-2
15	31	86.1	745	4	US-08-910-820-10
16	31	86.1	745	4	US-08-810-131A-2
17	31	86.1	756	2	US-08-887-518-4
18	31	86.1	756	2	US-09-023-321-4
19	31	86.1	756	2	US-08-890-853-2
20	31	86.1	756	2	US-09-032-475-4
21	31	86.1	756	2	US-09-099-125A-2
22	31	86.1	756	2	US-09-099-124A-2
23	31	86.1	756	4	US-09-032-476-2
24	31	86.1	756	4	US-08-890-854-2
25	31	86.1	756	4	US-09-023-324-2
26	31	86.1	756	4	US-09-168-629-15
27	31	86.1	756	4	US-08-910-820-9

28	31	86.1	758	1	US-07-756-250-16	Sequence 16, Appl
29	30	83.3	122	4	US-08-936-165A-397	Sequence 397, App
30	30	83.3	363	1	US-07-681-704A-2	Sequence 2, Appli
31	30	83.3	417	4	US-08-640-906-4	Sequence 4, Appli
32	30	83.3	417	4	US-08-640-906-18	Sequence 18, Appl
33	30	83.3	417	4	US-09-395-936-4	Sequence 4, Appli
34	30	83.3	417	4	US-09-395-936-18	Sequence 18, Appl
35	30	83.3	905	4	US-09-360-186-3	Sequence 3, Appli
36	29	80.6	45	2	US-08-637-759B-236	Sequence 236, App
37	29	80.6	45	3	US-08-871-355A-236	Sequence 236, App
38	29	80.6	45	4	US-09-201-945-236	Sequence 236, App
39	29	80.6	109	1	US-08-477-270-20	Sequence 20, Appl
40	29	80.6	109	2	US-08-585-585A-1	Sequence 1, Appli
41	29	80.6	109	2	US-08-249-037C-1	Sequence 1, Appli
42	29	80.6	109	2	US-08-788-622B-1	Sequence 1, Appli
43	29	80.6	109	3	US-08-788-621B-1	Sequence 1, Appli
44	29	80.6	117	4	US-08-936-165A-347	Sequence 347, App
45	29	80.6	343	4	US-08-853-948B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-134-001C-4300
; Sequence 4300, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4300
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4300

Query Match	88.9%	Score 32;	DB 4;	Length 462;
Best Local Similarity	100.0%	Pred. No. 2.4e+02;		
Matches	5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	LDWSY 5		
Db	159	LDWSY 163		

RESULT 2
US-08-484-105-16
; Sequence 16, Application US/08484105
; Patent No. 5589341
; GENERAL INFORMATION:
; APPLICANT: STILLMAN, Bruce
; APPLICANT: BELL, Stephen P
; APPLICANT: KOBAYASHI, Ryuji
; APPLICANT: KINE, Jasper
; APPLICANT: FOSS, Margit
; APPLICANT: MCNALLY, Francis J
; APPLICANT: LAURENSEN, Patricia
; APPLICANT: HERSKOWITZ, Ira
; APPLICANT: Li, Joachim J
; APPLICANT: GAVIN, Kimberly
; TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-105-16

Query Match 88.9%; Score 32; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSY 5
DB 193 LMSY 197

RESULT 3
US-08-484-106-16
Sequence 16, Application US/08484106
Patent No. 5614618
GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: McNALLY, Francis J
APPLICANT: LAURENSEN, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-106-16

Query Match 88.9%; Score 32; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSY 5
DB 193 LMSY 197

RESULT 4
US-08-596-985-2
Sequence 2, Application US/08596985
Patent No. 5736374
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Hucul, John A.
APPLICANT: Ward, Michael
TITLE OF INVENTION: Increased Production of
TITLE OF INVENTION: Beta-galactosidase in Aspergillus oryzae
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,985
FILING DATE: 05-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,631
FILING DATE: 29-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-596-985-2

Query Match

88.9%; Score 32; DB 1; Length 911;

Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 675 LDWKYL 680

RESULT 5

US-08-887-518-3
Sequence 3, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Wu, Lin

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;

Best Local Similarity 83.3%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 6

US-09-023-321-3

Sequence 3, Application US/09023321

Patent No. 5844073

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Wu, Lin

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;

Best Local Similarity 83.3%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 7

US-08-890-853-4

Sequence 4, Application US/08890853

Patent No. 5851812

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

APPLICANT: Woronicz, John

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/890,853

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
||||:|
Db 738 LDWSWL 743

RESULT 8
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.475
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
||||:|
Db 738 LDWSWL 743

RESULT 9
US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:

APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.125A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890.853
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
||||:|
Db 738 LDWSWL 743

RESULT 10
US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.124A
FILING DATE:
CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/890,853
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
DB 738 LDWSWL 743

RESULT 11
US-09-032-476-4
;; Sequence 4, Application US/09032476
;; Patent No. 6235492
;; GENERAL INFORMATION:
;; APPLICANT: Rothe, Mike
;; APPLICANT: Cao, Zhaodan
;; APPLICANT: R gnier, Catherine
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/032,476
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION NUMBER: 08/890,854
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 86.1%; Score 31; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSYL 6
DB 738 LDWSWL 743
RESULT 12
US-08-890-854-4
;; Sequence 4, Application US/08890854
;; Patent No. 6235512
;; GENERAL INFORMATION:
;; APPLICANT: Rothe, Mike
;; APPLICANT: Cao, Zhaodan
;; APPLICANT: R gnier, Catherine
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/890,854
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 86.1%; Score 31; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSYL 6
DB 738 LDWSWL 743

RESULT 13
US-09-023-324-4
;; Sequence 4, Application US/09023324
;; Patent No. 6235513
;; GENERAL INFORMATION:
;; APPLICANT: Rothe, Mike
;; APPLICANT: Cao, Zhaodan
;; APPLICANT: R gnier, Catherine
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/990,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 86.1%; Score 31; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 14
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 86.1%; Score 31; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 15
US-08-910-820-10
Sequence 10, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gian
APPLICANT: Murray, Brion W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 86.1%; Score 31; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 738 LDWSWL 743

Search completed: May 30, 2003, 14:41:31
Job time : 6.03947 secs

Result	Query No.	Score	Query		Length	DB	ID	Description
			Match	%				
1	36	100.0	6	23	ABB08737	Mutated IKKbeta NE		
2	36	100.0	6	23	AA048520	NBD mutant peptide		
3	36	100.0	756	23	ABB77301	Human IKKbeta muta		
4	34	94.4	98	22	AAG98962	E. coli growth and		
5	33	91.7	193	22	AAU04899	Micromonospora eve		
6	32	88.9	6	23	ABB08736	Mutated IKKbeta NE		
7	32	88.9	6	23	AA048519	NBD mutant peptide		
8	32	88.9	320	22	ABG13516	Novel human diagno		
9	32	88.9	320	22	ABG27654	Novel human diagno		
10	32	88.9	393	19	AA011025	H. pylori ORF 02qe		

AC ABB77301;
XX 14-JUN-2002 (first entry)
DT Human IKKbeta mutant W741Y.
DE
XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasclerotic; anti-allergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antitumor; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 741 /note= "Wildtype Trp substituted by Tyr"
FT
PN WO200183547-A2.
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US40654.
XX
XX 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S;
XX WPI: 2002-179350/23.
XX
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT Inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain
XX
XX Example 11; Page -: 82pp; English.
XX
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of I-kappaB. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC

CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of an IKKbeta
CC mutant, useful in examples of the invention.
CC Note: The present sequence is not given in the specification but is
CC derived from GenBank Accession No. O14920 (ABB77294).
XX
SQ Sequence 756 AA;
Query Match 100.0%; Score 36; DB 23; Length 756;
Best Local Similarity 100.0%; Pred. No. 26+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDWSYL 6
DB 737 LDWSYL 742
RESULT 4
AAG98962
ID AAG98962 standard; Protein; 98 AA.
XX
AC AAG98962;
XX
XX 26-SEP-2001 (first entry)
DT
DE E. coli growth and proliferation related protein sequence SEQ ID NO:432.
XX
XX Escherichia coli; growth; proliferation; microbial; antimicrobial;
KW bacterial infection; microorganism.
XX
XX Escherichia coli.
XX WO200134810-A2.
XX
PD 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US30950.
PF
XX 09-NOV-1999; 99US-0164415.
PR
XX (ELIT-) ELITRA PHARM INC.
XX
XX Forsyth RA, Ohlsen K, Zyskind J;
XX WPI: 2001-335933/35.
DR N-PSDB; AAH84633.
XX
XX Novel nucleic acids that inhibit Escherichia coli proliferation, useful
PT for screening for homologous genes and for designing expression vectors
PT
XX Claim 19; Page 490-491; 522pp; English.
PS
XX
XX AAH84373 to AAH84499 represent Escherichia coli growth and proliferation
CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli
CC growth and proliferation related proteins given in AAG99078 and AAG98830
CC to AAG98999. (I) can be used as potential targets for the generation of
CC new antimicrobial agents, and for identification of compounds which
CC interact with the gene products of (I). In addition the expression of
CC (I) and the purification of the proteins, the purified proteins can be
CC used to generate reagents and screen small molecule libraries or other
CC candidate compound libraries for compounds that can be further developed
CC to yield novel antimicrobial compounds. In addition, nucleic acid probes
CC complementary to (I) that are specific for particular species of
CC microorganisms can be used to identify particular microorganism species
CC in clinical specimens, therefore, providing a rapid and dependable
CC method by which to identify the causative agents of a bacterial
CC infection. Also, antibodies generated against proteins translated from
CC mRNA transcribed from proliferation-required sequences can also be used
CC

CC to screen for specific microorganisms that produce such proteins in a
 CC species-specific manner. AAH84371 and AAH84670 represent sequencing
 CC primers used in the isolation of *E. coli* growth and proliferation
 CC related sequence, which are used in an example from the present
 CC invention.

XX SQ Sequence 98 AA;

Query Match 94.4%; Score 34; DB 22; Length 98;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSYL 6
 :|||||
 Db 67 IDWSYL 72

RESULT 5

AAU04899
 ID AAU04899 standard; Protein; 193 AA.

XX AC

AAU04899;

DT 26-SEP-2001 (first entry)

XX Micromonospora everninomicin biosynthetic enzyme evrMR2.

DE Everninomicin; antibiotic; bottle-neck gene; orthomycin;
 KW fermentation; resistance mechanism gene; evrMR2.

XX Micromonospora carbonacea var. africana.

OS WO200151639-A2.

PN 19-JUL-2001.

PD 12-JAN-2001; 2001WO-US01187.

PF 12-JAN-2000; 2000US-0175751.

PR (SCHE) SCHERING CORP.

PA Hosted TJ, Horan AC, Wang TX;

PI WPI; 2001-442147/47.

XX N-PSDB; AAS08693.

PT New nucleic acid molecules encoding everninomicin pathway gene
 PT products, useful for improving yields of everninomicin, to produce new
 PT everninomicin and as probes to identify homologous sequences -

XX Claim 19; Fig 11; 109pp; English.

XX The sequence is a protein, evrMR2, encoded by a resistance mechanism
 CC gene. The protein comprises one of 98 enzymes of the
 CC everninomicin antibiotic biosynthetic pathway. A vector comprising a
 CC M. carbonacea everninomicin biosynthetic pathway resistance gene
 CC product is useful for selecting for a transfected or transformed host
 CC cell. An integrative version of the vector is useful for introducing a
 CC everninomicin pathway gene (a bottle-neck gene) into an actinomycete of
 CC the genus Micromonospora. The DNA encoding the biosynthetic proteins is
 CC useful for synthesising novel everninomicin-related compounds, arising
 CC from modifications of the DNA sequence designed to change glycosyl and
 CC modified ornithine acid groups contained in everninomicin, for
 CC expressing functional or mutant everninomicin biosynthetic enzyme for
 CC evaluation, diagnosis and preferably biosynthesis of everninomicin or
 CC other secondary metabolic products, improving the yield of everninomicin
 CC and to produce novel everninomicins and also as a hybridisation probe to
 CC identify homologous sequences. The encoded polypeptides are useful for
 CC combinatorial biosynthesis to generate libraries of orthomycins, e.g.
 CC everninomicin analogues/homologues and drug discovery. The
 CC DNA encoding the integrase allows for increasing a given gene dosage. The
 CC integrative vector can be used to permanently integrate copies of a

CC heterologous gene of choice into chromosomes of different hosts and to
 CC integrate genes which increase the yield of known products or to generate
 CC novel products such as hybrid antibiotics or other novel secondary
 CC metabolites. The vector can also be used to integrate antibiotic
 CC resistance genes in order to carry out bioconversions with compounds to
 CC which the strain is normally sensitive and is thus useful in fermentation
 CC processes involving e.g. Streptomyces antibioticus.

XX SQ Sequence 193 AA;

Query Match 91.7%; Score 33; DB 22; Length 193;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSYL 6
 :|||||

Db 139 LDWAYL 144

RESULT 6

ABB08736

ID ABB08736 standard; peptide; 6 AA.

XX AC ABB08736;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.

OS Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note= "Wildtype Trp substituted by Phe"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (UYUA) UNIV YALE.

XX May WJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain

XX Claim 23; Page 45; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of

CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.

Sequence 6 AA;

Query Match 88.9%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 |||||
 Db 1 LDWSFL 6

RESULT 7

AA48519
 ID AAM48519 standard; Peptide; 6 AA.
 AC AAM48519;

20-MAR-2002 (first entry)

NBD mutant peptide SEQ ID NO 14.

Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 antiarthritis; antiarthritic; osteopathic; antibacterial; virucide;
 immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 cytokine; NFkappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 autoimmune disorder; multiple sclerosis; transplant rejection;
 osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 ataxia telangiectasia; allergy; anaphylaxis; arthritis.

Synthetic.

WO200183554-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US14346.

02-MAY-2000; 2000US-201261P.

22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRACIS PHARM INC.
 PA (UYA) UNIV YALE.

May MJ, Ghosh S, Findeis MA, Phillips K;

WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation
 domain fused to NEMO binding sequence, useful for blocking nuclear
 factor kappaB activation, and for treating asthma, lung inflammation,
 psoriasis

Example 6; Page 48; 88pp; English.

The invention relates to an antiinflammatory compound (especially
 AAM48628-AAM48645), comprising a membrane translocation domain
 AAM48620-AAM48627 or AAM48646-AAM48651, which comprises from 6-15
 amino acid residues, fused to a NEMO binding sequence
 (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 cytostatic, antipsoriatic, antiinflammatory, antiarthritic, osteopathic,
 antibacterial, immunosuppressive, dermatological, neuroprotective,
 neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
 compounds act as selective inhibitors of cytokine-mediated NFkappaB
 activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 the NEMO binding domain that results in inhibition of IKKbeta kinase
 activation and subsequent decreased phosphorylation of IkkappaB. The
 compounds are useful for treating inflammatory disorders, e.g. asthma,
 lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 granulomatosis, multiple sclerosis; transplant rejection; and ataxia
 Alzheimer's disease; atherosclerosis; viral infections; and osteo
 telangiectasia. The compounds are also useful for treating
 pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 arthritis.

Sequence 6 AA;

Query Match 88.9%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 |||||
 Db 1 LDWSFL 6

RESULT 8

ABG13516
 ID ABG13516 standard; Protein; 320 AA.

AC ABG13516;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #13507.

Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS77703.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 43875; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 320 AA;
 SQ
 Query Match 88.9%; Score 32; DB 22; Length 320;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 DWSYL 6
 |||||
 Db 240 DWSYL 244
 RESULT 9
 ABG27654
 ID ABG27654 standard; Protein; 320 AA.
 XX AC ABG27654;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #27645.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.
 DR N-PSDB; AAS91841.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 58013; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 320 AA;
 SQ
 Query Match 88.9%; Score 32; DB 22; Length 320;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 DWSYL 6
 |||||
 Db 240 DWSYL 244
 RESULT 10
 AAY11025
 ID AAY11025 standard; Protein; 393 AA.
 XX AC AAY11025;
 XX DT 08-JUN-1999 (first entry)
 XX DE H. pylori ORF 02ge41622_14875000_c2_65 outer membrane protein.
 XX Vaccine; probe; diagnostic; ORF; cell envelope protein;
 KW secreted protein; cytoplasmic protein; cellular protein.
 XX OS Helicobacter pylori.
 XX PN WO9824475-A1.
 XX PD 11-JUN-1998.
 XX PF 05-DEC-1997; 97WO-US22104.
 XX PR 14-JUL-1997; 97US-0891928.
 XX PR 05-DEC-1996; 96US-0759625.
 XX PR 25-MAR-1997; 97US-0823745.
 XX PA (ASTR) ASTRA AB.
 XX PI Alm RA, Castriotta LM, Doig PC, Kabok Z, Smith D;

DR WPI; 1998-333051/29.
 XX N-PSDB; AAX30534.
 PT New isolated Helicobacter pylori nucleic acids - used to develop
 PT products for the diagnosis, prevention and treatment of infection by
 PT H. pylori and other Helicobacter species
 XX
 PS Claims 37, 41; Page 187-188; 339pp; English.
 XX
 CC Recombinant or substantially pure preparations of H. pylori polypeptides
 CC are disclosed, together with the nucleic acids encoding them. In all,
 CC 97 ORFs are shown. The proteins are variously cell envelope proteins,
 CC cytoplasmic proteins, secreted proteins or other cellular proteins.
 CC Vaccines containing the nucleic acids or proteins are claimed, as are
 CC probes containing at least 8 nucleotides from the nucleic acid
 CC sequences. The vaccines are useful for treating or reducing the risk of
 CC H. pylori infections, and the probes can be used diagnostically for
 CC detecting the presence of Helicobacter in a sample. The products are
 CC also of use in screening for compounds having the ability to interfere
 CC with the H. pylori life cycle or to inhibit H. pylori infection.
 XX
 SQ Sequence 393 AA;
 Query Match 88.9%; Score 32; DB 19; Length 393;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSYL 6
 Db 284 DWSYL 288
 |||||
 RESULT 11
 AAU76667
 ID AAU76667 standard; Protein; 393 AA.
 AC AAU76667;
 XX
 DT 21-MAY-2002 (first entry)
 DE Helicobacter pylori LPS biosynthesis enzyme HP1031 from strain J99.
 XX
 DE LPS; lipopolysaccharide; biosynthesis enzyme; HP1031; strain J99;
 KW antibiotic; vaccine; human self epitope.
 KW
 XX Helicobacter pylori.
 OS
 XX WO200207763-A2.
 PN
 XX
 PD 31-JAN-2002.
 XX
 PF 12-JUL-2001; 2001WO-IB01536.
 XX
 PR 12-JUL-2000; 2000GB-0017149.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Del Giudice G, Rappuoli R;
 XX
 DR WPI; 2002-217026/27.
 XX
 XX Novel Helicobacter pylori useful for prophylaxis and treatment of
 PT Helicobacter pylori infection, comprises mutation that prevents
 PT synthesis of auto-reactive lipopolysaccharide -
 XX
 PS Disclosure; Fig 1; 23pp; English.
 XX
 CC The present invention relates to a new Helicobacter pylori bacterium
 CC having a mutation that affects lipopolysaccharide (LPS) biosynthesis,
 CC where either LPS is not expressed or LPS which is expressed does not
 CC induce antibodies which cross-react with human self epitopes. The
 CC invention is useful for treating or preventing, and in the manufacture
 CC of a vaccine for treatment or prophylaxis of Helicobacter pylori

CC Infection. The vaccine does not induce antibodies which cross-react
 CC with human self epitopes. The present amino acid sequence represents
 CC the Helicobacter pylori LPS biosynthesis enzyme HP1031 that was
 CC isolated from strain J99 and was used in the methods of the invention.
 XX
 SQ Sequence 393 AA;
 Query Match 88.9%; Score 32; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSYL 6
 Db 284 DWSYL 288
 |||||
 RESULT 12
 AAG82777
 ID AAG82777 standard; Protein; 455 AA.
 XX
 AC AAG82777;
 XX
 DT 03-SEP-2001 (first entry)
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:2648.
 XX
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW vaccination; endocarditis.
 XX
 OS Staphylococcus epidermidis.
 XX
 PN WO200134809-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 09-NOV-2000; 2000WO-US30782.
 XX
 PR 09-NOV-1999; 99US-0164258.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Kimmery WJ;
 XX
 DR WPI; 2001-316495/33.
 DR N-PSDB; AAH53627.
 XX
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 PT
 PS Claim 18; Page 694-695; 2188pp; English.
 XX
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX
 SQ Sequence 455 AA;

Query Match 88.9%; Score 32; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
 Db 152 LDWSY 156
 |||||

RESULT 13
 ABP39455
 ID ABP39455 standard; Protein; 462 AA.
 XX
 AC ABP39455;
 XX
 DT 24-JUL-2002 (first entry)
 XX
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4300.
 XX
 KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 XX
 KW antibacterial; gene therapy.
 XX
 OS Staphylococcus epidermidis.
 XX
 PN US6380370-B1.
 XX
 PD 30-APR-2002.
 XX
 PF 13-AUG-1998; 98US-0134001.
 XX
 PR 14-AUG-1997; 97US-055779P.
 XX
 PR 08-NOV-1997; 97US-064964P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Doucette-Stamm LA, Bush D;
 XX
 DR WPI: 2002-381255/41.
 XX
 DR N-PSDB; ABN92000.
 XX
 PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
 PT polypeptide, useful for diagnosing and treating bacterial infections -
 XX
 PS Disclosure; SEQ ID 4300; 267pp; English.
 XX
 CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences
 CC can also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life
 CC cycle or inhibit S. epidermidis infection.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.
 XX
 SQ Sequence 462 AA;

Query Match 88.9%; Score 32; DB 23; Length 462;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
 Db 159 LDWSY 163
 |||||

RESULT 14
 ABG18718
 ID ABG18718 standard; Protein; 465 AA.
 XX

AC ABG18718;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #18709.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 XX
 DR N-PSDB; AAS82905.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 49077; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 465 AA;

Query Match 88.9%; Score 32; DB 22; Length 465;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
 Db 336 DWSYL 340
 |||||

RESULT 15
 AAU36508
 ID AAU36508 standard; Protein; 561 AA.
 XX
 AC AAU36508;
 XX

DT 14-FEB-2002 (first entry)
 XX Pseudomonas aeruginosa cellular proliferation protein #498.
 DE
 XX Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 KW
 XX Pseudomonas aeruginosa.
 OS
 XX WO200170955-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX
 XX 21-MAR-2001; 2001WO-US09180.
 PF
 XX 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS4367.
 DR
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PT
 XX Example 3; Seq ID No 12101; 511pp; English.
 PS
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX SQ Sequence 561 AA;
 Query Match 88.9%; Score 32; DB 22; Length 561;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DWSYL 6
 Db 117 DWSYL 121

Search completed: May 30, 2003, 14:50:01
 Job time : 20.7529 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62

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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	35	100.0	6	9	US-09-847-946A-14
3	32	91.4	6	9	US-09-847-940B-15
4	32	91.4	6	9	US-09-847-946A-15
5	32	91.4	56	10	US-09-764-877-1782
6	31	88.6	124	10	US-09-925-302-460
7	31	88.6	157	9	US-09-738-626-4783
8	31	88.6	184	9	US-10-078-770-86
9	31	88.6	238	9	US-10-078-770-96
10	31	88.6	305	9	US-10-078-770-90
11	30	85.7	6	9	US-09-847-940B-2
12	30	85.7	6	9	US-09-847-946A-33
13	30	85.7	7	9	US-09-847-946A-37
14	30	85.7	8	9	US-09-847-946A-30
15	30	85.7	8	9	US-09-847-946A-38
16	30	85.7	9	9	US-09-847-946A-29
17	30	85.7	9	9	US-09-847-946A-32
18	30	85.7	9	9	US-09-847-946A-35
19	30	85.7	9	9	US-09-847-946A-35

Sequence 36, Appl
Sequence 31, Appl
Sequence 34, Appl
Sequence 28, Appl
Sequence 132, Appl
Sequence 140, Appl
Sequence 143, Appl
Sequence 144, Appl
Sequence 145, Appl
Sequence 148, Appl
Sequence 141, Appl
Sequence 142, Appl
Sequence 146, Appl
Sequence 147, Appl
Sequence 131, Appl
Sequence 135, Appl
Sequence 136, Appl
Sequence 133, Appl
Sequence 134, Appl
Sequence 137, Appl
Sequence 138, Appl
Sequence 139, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 37, Appl
Sequence 30, Appl
Sequence 141, Appl

9 US-09-847-946A-36
10 US-09-847-946A-31
10 US-09-847-946A-34
11 US-09-847-946A-28
11 US-09-847-946A-132
11 US-09-847-946A-140
13 US-09-847-946A-143
13 US-09-847-946A-144
13 US-09-847-946A-145
13 US-09-847-946A-148
17 US-09-847-946A-141
17 US-09-847-946A-142
17 US-09-847-946A-146
17 US-09-847-946A-147
18 US-09-847-946A-131
18 US-09-847-946A-135
18 US-09-847-946A-136
22 US-09-847-946A-133
22 US-09-847-946A-134
22 US-09-847-946A-137
22 US-09-847-946A-138
22 US-09-847-946A-139
28 US-09-847-940B-18
28 US-09-847-946A-18
222 US-09-986-480-330
222 US-09-771-161A-141

ALIGNMENTS

RESULT 1

US-09-847-940B-14
; Sequence 14, Application US/09847940B
; Patent No. US20020156000A1

GENERAL INFORMATION:
; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sankar

; FILE REFERENCE: PPI-117CP

; CURRENT APPLICATION NUMBER: US/09/847,940B

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants

US-09-847-940B-14

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

Db 1 LDWSFL 6

RESULT 2

US-09-847-946A-14
; Sequence 14, Application US/09847946A
; Publication No. US20030054999A1

GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119

;; CURRENT APPLICATION NUMBER: US/09/847,946A

;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 60/201,261

;; PRIOR FILING DATE: 2000-05-02

;; PRIOR APPLICATION NUMBER: 09/643,260

;; PRIOR FILING DATE: 2000-08-22

;; NUMBER OF SEQ ID NOS: 160

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 14

;; LENGTH: 6

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-14

Query Match 100.0%; Score 35; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

Db 1 LDWSFL 6

RESULT 3

US-09-847-940B-15

;; Sequence 15, Application US/09847940B

;; Patent No. US20020156000A1

;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J.

;; APPLICANT: Ghosh, Sankar

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;; FILE REFERENCE: PPI-117CP

;; CURRENT APPLICATION NUMBER: US/09/847,940B

;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 09/643,260

;; PRIOR FILING DATE: 2000-08-22

;; NUMBER OF SEQ ID NOS: 27

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 15

;; LENGTH: 6

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants

US-09-847-940B-15

Query Match 91.4%; Score 32; DB 9; Length 6;

Best Local Similarity 83.3%; Pred. No. 3.4e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

Db 1 LDWSYL 6

RESULT 4

US-09-847-946A-15

;; Sequence 15, Application US/09847946A

;; Publication No. US20030054999A1

;; GENERAL INFORMATION:

;; APPLICANT: May, Michael J

;; APPLICANT: Ghosh, Sankar

;; APPLICANT: Findels, Mark A

;; APPLICANT: Phillips, Kathryn

;; APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;; FILE REFERENCE: PPI-119

;; CURRENT APPLICATION NUMBER: US/09/847,946A

;; CURRENT FILING DATE: 2001-05-02

;; PRIOR APPLICATION NUMBER: 60/201,261

;; PRIOR FILING DATE: 2000-05-02

;; PRIOR APPLICATION NUMBER: 09/643,260

;; PRIOR FILING DATE: 2000-08-22

;; NUMBER OF SEQ ID NOS: 160

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 15

;; LENGTH: 6

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-15

Query Match 91.4%; Score 32; DB 9; Length 6;

Best Local Similarity 83.3%; Pred. No. 3.4e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

Db 1 LDWSYL 6

RESULT 5

US-09-764-877-1782

;; Sequence 1782, Application US/09764877

;; Patent No. US20020147140A1

;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

;; FILE REFERENCE: PC005

;; CURRENT APPLICATION NUMBER: US/09/764,877

;; CURRENT FILING DATE: 2001-01-17

;; Prior application data removed - refer to PALM or file wrapper

;; NUMBER OF SEQ ID NOS: 4031

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 1782

;; LENGTH: 56

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: SITE

;; LOCATION: (51)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

;; NAME/KEY: SITE

;; LOCATION: (56)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-877-1782

Query Match 91.4%; Score 32; DB 10; Length 56;

Best Local Similarity 83.3%; Pred. No. 59;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

Db 27 LDWNFL 32

RESULT 6

US-09-925-302-460

;; Sequence 460, Application US/09925302

;; Patent No. US20020044941A1

;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

;; FILE REFERENCE: PA104

;; CURRENT APPLICATION NUMBER: US/09/925,302

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: PCT/US00/05918

;; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270

;; PRIOR FILING DATE: 1999-03-12

;; NUMBER OF SEQ ID NOS: 896

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-302-460

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Query Match 88.6%; Score 31; DB 10; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSLF 6
 Db 50 DWSLF 54

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RESULT 7
US-09-738-626-4783
; Sequence 4783, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4783
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-4783

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Query Match 88.6%; Score 31; DB 9; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
 Db 72 LDWSF 76

RESULT 8
 US-10-078-770-86

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; Sequence 86, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 86
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (98)
; NAME/KEY: UNSURE
; LOCATION: (104)..(105)
; NAME/KEY: UNSURE
; LOCATION: (115)
; NAME/KEY: UNSURE
; LOCATION: (117)
; NAME/KEY: UNSURE
; LOCATION: (123)
; NAME/KEY: UNSURE
; LOCATION: (126)..(127)
; NAME/KEY: UNSURE
; LOCATION: (136)
; NAME/KEY: UNSURE
; LOCATION: (159)
; NAME/KEY: UNSURE
; LOCATION: (174)..(175)
; US-10-078-770-86

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Query Match 88.6%; Score 31; DB 9; Length 184;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
 Db 18 LDWSF 22

```

RESULT 9
US-10-078-770-96
; Sequence 96, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770

```

;; CURRENT FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 09/614,188
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 96
;; LENGTH: 238
;; TYPE: PRT
;; ORGANISM: Zea mays
US-10-078-770-96

Query Match 88.6%; Score 31; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
| | | | |
DB 26 LDWSF 30

RESULT 10
US-10-078-770-90
;; Sequence 90, Application US/10078770
;; Publication No. US20030003471A1
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Forge, Charlie
;; APPLICANT: Miao, Guo-Hua
;; TITLE OF INVENTION: cDNAs Encoding Polypeptides
;; FILE REFERENCE: BB-1365 US NA
;; CURRENT APPLICATION NUMBER: US/10/078,770
;; CURRENT FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 09/614,188
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 90
;; LENGTH: 305
;; TYPE: PRT
;; ORGANISM: Triticum aestivum
US-10-078-770-90

Query Match 88.6%; Score 31; DB 9; Length 305;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
| | | | |
DB 93 LDWSF 97

RESULT 11
US-09-847-940B-2
;; Sequence 2, Application US/09847940B
;; Patent No. US20020156000A1
;; GENERAL INFORMATION:
;; APPLICANT: May, Michael J.
;; APPLICANT: Ghosh, Sankar
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-117CP
;; CURRENT APPLICATION NUMBER: US/09/847,940B
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 85.7%; Score 30; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
DB 1 LDWSWL 6

RESULT 12
US-09-847-946A-2
;; Sequence 2, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:
;; APPLICANT: May, Michael J
;; APPLICANT: Ghosh, Sankar
;; APPLICANT: Findels, Mark A
;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Hannig, Gerhard
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2

Query Match 85.7%; Score 30; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
DB 1 LDWSWL 6

RESULT 13

US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-33

Query Match 85.7%; Score 30; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 1 LDWSWL 6

RESULT 14

US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-37

Query Match 85.7%; Score 30; DB 9; Length 7;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 1 LDWSWL 6

RESULT 15

US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-30

Query Match 85.7%; Score 30; DB 9; Length 8;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 3 LDWSWL 8

Search completed: May 30, 2003, 15:53:20
Job time : 10.4605 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs; 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	91.4	404	1 YCFD_HAEIN	P44683 haemophilus
2	31	88.6	135	1 VAL2_CLVK	P14976 cassava lat
3	31	88.6	135	1 VAL2_CLVN	P14968 cassava lat
4	31	88.6	135	1 VAL2_TYLCV	P27262 tomato yell
5	31	88.6	204	1 HIS2_YERPE	Q82fy1 yersinia pe
6	31	88.6	240	1 LECS_VATMA	P81371 vatairea ma
7	31	88.6	355	1 CXA5_RAT	P28234 rattus norv
8	31	88.6	356	1 CXA5_CANFA	P33725 canis famil
9	31	88.6	357	1 CXA5_HUMAN	P36382 homo sapien
10	31	88.6	357	1 CXA5_MOUSE	Q01231 mus musculu
11	31	88.6	368	1 CXA5_CHICK	P18860 gallus gall
12	31	88.6	382	1 LYS1_CANAL	P43065 candida alb
13	31	88.6	383	1 P2C4_SCHPO	O14156 schizosacch
14	31	88.6	399	1 CXA8_CHICK	P36381 gallus gall
15	31	88.6	400	1 NUCM_PROVI	Q37619 prototheca
16	31	88.6	406	1 CXA3_BOVIN	P41987 bos taurus
17	31	88.6	415	1 CXA3_RAT	P29414 rattus norv
18	31	88.6	416	1 CXA3_MOUSE	Q64448 mus musculu
19	31	88.6	432	1 CXA8_HUMAN	P48165 homo sapien
20	31	88.6	434	1 CXA3_HUMAN	Q9y6h8 homo sapien
21	31	88.6	439	1 CXA8_MOUSE	P28236 mus musculu
22	31	88.6	439	1 CXA8_SHEEP	P55917 ovis aries
23	31	88.6	510	1 CX56_CHICK	P29415 gallus gall
24	31	88.6	1363	1 ILPR_BRALA	O02466 branchiosto
25	30	85.7	98	1 YDAS_ECOLI	P76063 escherichia
26	30	85.7	225	1 TRPF_CANAL	P43073 candida alb
27	30	85.7	570	1 MKKS_HUMAN	Q9np11 homo sapien
28	30	85.7	654	1 CBPI_YEAST	P07252 saccharomyc
29	30	85.7	709	1 KRPI_SCHPO	Q09175 schizosacch
30	30	85.7	745	1 IKKA_HUMAN	O15111 h inhibitor
31	30	85.7	745	1 IKKA_MOUSE	Q60680 m inhibitor
32	30	85.7	751	1 TALA_POVHA	P03075 hamster pol
33	30	85.7	756	1 IKKB_HUMAN	O14920 homo sapien

34	30	85.7	757	1 IKKB_MOUSE	O88351 mus musculu
35	30	85.7	757	1 IKKB_RAT	Q9qy78 rattus norv
36	30	85.7	3746	1 ACVS_PENCH	P19787 penicillium
37	30	85.7	3791	1 ACVT_PENCH	P26046 penicillium
38	29	82.9	139	1 YOR2_ADEG1	P20744 avian adeno
39	29	82.9	228	1 Y268_MYCGE	P47510 mycoplasma
40	29	82.9	233	1 CR29_ENTHI	P19476 entamoeba h
41	29	82.9	328	1 NIR3_AZOBR	P45672 azospirillu
42	29	82.9	330	1 YETK_BACSU	O31540 bacillus su
43	29	82.9	453	1 AAT5_ARATH	P46248 arabidopsis
44	29	82.9	454	1 AATM_LUPAN	P26563 lupinus ang
45	29	82.9	479	1 CATA_BOTCI	P55304 botrytis ci

ALIGNMENTS

RESULT 1

ID	YCFD_HAEIN	STANDARD;	PRT;	404 AA
AC	P44683;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Protein HI0396.			
GN	HI0396.			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Rd / KW20 / ATCC 51907;			
RX	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Cloutier B.A., Merrick J.M.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Kinkness E.F.,			
RA	McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,			
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,			
RA	Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae			
RL	Rd.";			
RL	Science 269:496-512(1995).			
RN	[2]			
RP	IDENTIFICATION BY MASS SPECTROMETRY.			
RX	MEDLINE=20137488; PubMed=10675023;			
RA	Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,			
RA	Gray C., Fountoulakis M.;			
RT	"Two-dimensional map of the proteome of Haemophilus influenzae.";			
RL	Electrophoresis 21:411-429(2000).			
CC	-1- SIMILARITY: STRONG, TO E.COLI YCFD.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U32723; AAC22055.1; -			
DR	TIGR; HI0396; -			
KW	Complete proteome.			
SQ	SEQUENCE 404 AA; 46419 MW; A3FF26064D3F8B4C CRC64;			

Query Match 91.4%; Score 32; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

```
Db 366 LWAF 371
|||||
RESULT 2
VAL2_CLVK STANDARD; PRT; 135 AA.
AC P14976;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (15.2 kDa protein).
GN AC2.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
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CC
CC EMBL; J02057; ; NOT_ANNOTATED_CDS.
DR InterPro; IPR000942; Gemin1_AL2.
DR Pfam; PF01440; Gemin1_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin1_AL2; 1.
DR SEQUENCE 135 AA; 15159 MW; 75D24A8CD6368848 CRC64;
SQ
Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSFL 6
DB 128 DWSFL 132
|||||
RESULT 3
VAL2_CLVK STANDARD; PRT; 135 AA.
AC P14968;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (15.2 kDa protein).
GN AC2.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
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CC
CC EMBL; X17095; CAA34952.1;
DR PIR; S07593; S07593.
DR InterPro; IPR000942; Gemin1_AL2.
DR Pfam; PF01440; Gemin1_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin1_AL2; 1.
DR SEQUENCE 135 AA; 15178 MW; 2825C2F42E5E1F49 CRC64;
SQ
Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSFL 6
DB 128 DWSFL 132
|||||
RESULT 4
VAL2_TYLCV STANDARD; PRT; 135 AA.
AC P27262;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (C2 protein).
GN C2.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
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CC
CC EMBL; X15656; CAA33689.1;
DR PIR; C40779; QQCVC4.
DR InterPro; IPR000942; Gemin1_AL2.
DR Pfam; PF01440; Gemin1_AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin1_AL2; 1.
DR SEQUENCE 135 AA; 15611 MW; F111C8C2F7E9DD32 CRC64;
SQ
Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSFL 6
DB 128 DWSFL 132
|||||
RESULT 5
HIS2_YERPE STANDARD; PRT; 204 AA.
AC Q82FY1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
SQ
```

DE Histidine biosynthesis bifunctional protein HISIE [Includes:
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].
 GN HISI OR HISIE OR YPO1542.
 OS versinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Versinia.
 OX NCBI_TaxID=632;
 RN
 RP SEQUENCE FROM N.A.
 RX STRAIN=CO-92 / Biovar Orientalis;
 RC MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of *Versinia pestis*, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-
 CC phosphoribosyl)-AMP + diphosphate.
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + 1-(5-
 CC phosphoribosyl)-5-[(5-
 CC phosphoribosylamino)methylidenamino]imidazole-4-carboxamide.
 CC -1- PATHWAY: Histidine biosynthesis; second step.
 CC -1- PATHWAY: Histidine biosynthesis; third step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH
 CC FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PRA-PH
 CC FAMILY.
 CC
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 CC
 CC EMBL: AJ414149; CAC90365.1;
 DR InterPro: IPR002496; PRA-CH.
 DR InterPro: IPR002497; PRA-PH.
 DR Pfam: PF01502; PRA-CH; 1.
 DR Pfam: PF01503; PRA-PH; 1.
 DR ProDom: PD002610; PRA-CH; 1.
 DR ProDom: PD002611; PRA-PH; 1.
 KW Histidine biosynthesis; Multifunctional enzyme; Hydrolase;
 KW Complete proteome.
 FT DOMAIN 1 114 PHOSPHORIBOSYL-AMP CYCLOHYDROLASE.
 FT DOMAIN 115 204 PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE.
 SQ SEQUENCE 204 AA; 22807 MW; BF3328DF1C0A8C79 CRC64;

Query Match 88.68; Score 31; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
 DB 111 DWSFL 115
 |||||

RESULT 6
 LECS_VATNA STANDARD; PRT; 240 AA.
 AC P81371;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Seed Lentin (VML).
 OS Vatairea macrocarpa.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Dalbergiaceae; Vatairea.
 OX NCBI_TaxID=77050;
 RN
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=98218569; PubMed=9559667;
 RA Calvete J.J., Santos C.F., Mann K., Grangeiro T.B., Nimtz M.,
 RA Urbanké C., Sousa-Cavada B.;
 RT "Amino acid sequence, glycan structure, and proteolytic processing of
 RL the lectin of *Vatairea macrocarpa* seeds.";
 RL FEBS Lett. 425:286-292(1998).
 CC -1- FUNCTION: LECTIN THAT BINDS GALACTOSE.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- TISSUE SPECIFICITY: SEED.
 CC -1- PTM: PARTIALLY N-GLYCOSYLATED AT POSITIONS 111 AND 183 WITH
 CC THE HEPTASACCHARIDE [(BETA-Xylosyl-1,2)(ALPHA-MANNOSYL-1,6)(ALPHA-
 CC MANNOSYL-1,3)]BETA-MANOSYL-1,4-GLCNAC-BETA-1,4-GLCNAC-BETA-1,4
 CC PROTEOLYTICALLY CLEAVED AT 114-115 INTO GAMMA AND BETA CHAINS.
 CC THIS IS PROBABLY DEPENDENT ON THE DEGLYCOSYLATION OF N-111.
 CC -1- MISCELLANEOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION
 CC AND ONE CALCIUM ION. THE METAL IONS ARE ESSENTIAL FOR THE
 CC SACCHARIDE-BINDING AND CELL-AGGLUTINATING ACTIVITIES (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
 CC HSSP: P19588; 1LUL.
 DR GlycoSuiteDB: P81371;
 DR InterPro: IPR000985; Lentin_legA.
 DR InterPro: IPR001220; Lentin_legB.
 DR Pfam: PF00138; Lentin_legA; 1.
 DR Pfam: PF00139; Lentin_legB; 1.
 DR ProDom: PD000671; Lentin_legA; 1.
 DR ProDom: PD000711; Lentin_legB; 1.
 DR PROSITE: PS00307; LECTIN_LEGUE_BETA; 1.
 DR PROSITE: PS00308; LECTIN_LEGUE_ALPHA; 1.
 KW Lentin; Calcium; Manganese; Glycoprotein.
 FT CHAIN 1 240
 FT CHAIN 1 114 SEED LECTIN ALPHA CHAIN.
 FT CHAIN 123 239 SEED LECTIN BETA CHAIN.
 FT METAL 115 123 SEED LECTIN BETA CHAIN.
 FT METAL 125 125 MANGANESE (BY SIMILARITY).
 FT METAL 129 129 MANGANESE AND CALCIUM (BY SIMILARITY).
 FT METAL 132 132 CALCIUM (BY SIMILARITY).
 FT METAL 137 137 MANGANESE AND CALCIUM (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .).
 FT VARIANT 117 117 I -> V.
 FT VARIANT 148 148 M -> K.
 FT VARIANT 154 154 G -> A.
 FT VARIANT 168 168 E -> Q.
 FT UNSURE 239 240
 SQ SEQUENCE 240 AA; 26197 MW; C17DF6B2568C65C1 CRC64;

Query Match 88.68; Score 31; DB 1; Length 240;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
 DB 224 LDWSF 228
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RESULT 7
 CXAS_RAT STANDARD; PRT; 355 AA.
 AC P28234;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE gap junction alpha-5 protein (Connexin 40) (Cx40).
 GN GJA5 OR CXN-40.

OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE=92112940; PubMed=1370487;
 RA Haefliger J.-A., Bruzzone R., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Paul D.L.;
 RT "Four novel members of the connexin family of gap junction proteins.
 RT Molecular cloning, expression, and chromosome mapping.";
 RL J. Biol. Chem. 267:2057-2064(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93021055; PubMed=1328644;
 RA Beyer E.C., Reed K.E., Westphale E.M., Kanter H.L., Larson D.M.;
 RT "Molecular cloning and expression of rat connexin40, a gap junction
 RT protein expressed in vascular smooth muscle.";
 RL J. Membr. Biol. 127:69-76(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98066770; PubMed=9403066;
 RA Seul K.H., Tadros P.N., Beyer E.C.;
 RT "Mouse connexin40: gene structure and promoter analysis.";
 RL Genomics 46:120-126(1997).
 CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
 CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
 CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
 CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG.
 CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC
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 CC -----
 DR EMBL; M76535; AAA41000.1; -;
 DR EMBL; M83092; AAA41194.1; -;
 DR EMBL; AF021806; AAC33502.1; -;
 DR EMBL; AF022136; AAC33503.1; -;
 DR PIR; A42053; A42053.
 DR InterPro; IPR000500; Connexin.
 DR Pfam; PF00029; connexin; 1.
 DR PRINTS; PR00206; CONNEXIN.
 DR SMART; SM00037; CNX; 1.
 DR PROSITE; PS00407; CONNEXINS_1; 1.
 DR PROSITE; PS00408; CONNEXINS_2; 1.
 KW Gap junction; Transmembrane.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 19 39 POTENTIAL.
 FT DOMAIN 40 75 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 76 96 POTENTIAL.
 FT DOMAIN 97 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 183 POTENTIAL.
 FT DOMAIN 184 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 224 POTENTIAL.
 FT DOMAIN 225 355 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 355 AA; 40102 MW; 4F859438686000B9 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 DWSFL 6
 |||||

RESULT 9
 ID CXAS_HUMAN STANDARD; PRT; 357 AA.
 AC P36382;
 DT 01-JUN-1994 (Rel. 29, Created)

Db 2 DWSFL 6

RESULT 8
 ID CXAS_CANFA STANDARD; PRT; 356 AA.
 AC P33725;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
 GN GJAS.
 OS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92136511; PubMed=1310450;
 RA Kanter H.L., Saffitz J.E., Beyer E.C.;
 RT "Cardiac myocytes express multiple gap junction proteins.";
 RL Circ. Res. 70:438-444(1992).
 CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
 CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
 CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
 CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC
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 CC -----
 DR EMBL; M81347; AAA30838.1; -;
 DR PIR; A49024; A49024.
 DR InterPro; IPR000500; Connexin.
 DR Pfam; PF00029; connexin; 1.
 DR PRINTS; PR00206; CONNEXIN.
 DR SMART; SM00037; CNX; 1.
 DR PROSITE; PS00407; CONNEXINS_1; 1.
 DR PROSITE; PS00408; CONNEXINS_2; 1.
 KW Gap junction; Transmembrane.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 19 39 POTENTIAL.
 FT DOMAIN 40 75 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 76 96 POTENTIAL.
 FT DOMAIN 97 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 183 POTENTIAL.
 FT DOMAIN 184 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 224 POTENTIAL.
 FT DOMAIN 225 356 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 356 AA; 39801 MW; C8431D65CF9E78FE CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 356;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 DWSFL 6
 |||||

RESULT 9
 ID CXAS_HUMAN STANDARD; PRT; 357 AA.
 AC P36382;
 DT 01-JUN-1994 (Rel. 29, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Gap Junction alpha-5 protein (Connexin 40) (Cx40).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95055780; PubMed=7966354;
RA Kanter H.L., Saffitz J.E., Beyer E.C.;
RT "Molecular cloning of two human cardiac gap junction proteins,
connexin40 and connexin45.";
RL J. Mol. Cell. Cardiol. 26:861-868(1994).
RN [2]
RP REVISIONS.
RA Beyer E.C., Christensen E.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lin H.H., Jin N., Kiang D.T.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Hefflinger J.-A., Goy J.J., Waerber G.;
RT "Sporadic cases of dilated cardiomyopathies associated with
RT atrioventricular conduction defects are not linked to mutation within
RT the connexins 40 and 43 genes.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRausberg R.;
RA Tissue=Placenta;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
CC -1- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U03486; AAA60457.2; -;
CC EMBL; L34954; AAA91833.1; -;
CC EMBL; AF151979; AAD37801.1; -;
CC EMBL; BC013313; AAI13313.1; -;
CC Genew; HGNC:4279; GJA5.
CC MIM; 121013; -;
CC InterPro; IPR000500; Connexin.
CC Pfam; PF00029; connexin; 1.
CC PRINTS; PR00206; CONNEXIN.
CC SMART; SM00037; CNX; 1.
CC PROSITE; PS00407; CONNEXINS_1; 1.
CC PROSITE; PS00408; CONNEXINS_2; 1.
CC Gap junction; Transmembrane.
CC INIT_MET 0 0
CC BY SIMILARITY.
CC DOMAIN 1 18
CC CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 19 39
CC POTENTIAL.
CC DOMAIN 40 75
CC EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 76 96
CC POTENTIAL.
CC DOMAIN 97 163
CC CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 164 184
CC POTENTIAL.
CC DOMAIN 185 204
CC EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 205 225
CC POTENTIAL.

FT DOMAIN 226 357 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 357 AA; 40249 MW; 63FF9AA3CAED760 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSFL 6
DB 2 DWSFL 6
RESULT 10
CXAS_MOUSE
ID CXAS_MOUSE STANDARD; PRT; 357 AA.
AC Q01231;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gap Junction alpha-5 protein (Connexin 40) (Cx40).
GN GJA5 OR CXN-40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=92299686; PubMed=1318884;
RA Hennemann J., Suchyna T., Lichtenberg-Frate H., Jungbluth S.,
RA Dahl E., Schwarz J., Nicholson B.J., Willecke K.;
RT "Molecular cloning and functional expression of mouse connexin40, a
RT second gap junction gene preferentially expressed in lung.";
RL J. Cell Biol. 117:1299-1310(1992).
CC -1- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
CC -1- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: KIDNEY, HEART AND SKIN, BUT MOST ABUNDANT
CC IN LUNG.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X61675; CAA43850.1; -;
CC PIR; S23111; S23111.
CC MGD; MGI:95716; Gja5.
CC InterPro; IPR000500; Connexin.
CC Pfam; PF00029; connexin; 1.
CC PRINTS; PR00206; CONNEXIN.
CC SMART; SM00037; CNX; 1.
CC PROSITE; PS00407; CONNEXINS_1; 1.
CC PROSITE; PS00408; CONNEXINS_2; 1.
CC Gap junction; Transmembrane.
CC INIT_MET 0 0
CC BY SIMILARITY.
CC DOMAIN 1 18
CC CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 19 39
CC POTENTIAL.
CC DOMAIN 40 75
CC EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 76 96
CC POTENTIAL.
CC DOMAIN 97 163
CC CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 164 184
CC POTENTIAL.
CC DOMAIN 185 204
CC EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 205 225
CC POTENTIAL.
CC DOMAIN 226 357
CC CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 357 AA; 40282 MW; 7823CDA57A9C7C90 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 2 DWSFL 6

RESULT 11

QY 2 DWSFL 6
DB 2 DWSFL 6

RESULT 11
CXA5_CHICK
ID CXA5_CHICK STANDARD; PRT; 368 AA.
AC P18860;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gap junction alpha-5 protein (Connexin 42) (Cx42).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90354434; PubMed=2167316;
RA Beyer E.C.;
RT "Molecular cloning and developmental expression of two chick embryo gap junction proteins";
RL J. Biol. Chem. 265:14439-14443(1990).
CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: MOSTLY IN HEART, AND IN THE WHOLE EMBRYO, LIVER, STOMACH, AND PECTORAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II) SUBFAMILY.

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EMBL; M35043; AAA48716.1; -
DR PIR; B37819; B37819.
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 43 POTENTIAL.
FT DOMAIN 44 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 96 POTENTIAL.
FT DOMAIN 97 168 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 169 189 POTENTIAL.
FT DOMAIN 190 209 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 210 230 POTENTIAL.
FT DOMAIN 231 368 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 368 AA; 41613 MW; 853A042FF51DACB CRC64;

Query Match 88.6%; Score 31; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 2 DWSFL 6

RESULT 12

QY 2 DWSFL 6
DB 2 DWSFL 6

RESULT 12
LYSL_CANAL
ID LYS1_CANAL STANDARD; PRT; 382 AA.
AC P43065;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Saccharopine dehydrogenase [NAD+, L-lysine forming] (EC 1.5.1.7)
DE (Lysine--2-oxoglutarate reductase) (SDH).
GN LYS1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95012722; PubMed=7927784;
RA Garrad R.C.; Schmidt T.M.; Bhattacharjee J.K.;
RT "Molecular and functional analysis of the LYS1 gene of Candida albicans";
RL Infect. Immun. 62:5027-5031(1994).
CC -!- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+) + H(2)O = L-lysine + 2-oxoglutarate + NADH.
CC -!- PATHWAY: Lysine biosynthesis; eighth step.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER FUNGAL SACCHAROPINE DEHYDROGENASE.

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EMBL; U13233; AAA21362.1; -
DR InterPro; IPR004002; AlaDh_PNT.
DR Pfam; PF01262; AlaDh_PNT; 1.
KW Lysine biosynthesis; Oxidoreductase; NAD.
FT ACT_SITE 217 217 BY SIMILARITY.
SQ SEQUENCE 382 AA; 42394 MW; A3620191DF04B88F CRC64;

Query Match 88.6%; Score 31; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
DB 151 LDWSF 155

RESULT 13

QY 1 LDWSF 5
DB 151 LDWSF 155

RESULT 13
P2C4_SCHPO
ID P2C4_SCHPO STANDARD; PRT; 383 AA.
AC O14156; Q9UR02;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 4 (EC 3.1.3.16) (P2C-4).
GN PTC4 OR SPAC4A8.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.; SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION.
RC STRAIN=972;

RX MEDLINE=99365157; PubMed=10436019;
RA Gaits F., Russell P.;
RT "Vacuole fusion regulated by protein phosphatase 2C in fission
RL yeast.";
RL Mol. Biol. Cell 10:2647-2654(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson S., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor J., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voickaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: HAS A ROLE IN THE REGULATION OF VACUOLE FUSION.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. VACUOLAR.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC
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CC -----
DR EMBL; AF140285; AAD27651.1; -;
DR EMBL; Z98762; CAB58554.1; -;
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
DR Hydrolase; Magnesium; Manganese; Multigene family.
KW METAL 92 92 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 308 308 MANGANESE 2 (BY SIMILARITY).
FT METAL 347 347 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 383 AA; 43569 MW; 88E00C2BDAE4B9BF CRC64;
Query Match 88.6%; Score 31; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSFL 6
Db 299 DWSFL 303

RESULT 14
CXAB_CHICK STANDARD; PRT: 399 AA.
ID AC P36381; Q92144;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gap junction alpha-8 protein (Connexin 45.6) (Cx45.6).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=94325667; PubMed=8049527;
RT "Molecular cloning and functional characterization of chick lens
fiber connexin 45.6.";
RL Mol. Biol. Cell 5:363-373(1994).
RN [2]
RP SEQUENCE OF 1-235 FROM N.A.
RC TISSUE=Lens fibers;
RX MEDLINE=96437509; PubMed=8840185;
RA Sawada K., Agata K., Eguchi G.;
RT "Characterization of terminally differentiated cell state by
categorizing cDNA clones derived from chicken lens fibers.";
RL Int. J. Dev. Biol. 40:531-535(1996).
CC -1- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
CC -1- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC
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CC -----
DR EMBL; L24799; AAA57134.1; -;
DR EMBL; D26333; BAA05381.1; -;
DR InterPro; IPR000500; Connexin.
DR InterPro; IPR002266; Connexin50.
DR Pfam; PF00029; connexin; 1.
DR Pfam; PF03509; Connexin50; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT_MET 0 0
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 43 POTENTIAL.
FT DOMAIN 44 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 96 POTENTIAL.
FT DOMAIN 97 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 176 POTENTIAL.
FT DOMAIN 177 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 POTENTIAL.
FT DOMAIN 226 399 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 145 146 EG -> DL (IN REF. 2).
FT CONFLICT 187 188 WP -> D (IN REF. 2).
FT CONFLICT 233 235 IRR -> SEL (IN REF. 2).
SQ SEQUENCE 399 AA; 45485 MW; 4197392ADB6CB5CA CRC64;
Query Match 88.6%; Score 31; DB 1; Length 399;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
|||||
DB 2 DWSFL 6

RESULT 15

NUCM_PROWI STANDARD; PRT; 400 AA.
AC Q37619;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADH-ubiquinone oxidoreductase 49 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (NADH dehydrogenase subunit 7).
GN NAD7.
OS Prototheca wickerhamii.
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Prototheca.
OX NCBI_TaxID=3111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=263-11;
RX MEDLINE=94180393; PubMed=8133522;
RA Wolff G., Plante I., Lang B.F., Kueck U., Burger G.;
RT "Complete sequence of the mitochondrial DNA of the chlorophyte alga
RT Prototheca wickerhamii. Gene content and genome organization.";
RL J. Mol. Biol. 237:75-86(1994).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
CC THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: BINDS 1 4Fe-4S CLUSTER.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 49 kDa SUBUNIT FAMILY.
CC -----
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CC -----
DR EMBL; U02970; A012640.1; -
DR InterPro; IPR001135; Oxidored_49kDa.
DR Pfam; PF00346; complex1_49kd; 1.
DR PROSITE; PS00535; COMPLEX1_49K; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Iron-sulfur; 4Fe-4S.
SQ SEQUENCE 400 AA; 45810 MW; 722758FE80BC9D2 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
|||||
DB 221 LDWSF 225

Search completed: May 30, 2003, 15:49:00
Job time : 4.11842 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-14
Perfect score: 35
Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	88.6	277	1	US-08-118-270-68
2	31	88.6	277	5	Sequence 68, Appl
3	31	88.6	382	2	Sequence 68, Appl
4	30	85.7	745	2	Sequence 30, Appl
5	30	85.7	745	2	Sequence 3, Appl
6	30	85.7	745	2	Sequence 3, Appl
7	30	85.7	745	2	Sequence 4, Appl
8	30	85.7	745	2	Sequence 3, Appl
9	30	85.7	745	2	Sequence 4, Appl
10	30	85.7	745	4	Sequence 4, Appl
11	30	85.7	745	4	Sequence 4, Appl
12	30	85.7	745	4	Sequence 4, Appl
13	30	85.7	745	4	Sequence 2, Appl
14	30	85.7	745	4	Sequence 10, Appl
15	30	85.7	745	4	Sequence 2, Appl
16	30	85.7	756	2	Sequence 4, Appl
17	30	85.7	756	2	Sequence 4, Appl
18	30	85.7	756	2	Sequence 2, Appl
19	30	85.7	756	2	Sequence 4, Appl
20	30	85.7	756	2	Sequence 2, Appl
21	30	85.7	756	2	Sequence 2, Appl
22	30	85.7	756	4	Sequence 2, Appl
23	30	85.7	756	4	Sequence 2, Appl
24	30	85.7	756	4	Sequence 2, Appl
25	30	85.7	756	4	Sequence 15, Appl
26	30	85.7	756	4	Sequence 9, Appl
27	30	85.7	768	2	Sequence 5, Appl

28 30 85.7 3656 2 US-08-222-617A-12 Sequence 12, Appl
29 30 85.7 3727 2 US-08-222-617A-27 Sequence 27, Appl
30 30 85.7 3778 2 US-08-222-617A-2 Sequence 2, Appl
31 29 82.9 70 4 US-09-242-050-4 Sequence 4, Appl
32 29 82.9 139 4 US-09-171-461-42 Sequence 4, Appl
33 29 82.9 415 4 US-09-242-050-2 Sequence 2, Appl
34 29 82.9 532 4 US-09-242-050-2 Sequence 3, Appl
35 29 82.9 532 4 US-09-555-270A-3 Sequence 3, Appl
36 29 82.9 532 4 US-09-955-597-3 Sequence 3, Appl
37 29 82.9 727 4 US-09-134-001C-4067 Sequence 4067, Ap
38 29 82.9 2595 4 US-09-036-987A-2 Sequence 2, Appl
39 29 82.9 2595 4 US-09-370-700-2 Sequence 2, Appl
40 28 80.0 48 2 US-08-637-759B-253 Sequence 253, App
41 28 80.0 48 3 US-08-871-355A-253 Sequence 253, App
42 28 80.0 48 4 US-09-201-945-253 Sequence 253, App
43 28 80.0 336 3 US-08-749-816-2 Sequence 2, Appl
44 28 80.0 336 4 US-09-144-914-2 Sequence 2, Appl
45 28 80.0 345 3 US-08-858-003-34 Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-118-270-68
; Sequence 68, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-68

Query Match 88.6%; Score 31; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6

Db 81 DWSFL 85

RESULT 2
PCT-US93-08528-68
; Sequence 68, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633

INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-68

Query Match 88.6%; Score 31; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSFL 6
Db 81 DWSFL 85

RESULT 3
US-08-360-606B-30
; Sequence 30, Application US/08360606B
; Patent No. 5919617
; GENERAL INFORMATION:
; APPLICANT: Jnanendra K. Bhattacharjee
; APPLICANT: Richard C. Garrad
; APPLICANT: Paul L. Skatrud
; APPLICANT: Robert P. Peery
; TITLE OF INVENTION: Methods and Reagents for
; TITLE OF INVENTION: Detecting Fungal Pathogens in a
; TITLE OF INVENTION: Biological Sample
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive Suite 3200
; CITY: Chicago

STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,606B
; FILING DATE: December 21, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berghoff, Paul H.
; REGISTRATION NUMBER: 30,243
; REFERENCE/DOCKET NUMBER: 94,319
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: Yes
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-360-606B-30

Query Match 88.6%; Score 31; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSF 5
Db 151 LDWSF 155

RESULT 4
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 5
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 6
US-08-890-853-4
; Sequence 4, Application US/08890853

; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 7
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. NO. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 8
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. NO. 9.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 9
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. NO. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 10
US-09-032-476-4
Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 85.7%; Score 30; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 11
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 85.7%; Score 30; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 12
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 85.7%; Score 30; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 13
US-09-168-629-2
; Sequence 2, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: IKB Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 85.7%; Score 30; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 14
US-08-910-820-10
; Sequence 10, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brian W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: linear
US-08-910-820-10
Query Match 85.7%; Score 30; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 15
US-08-810-131A-2
; Sequence 2, Application US/08810131A
; Patent No. 6268194
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
; TITLE OF INVENTION: Same
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,131A
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-131A-2

Query Match 85.7%; Score 30; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 9.6e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSFL 6
Db 738 LDWSWL 743

Search completed: May 30, 2003, 14:41:31
Job time : 7.03947 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	35	100.0	6	23	ABB08736		Mutated IKKbeta NE
2	35	100.0	6	23	AA048519		NBD mutant peptide
3	35	100.0	756	23	ABB77300		Human IKKbeta muta
4	33	94.3	59	22	AAU58740		Propionibacterium
5	33	94.3	208	23	ABP30274		Streptococcus poly
6	33	94.3	216	23	ABP29552		Streptococcus poly
7	33	94.3	788	22	ABB64315		Drosophila melanog
8	32	91.4	6	23	ABB08737		Mutated IKKbeta NE
9	32	91.4	6	23	AA048520		NBD mutant peptide
10	32	91.4	37	21	AA059894		Arabidopsis thalia

11	32	91.4	37	21	AAG60632	Arabidopsis thalia
12	32	91.4	56	22	ABB03835	Human musculoskele
13	32	91.4	339	23	ABB55349	Lactococcus lactis
14	32	91.4	756	23	ABB77301	Human IKKbeta muta
15	32	91.4	927	23	ABB49720	Listeria monocytog
16	31	88.6	71	22	AAU63276	Propionibacterium
17	31	88.6	83	21	AAG00107	Human secreted pro
18	31	88.6	97	22	AAU55876	Propionibacterium
19	31	88.6	124	21	AA058122	Lung cancer associ
20	31	88.6	137	22	AAG67051	Human dihydrorota
21	31	88.6	149	21	AAG23584	Arabidopsis thalia
22	31	88.6	150	21	AA035712	CLCIV AC3 protein
23	31	88.6	157	22	AAG91029	C glutamicum prote
24	31	88.6	178	21	AAG23583	Arabidopsis thalia
25	31	88.6	234	21	AAG49093	Arabidopsis thalia
26	31	88.6	234	21	AAG49116	Arabidopsis thalia
27	31	88.6	242	23	ABB91342	Herbicidally activ
28	31	88.6	259	21	AA026244	Zea mays zmet2b me
29	31	88.6	264	21	AA016701	Bacteriophage Dp-1
30	31	88.6	266	21	AA011935	Arabidopsis thalia
31	31	88.6	277	15	AA048747	G-protein coupled
32	31	88.6	277	17	AA02719	G-protein coupled
33	31	88.6	280	21	AAG11934	Arabidopsis thalia
34	31	88.6	315	21	AAG49092	Arabidopsis thalia
35	31	88.6	315	21	AA049115	Arabidopsis thalia
36	31	88.6	317	22	AA069701	Bifidobacterium lo
37	31	88.6	343	21	AA049114	Arabidopsis thalia
38	31	88.6	358	19	AA023968	Connexin protein C
39	31	88.6	382	17	AA000496	Candida albicans s
40	31	88.6	417	19	AA049009	Mouse alpha 3 conn
41	31	88.6	442	21	AA049091	Arabidopsis thalia
42	31	88.6	597	22	ABB62635	Drosophila melanog
43	31	88.6	912	21	AA026242	Zea mays zmet2a me
44	31	88.6	932	21	AA026243	Zea mays zmet2a me
45	31	88.6	975	22	ABB64661	Drosophila melanog

ALIGNMENTS

RESULT 1

ABB08736
ID ABB08736 standard; peptide; 6 AA.

XX ABB08736;

XX AC ABB08736;

XX DT 14-JUN-2002 (first entry)

XX DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
autoimmune disease; transplant rejection; osteoporosis; cancer;
Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
osteopathic; cytostatic; nontropic; neuroprotective; anti-HIV; human;
antiartherosclerotic; virucide; antipathogenic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX FT Misc-difference 5 /note= "Wildtype Trp substituted by Phe"

XX PN WO200183547-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYVA) UNIV YALE.
 PA
 PI May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Claim 23; Page 45; 82pp; English.
 PS
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKBeta at the NEMO binding domain. Blockage of IKBeta-NEMO
 CC interaction results in inhibition of IKBeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKBeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 Db 1 LDWSFL 6
 |||||
 RESULT 2
 AAM48519
 ID AAM48519 standard; Peptide; 6 AA.
 AC AAM48519;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 14.
 XX

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkkappaB kinase beta; IKBeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS
 XX Example 6; Page 48; 88pp; English.
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM4828-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkkappaB Kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 Db 1 LDWSFL 6
 |||||
 RESULT 3
 ABB77300
 ID ABB77300 standard; protein; 756 AA.
 XX

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. These antibodies can be used to
 CC downregulate expression and activity of *P. acnes* polypeptides and
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 59 AA;
 Query Match 94.3%; Score 33; DB 22; Length 59;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSFL 6
 :|||||
 DB 18 LDWSFL 23

RESULT 5
 ABP30274
 ID ABP30274 standard; Protein; 208 AA.

XX AC ABP30274;

XX DT 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 9724.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus agalactiae.

XX PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;

XX PI Tettelin H;

XX DR WPI; 2002-352536/38.

XX DR N-PSDB; ABN70905.

XX PS Claim 1; Page 4099; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
 CC Nucleic acids encoding (I) are used to determine whether a compound binds to
 CC biological sample. (I) is used to determine whether a compound binds to
 CC Streptococcus comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX Sequence 208 AA;

Query Match 94.3%; Score 33; DB 23; Length 208;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSFL 6
 :|||||

DB 198 MDWSFL 203

RESULT 6
 ABP25952
 ID ABP25952 standard; Protein; 216 AA.

XX AC ABP25952;

XX DT 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 1080.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus agalactiae.

XX PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C;

XX PI Tettelin H;

XX DR WPI; 2002-352536/38.

XX DR N-PSDB; ABN66583.

XX PS Claim 1; Page 3263; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
 CC Nucleic acids encoding (I) are used to determine whether a compound binds to
 CC biological sample. (I) is used to determine whether a compound binds to
 CC Streptococcus comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

SQ Sequence 216 AA;

Query Match 94.3%; Score 33; DB 23; Length 216;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSFL 6
Db 206 MDWSFL 211

RESULT 7

ABBB64315
ID ABB64315 standard; Protein; 788 AA.

AC ABB64315;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 19737.

XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

OS Drosophila melanogaster.

PN W0200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL0841b.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions

XX Disclosure; SEQ ID NO 19737; 2lpp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 788 AA;

Query Match 94.3%; Score 33; DB 22; Length 788;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSFL 6

Db 331 LDWSFI 336

RESULT 8

ABB08737

ID ABB08737 standard; peptide; 6 AA.

XX ABB08737;

XX 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutetin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 5 /note= "Wildtype Trp substituted by Tyr"

XX W0200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain

XX Claim 23; Page 45; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprising contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkbppaB. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, psoriasis,
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and

CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arthritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.

XX SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
 ||||:|
 Db 1 LDWSYL 6

RESULT 9

AAM48520
 ID AAM48520 standard; Peptide; 6 AA.

AC AAM48520;

DT 20-MAR-2002 (first entry)

DE NBD mutant peptide SEQ ID NO 15.

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

OS WO200183554-A2.

PN 08-NOV-2001.

PD 02-MAY-2001; 2001WO-US14346.

PF 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYIA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPT; 2002-121889/16.

XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis

XX Example 6; Page 48; 88pp; English.

XX The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, The
 CC neutropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
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 Db 1 LDWSYL 6

RESULT 10

AAG59894

ID AAG59894 standard; Protein; 37 AA.

XX AAG59894;

AC AAG59894;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 77522.

DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

PN 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 16-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

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 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
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 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
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PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 91.4%; Score 32; DB 21; Length 37;

Best Local Similarity 83.3%; Pred. No. 48;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSFL 6

Db 3 LDWAF 8

RESULT 11

AAG60632
ID AAG60632 standard; Protein; 37 AA.

XX AC AAG60632;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 78557.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PP 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0123789.

PR 29-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0126785.

PR 06-APR-1999; 99US-0127462.

PR 08-APR-1999; 99US-0128234.

PR 16-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130449.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
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PR 26-JUL-1999; 99US-0145276.
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PR 09-AUG-1999;	99US-0147493.		
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PR 27-AUG-1999;	99US-0151080.		
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PR 28-OCT-1999;	99US-0161922.
PR 28-OCT-1999;	99US-0161993.
PR 28-OCT-1999;	99US-0161993.
PR 29-OCT-1999;	99US-0162142.

Query Match 91.4%; Score 32; DB 21; Length 37;
 Best Local Similarity 83.3%; Pred. NO. 48;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
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 Db 3 LDWAF 8

RESULT 12
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 ID ABB03835 standard; Protein; 56 AA.
 AC ABB03835;
 XX
 XX 08-JAN-2002 (first entry)
 DT
 XX Human musculoskeletal system related polypeptide SEQ ID NO 1782.
 DE
 XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system.
 XX
 XX Homo sapiens.
 OS
 XX WO200155367-A1.
 PN
 XX 02-AUG-2001.
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 XX 17-JAN-2001; 2001WO-US01338.
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 XX 31-JAN-2000; 2000US-0179065.
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 PR 19-MAY-2000; 2000US-0205515.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX
DR WPI; 2001-451937/48.
DR N-PSDB; AAL35417.
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
PS Claim 11; SEQ ID NO 1782; 781pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABH03087-ABH04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 56 AA;

Query Match 91.4%; Score 32; DB 22; Length 56;
Best Local Similarity 83.3%; Pred No. 74;
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CC derived from GenBank Accession No. O14920 (ABB77294).

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Query Match 91.4%; Score 32; DB 23; Length 756;
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AA ABB49720;

DT 05-FEB-2002 (first entry)

DE *Listeria monocytogenes* protein #2424.

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW
vitamin B12; bacterial infection; disease.
KW

OS *Listeria monocytogenes*.

PN WO200177335-A2.

18-OCT-2001.

11-APR-2001: 2001WO-FR01118.

PR 11-APR-2000; 2000FR-0004629.

PA (INSP) INST PASTEUR.

AA Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurgeat O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kref J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueto E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;

WPI: 2002-010914/01.

Genomic sequence for *Listeria* monocytogenes, useful e.g. for treatment and prevention of *Listeria* and related bacterial infections, and related polypeptides -

PS Claim 6; SEQ ID No 2425; 192pp; French.

The present invention relates to the genome sequence of *Listeria* monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in *L. monocytogenes* and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of *L. monocytogenes* and related organisms, for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate *L. monocytogenes*-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by *L. monocytogenes* and related organisms.

CC monocyctogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published/pct/sequences.

XX
SQ Sequence 927 AA;

Query Match 91.4%; Score 32; DB 23; Length 927;
Best Local Similarity 83.3%; Pred. NO. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

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SUMMARIES

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4	31	93.9	502	10	US-09-896-552-13
5	31	93.9	984	9	US-10-029-905-10
6	30	90.9	516	9	US-10-119-635-2
7	29	87.9	297	9	US-09-557-796-30
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9	29	87.9	636	9	US-09-905-291A-175
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24	29	87.9	636	9	US-10-180-552-22	Sequence 22, Appl
25	29	87.9	636	9	US-10-180-557-22	Sequence 22, Appl
26	29	87.9	636	9	US-09-908-838-175	Sequence 175, App
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ALIGNMENTS

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; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
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; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-13

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DB 1 LDWSAL 6

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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Fideles, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; Patent No. US2002002550A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 210119USOCNT
; CURRENT APPLICATION NUMBER: US/09/895,072
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: US 09/635,872
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 52
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Db 372 LDWSAM 377

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; Patent No. US20020150981A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 215089US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
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US-09-986-552-13

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; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying compounds which positively
; FILE REFERENCE: 1/1177
; CURRENT APPLICATION NUMBER: US/10/029,905
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/257,854
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 12
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US-10-029-905-10

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RESULT 6
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; Publication No. US20020193581A1
; GENERAL INFORMATION:
; APPLICANT: Karavorgou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/10/119,635
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/277,262
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 9
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; ORGANISM: Homo sapiens
US-10-119-635-2

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RESULT 7

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; Publication No. US20030073140A1
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/557,796
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/172,952
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Ylar-EC
US-09-557-796-30

Query Match 87.9%; Score 29; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSA 5
Db 59 LDWSA 63

RESULT 8

US-09-735-056-34
; Sequence 34, Application US/09735056
; Publication No. US20030013662A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Leonard
; APPLICANT: Stassi, Diane L.
; APPLICANT: Summers Jr., Richard G.
; APPLICANT: Ruan, Xiaolan
; APPLICANT: Pereda-Lopez, Ana
; APPLICANT: Kakavas, Stephan J.
; TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd.
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/735,056
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/858,003
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne Casuto
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 4952.US.P2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030013662A1e
US-09-735-056-34

Query Match 87.9%; Score 29; DB 9; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 43 LDWSSL 48

RESULT 9

US-09-905-291A-175
; Sequence 175, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 175
;; LENGTH: 636
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MOD.RES
;; LOCATION: (539)
;; OTHER INFORMATION: Any amino acid
US-09-905-291A-175

Query Match 87.9%; Score 29; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
|||||
DB 30 LDWSTL 35

RESULT 10

US-09-902-853-175
; Sequence 175, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902.853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350

;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 175
;; LENGTH: 636
;; TYPE: PRT
;; ORGANISM: Homo Sapien
;; NAME/KEY: unsure
;; LOCATION: 539
;; OTHER INFORMATION: unknown amino acid
US-09-902-853-175

Query Match 87.9%; Score 29; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
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DB 30 LDWSTL 35

RESULT 11

US-09-907-824-175
; Sequence 175, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/907,824
 ; PRIOR FILING DATE: 2001-07-17
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 175
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 539
 ; OTHER INFORMATION: unknown amino acid
 US-09-907-824-175

Query Match 87.9%; Score 29; DB 9; Length 636;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWSAL 6
 Db 30 LDWSTL 35

RESULT 12
 US-09-907-841-175

; Sequence 175, Application US/09907841
 ; Publication No. US20020198366A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/907,841
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 175
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (539)
 ; OTHER INFORMATION: Any amino acid
 US-09-907-841-175

Query Match 87.9%; Score 29; DB 9; Length 636;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWSAL 6
 Db 30 LDWSTL 35

RESULT 13

US-09-904-011-175
; Sequence 175, Application US/09904011
; Publication No. US2003003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 175
; LENGTH: 636
; TYPE: PRT

; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 539
; OTHER INFORMATION: unknown amino acid
US-09-904-011-175

Query Match 87.9%; Score 29; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDWSAL 6
 |||||
DB 30 LDWSTL 35

RESULT 14

US-10-174-590-22
; Sequence 22, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 22
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 539
; OTHER INFORMATION: unknown amino acid
US-10-174-590-22

Query Match 87.9%; Score 29; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDWSAL 6
 |||||
DB 30 LDWSTL 35

RESULT 15

US-10-176-758-22
; Sequence 22, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James


```

; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 22
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 539
; OTHER INFORMATION: unknown amino acid
US-10-176-758-22

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Query Match      87.9%; Score 29; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 LDWSAL 6
      |||||
Db      30 LDWSTL 35

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Search completed: May 30, 2003, 15:53:20
Job time : 11.4605 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDWSAL 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	93.9	226	1	P46691 ovis aries
2	31	93.9	333	1	Y237 SYN3
3	31	93.9	666	1	CO14 BRAJA
4	31	93.9	984	1	PKL2 HUMAN
5	30	90.9	261	1	YFJR_BACSU
6	30	90.9	377	1	Y4WD_RHISN
7	30	90.9	516	1	PROD_HUMAN
8	29	87.9	223	1	SAMP_HUMAN
9	29	87.9	224	1	SAMP_PIG
10	29	87.9	234	1	SAMP_MESAU
11	29	87.9	286	1	CXAC_RAT
12	29	87.9	286	1	SGBU_ECOLI
13	29	87.9	296	1	CYCG_RHOSH
14	29	87.9	313	1	Y763_TREPA
15	29	87.9	378	1	CXAL_XENLA
16	29	87.9	380	1	CXAL_BRARE
17	29	87.9	380	1	CXAL_CHICK
18	29	87.9	381	1	CXAL_HUMAN
19	29	87.9	381	1	CXAL_MOUSE
20	29	87.9	381	1	CXAL_RAT
21	29	87.9	382	1	CXAL_BOVIN
22	29	87.9	394	1	PGK_BACST
23	29	87.9	446	1	5HT_BOMMO
24	29	87.9	451	1	GUDH_PSEPU
25	29	87.9	455	1	UHPT_CHLPN
26	29	87.9	456	1	UHPT_CHLMU
27	29	87.9	456	1	UHPT_CHLTY
28	29	87.9	482	1	TRPE_SPIAU
29	29	87.9	517	1	LADI_HUMAN
30	29	87.9	528	1	LADI_MOUSE
31	29	87.9	600	1	GLMS_HAIN1
32	29	87.9	630	1	GLMS_SYN3
33	29	87.9	644	1	VP4_BTvl1

34	29	87.9	644	1	VP4_BTvl13
35	29	87.9	644	1	VP4_BTv2A
36	29	87.9	654	1	VP4_BTv10
37	29	87.9	754	1	RIR1_BPT4
38	29	87.9	842	1	PKL2_RAT
39	29	87.9	926	1	MAY3_SCHCO
40	29	87.9	941	1	GCSP_MYCTU
41	29	87.9	946	1	PKL1_RAT
42	29	87.9	958	1	YA7B_SCHPO
43	29	87.9	1036	1	P200_MYCPN
44	29	87.9	1199	1	MFD_SYN3
45	29	87.9	1693	1	Y163_SYN3

ALIGNMENTS

RESULT 1

ID	CXB2_SHEEP	STANDARD;	PRT;	226 AA.
AC	P46691;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Gap junction beta-2 protein (Connexin 26) (Cx26).			
GN	GJB2.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Rovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cornea;			
RA	Dong Y., Green C., Donaldson P.J., Kistler J.J.			
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED			
CC	PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH			
CC	MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.			
CC	-1- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP 1)			
CC	SUBFAMILY.			

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CC	EMBL; U17592; AAA67446.1; -
DR	InterPro; IPR000500; Connexin.
DR	Pfam; PF00029; connexin; 1.
DR	PRINTS; PRO0206; CONNEXIN.
DR	SMART; SM00037; CNX; 1.
DR	PROSITE; PS00407; CONNEXINS_1; 1.
DR	PROSITE; PS00408; CONNEXINS_2; 1.
KW	Gap junction; Transmembrane.
FT	DOMAIN 1 19 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 20 40 POTENTIAL.
FT	DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 76 96 POTENTIAL.
FT	DOMAIN 97 143 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 144 164 POTENTIAL.
FT	DOMAIN 165 189 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 190 210 POTENTIAL.
FT	DOMAIN 211 226 CYTOPLASMIC (POTENTIAL).
SQ	SEQUENCE 226 AA; 26215 MW; DCE2F0C1B4FCE7D CRC64;

Query Match 93.9%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 49;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 1 MDWSAL 6

RESULT 2

YZ37_SYNY3
ID YZ37_SYNY3 STANDARD; PRT; 333 AA.
AC Q55480;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical sugar kinase slr0537.
GN SLR0537.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.

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CC EMBL; D64006; BAAL0827.1; -
CC HSP; Q9TVM2; IDG.
CC InterPro; IPR002173; PfkB.
CC Pfam; PF00294; pfkb; 1.
CC PROSITE; PS00583; PFKB_KINASES.1; FALSE_NEG.
CC PROSITE; PS00584; PFKB_KINASES.2; 1
KW Hypothetical protein; transferase; Kinase; Complete proteome.
SQ SEQUENCE 333 AA; 35184 MW; CBCE13D0F7EEF90D CRC64;

Query Match 93.9%; Score 31; DB 1; Length 333;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 146 MDWSAL 151

RESULT 3

CO14_BRAJA
ID CO14_BRAJA STANDARD; PRT; 666 AA.
AC P98057;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fourth
DE terminal oxidase).
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94259305; PubMed=8200541;
RA Surpin M.A., Moshiri F., Murphy A.M., Maier R.J.;

Genetic evidence for a fourth terminal oxidase in Bradyrhizobium japonicum.;
Gene 143:73-77(1994).
-1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) - 4 ferrocyclochrome c + 2 H(2)O.
-1- PATHWAY: Respiratory chain; terminal step.
-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

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CC EMBL; L25841; AAA26210.1; -
CC HSP; P18401; 1FFT.
CC InterPro; IPR000883; COX1.
CC Pfam; PF00115; COX1; 1.
CC PRINTS; PR01165; CYCOXIDASE1.
CC PROSITE; PS00077; COX1; 1.
KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain.
FT METAL 105
FT METAL 283
FT METAL 287
FT METAL 332
FT METAL 333
FT METAL 418
FT METAL 420
SQ SEQUENCE 666 AA; 74537 MW; 326E05BD13B1AAEC CRC64;

Query Match 93.9%; Score 31; DB 1; Length 666;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 5 LDWSAI 10

RESULT 4

PKL2_HUMAN
ID PKL2_HUMAN STANDARD; PRT; 984 AA.
AC Q16513; Q9H1W4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C-like 2 (EC 2.7.1.1-) (Protein-kinase C-related kinase
DE 2).
GN PRKCL2 OR PRK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95080426; PubMed=7988719;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
RT products.";
RL FEBS Lett. 356:5-8(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=95154310; PubMed=7851406;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Cloning and expression patterns of two members of a novel protein-
RT kinase-C-related kinase family.";
RL Eur. J. Biochem. 227:344-351(1995).
RN [3]
RP SEQUENCE OF 17-984 FROM N.A.
RA Brown A.;

```

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: EXHIBITS A PREFERENCE FOR HIGHLY BASIC PROTEIN
CC SUBSTRATES (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
CC AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS AND
CC -1- UNSATURATED FATTY ACIDS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U33052; AAC50208.1; -
DR EMBL; S75548; AAB33346.1; -
DR EMBL; AL136381; CAC17575.1; -
DR HSP; Q63450; IAO6
DR Genew; HGNC:9406; PRKCL2.
DR MIM; 602549; -
DR InterPro; IPR000008; C2.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; pkinase_C.
DR InterPro; IPR000861; REM_repeat.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase_1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF02185; HR1; 3.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00074; HR1; 3.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase; ATP-binding; Serine/threonine-protein kinase;
DR Phosphorylation.
FT DOMAIN 657 916 PROTEIN KINASE.
FT NP_BIND 663 671 ATP (BY SIMILARITY).
FT BINDING 686 686 ATP (BY SIMILARITY).
FT ACT_SITE 782 782 BY SIMILARITY.
FT CONFLICT 207 207 N -> KGDGNCPPSYEHN (IN REF. 3).
SQ SEQUENCE 984 AA; 112034 MW; 687EC417A0F51C1D CRC64;

Query Match 93.9%; Score 31; DB 1; Length 984;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 919 IDWSAL 924

RESULT 5
YFJR_BACSU STANDARD; PRT; 261 AA.
AC O34969;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase yfjR (EC 1.1.1.-.-).
GN YFJR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;

RN SEQUENCE FROM N.A.
RP STRAIN-AC327;
RX MEDLINE-97124190; PubMed-8969503;
RA Yamamoto H., Uchiyama S., Sekiguchi J.;
RT "Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76
RT degrees region of the Bacillus subtilis chromosome containing genes
RT for trehalose metabolism and acetoin utilization.";
RL Microbiology 142:3057-3065(1996).
RN SEQUENCE FROM N.A.
RP STRAIN-168;
RX MEDLINE-98044033; PubMed-9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconelli E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: BELONGS TO THE 3-HYDROXYISOBUTYRATE DEHYDROGENASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; D83967; BAA23388.1; -
DR EMBL; D78509; BAA24303.1; -
DR EMBL; Z99108; CAB12628.1; -
DR Subtilist; BG12914; yfjR.
DR InterPro; IPR002204; 3hydroxisobut_dh.
DR PROSITE; PS00895; 3-HYDROXYISOBUT_DH; FALSE_NEG.
RW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 261 AA; 27866 MW; 6C9A8CAC8C71CA66 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 261;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 251 LDWSAL 256

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RESULT 6
Y4WD_RHISN          STANDARD;          PRT;          377 AA.
ID Y4WD_RHISN          STANDARD;          PRT;          377 AA.
AC P55682;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical transport protein Y4WD.
GN Y4WD.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- FUNCTION: COULD BE INVOLVED IN A TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: TO R.MELILOTI MOSC.
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-----
DR EMBL; AE000103; AAB91911.1;
KW Hypothetical protein; Transmembrane; Transport; Plasmid.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 85 105 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 192 212 POTENTIAL.
FT TRANSMEM 278 298 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 327 347 POTENTIAL.
FT TRANSMEM 356 376 POTENTIAL.
SQ SEQUENCE 377 AA; 39051 MW; 49CF6E44AA0D74BD CRC64;

Query Match          90.9%; Score 30; DB 1; Length 377;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
| | | | |
Db 221 LDWSAV 226

RESULT 7
PROD_HUMAN
ID PROD_HUMAN          STANDARD;          PRT;          516 AA.
AC O43272;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proline oxidase, mitochondrial precursor (EC 1.5.3.-) (Proline
DE dehydrogenase).
GN PRODH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RX MEDLINE=98046348; PubMed=9385373;
RA Campbell H.D., Webb G.C., Young I.G.;
RT "A human homologue of the Drosophila melanogaster sluggish-A (proline
RT oxidase) gene maps to 22q11.2, and is a candidate gene for type-I
RL hyperprolinaemia.";
RN Hum. Genet. 101:69-74(1997).
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum, and Kidney;
RX MEDLINE=99208616; PubMed=10192398;
RA Gogos J.A., Santha M., Takacs Z., Beck K.D., Luine V., Lucas L.R.,
RA Nadler J.V., Karayorgou M.;
RT "The gene encoding proline dehydrogenase modulates sensorimotor gating
RT in mice.";
RL Nat. Genet. 21:434-439(1999).
CC -1- FUNCTION: CONVERTS PROLINE TO DELTA-1-PYRROLINE-5-CARBOXYLATE.
CC -1- PATHWAY: Conversion from proline to glutamate; first step.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKELETAL MUSCLE AND BRAIN,
CC TO A LESSER EXTENT IN HEART AND KIDNEY, AND WEAKLY IN LIVER,
CC PLACENTA AND PANCREAS.
CC -1- DISEASE: DEFECTS IN PRODH ARE A CAUSE OF TYPE-1 HYPERPROLINEMIA.
CC A DISORDER WHERE SERUM PROLINE LEVELS ARE ELEVATED. MAY BE
CC INVOLVED IN THE 22Q11 ASSOCIATED PSYCHIATRIC AND BEHAVIORAL
CC PHENOTYPES.
CC -1- SIMILARITY: BELONGS TO THE PROLINE OXIDASE FAMILY.
-----
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-----
DR EMBL; U82381; AAB88789.1;
DR EMBL; AF120278; AAD24775.1;
DR Genew; HGNC:9453; PRODH.
DR MIN; 606810;
DR MIN; 239500;
DR InterPro; IPR002872; Pro_dh.
DR Pfam; PF01619; Pro_dh; 1.
DR Oxidoreductase; Proline metabolism; Mitochondrion; Transit peptide.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 516 PROLINE OXIDASE.
FT CONFLICT 80 80 S -> T (IN REF. 2).
SQ SEQUENCE 516 AA; 59216 MW; 2FA5B1E4481C450A CRC64;

Query Match          90.9%; Score 30; DB 1; Length 516;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
| | | | |
Db 231 LDWSSL 236

RESULT 8
SAMP_HUMAN
ID SAMP_HUMAN          STANDARD;          PRT;          223 AA.
AC P02743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glycoprotein).
DE APCs OR FFX2.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=85207828; PubMed=2987268;
 RA Mantouranis E.C., Dowton S.B., Whitehead A.S., Edge M.D.,
 RA Bruns G.A.P., Colten H.R.;
 RT "Human serum amyloid P component. cDNA isolation, complete sequence
 RT of pre-serum amyloid P component, and localization of the gene to
 RT chromosome 1.";
 RL J. Biol. Chem. 260:7752-7756(1985).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87137351; PubMed=3029048;
 RA Ohnishi S., Maeda S., Shimada K., Arao T.;
 RT "Isolation and characterization of the complete complementary and
 RT genomic DNA sequences of human serum amyloid P component.";
 RL J. Biochem. 100:849-858(1986).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE OF 20-223.
 RX MEDLINE=86033713; PubMed=4055725;
 RA Prelli F., Pras M., Frangione B.;
 RT "The primary structure of human tissue amyloid P component from a
 RT patient with primary idiopathic amyloidosis.";
 RL J. Biol. Chem. 260:12895-12898(1985).
 RN [5]
 RN SEQUENCE OF 20-49.
 RX MEDLINE=79042150; PubMed=81686;
 RA Thompson A.R., Enfield D.L.;
 RT "Human plasma P component: isolation and characterization.";
 RL Biochemistry 17:4304-4311(1978).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94159098; PubMed=8114934;
 RA Emsley J., White H.E., O'Hara B., Oliva G., Srinivasan N.,
 RA Tickle I.J., Blundell T.L., Pepys M.B., Wood S.P.;
 RT "Structure of pentameric human serum amyloid P component.";
 RL Nature 367:338-345(1994).
 RN [7]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=97360233; PubMed=9217261;
 RA Hohenester E., Hutchinson W.L., Pepys M.B., Wood S.P.;
 RT "Crystal structure of a decameric complex of human serum amyloid P
 RT component with bound DAMP.";
 RL J. Mol. Biol. 269:570-578(1997).
 CC -1- FUNCTION: CAN INTERACT WITH DNA AND HISTONES AND MAY SCAVENGE
 CC NUCLEAR MATERIAL RELEASED FROM DAMAGED CIRCULATING CELLS. MAY ALSO
 CC FUNCTION AS A CALCIUM-DEPENDENT LECTIN.
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
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 CC -----
 DR EMBL; D00097; BAA00060.1;
 DR EMBL; M10944; AAA60302.1;
 DR EMBL; X04608; CAA28275.1;
 DR EMBL; BC007039; AAH07039.1;
 DR EMBL; BC007058; AAH07058.1;
 DR PIR; A03203; YLHUP.
 DR PIR; A24080; A24080.
 DR PIR; A25503; A25503.
 DR PDB; 1SAC; 31-JUL-94.
 DR PDB; 1LGN; 24-DEC-97.

DR GlycoSuiteDB; P02743;
 DR SWISS-2DPAGE; P02743; HUMAN.
 DR Genew; HGNC:584; APCs.
 DR MTM; 104770;
 DR InterPro; IPR001759; Pentaxin.
 DR Pfam; PF00354; Pentaxin; 1.
 DR PRINTS; PR00895; PENTAXIN.
 DR PRODOM; PD002153; Pentaxin; 1.
 DR SMART; SM00159; PTX; 1.
 DR PROSITE; PS00289; PENTAXIN; 1.
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal; Polymorphism;
 KW 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 223
 FT DOMAIN 20 223
 FT DISULFID 55 114
 FT CARBOHYD 51 51
 FT VARIANT 152 152
 FT VARIANT 155 155
 FT VARIANT 158 158
 FT CONFLICT 101 101
 FT SEQUENCE 223 AA; 23387 MW; 6C88A515FE88B393 CRC64;
 SQ
 Query Match 87.9%; Score 29; DB 1; Length 223;
 Best Local Similarity 83.3%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 DB 202 LDWQAL 207
 III II
 RESULT 9
 SAMP_PIG STANDARD; PRT; 224 AA.
 ID SAMP_PIG
 AC 019063;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serum amyloid P-component precursor (SAP).
 GN ACPS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace; TISSUE=Liver;
 RA Ozawa A., Matsumoto M., Kajikawa M., Hanazono M., Yasue H.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
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 CC -----
 DR EMBL; AB005546; BAA21474.1;
 DR HSSP; P02743; 1SAC.
 DR InterPro; IPR001759; Pentaxin.
 DR Pfam; PF00354; Pentaxin; 1.
 DR PRINTS; PR00895; PENTAXIN.

DR ProDom: PD002153; Pentaxin; 1.
 DR SMART; SM00159; PTX; 1.
 DR PROSITE; PS00289; PENTAXIN; 1.
 KW Lentin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 224 SERUM AMYLOID P-COMPONENT.
 FT DOMAIN 20 224 PENTAXIN.
 FT DISULFID 55 114 BY SIMILARITY.
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 224 AA; 25641 MW; 9D1867691EBEDC66 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 224;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDWSAL 6
 DB 203 LDWQAL 208

RESULT 10
 SAMP_MESAU STANDARD; PRT; 234 AA.
 AC P07629;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Serum amyloid P-component precursor (Female protein) (FP) (SAP(FP)).
 GN PTX2 OR SAP.
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94012761; PubMed=7691816;
 RA Rudnick C.M., Dowton S.B.;
 RT "Serum amyloid P (female protein) of the Syrian hamster. Gene
 structure and expression."
 RL J. Biol. Chem. 268:21760-21769(1993).
 RN [2]
 RP SEQUENCE OF 24-234 FROM N.A.
 RX MEDLINE=85218787; PubMed=2408337;
 RA Dowton S.B., Woods D.E., Mantzouranis E.C., Colten H.R.;
 RT "Syrian hamster female protein: analysis of female protein primary
 structure and gene expression."
 RL Science 228:1206-1208(1985).
 RN [3]
 RP SEQUENCE OF 25-48.
 RX MEDLINE=81241327; PubMed=6166709;
 RA Coe J.E., Margossian S.S., Slayter H.S., Sogn J.A.;
 RT "Hamster female protein. A new Pentraxin structurally and
 functionally similar to C-reactive protein and amyloid P component."
 RL J. Exp. Med. 153:977-991(1981).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=95187705; PubMed=7881902;
 RA Srinivasan N., White H.E., Emsley J., Wood S.P., Pepys M.B.,
 RA Blundell T.L.;
 RT "Comparative analyses of pentraxins: implications for protomer
 assembly and ligand binding."
 RL Structure 2:1017-1027(1994).
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
 ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- MISCELLANEOUS: PLASMA CONCENTRATION OF FP ARE ALTERED BY SEX
 STEROIDS AND BY STIMULI THAT ELICIT AN ACUTE PHASE RESPONSE.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L22024; AAA03577.1; -
 DR EMBL; M11342; AAA36980.1; -
 DR PIR; A19828; A19828.
 DR PIR; A44177; A44177.
 DR PIR; A48593; A48593.
 DR PDB; 1HAS; 15-OCT-95.
 DR InterPro: IPR001759; Pentaxin.
 DR Pfam; PF00354; pentaxin; 1.
 DR PRINTS; PR00895; PENTAXIN.
 DR ProDom; PD002153; Pentaxin; 1.
 DR SMART; SM00159; PTX; 1.
 DR PROSITE; PS00289; PENTAXIN; 1.
 KW Lentin; Pentaxin; Plasma; Acute phase; Signal; Amyloid; Glycoprotein;
 KW 3D-structure.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 234 SERUM AMYLOID P-COMPONENT.
 FT DOMAIN 23 234 PENTAXIN.
 FT DISULFID 58 117 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 27 27 T -> S (IN REF. 3).
 FT CONFLICT 43 43 K -> N (IN REF. 3).
 FT CONFLICT 76 76 A -> T (IN REF. 2).
 SQ SEQUENCE 234 AA; 26463 MW; 6161F0383062D2DB CRC64;

Query Match 87.9%; Score 29; DB 1; Length 234;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDWSAL 6
 DB 205 LDWQAL 210

RESULT 11
 CXA6_RAT
 ID CXA6_RAT STANDARD; PRT; 286 AA.
 AC P28233;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gap junction alpha-6 protein (Connexin 33) (Cx33).
 GN GJA6 OR CXN-33.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92112940; PubMed=1370487;
 RA Haefliger J.-A., Bruzzese R., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Paul D.L.;
 RT "Four novel members of the connexin family of gap junction proteins.
 Molecular cloning, expression, and chromosome mapping."
 RL J. Biol. Chem. 267:2057-2064(1992).
 CC -1- FUNCTION: ONE GAP JUNCTION CHANNELS, THE CONNEXONS, THROUGH WHICH
 PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
 MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
 CC -1- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 SUBFAMILY.
 CC
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CC EMBL; M76534; AAA40998.1; -
CC PIR; C42053;
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin.1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT DOMAIN 42 76 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 77 97 POTENTIAL.
FT DOMAIN 98 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 184 POTENTIAL.
FT DOMAIN 185 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 229 POTENTIAL.
FT DOMAIN 230 286 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 286 AA; 32860 MW; A585266ACA2ACCF2 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 DWSAL 6
DB 3 DWSAL 7

RESULT 12
SGBU_ECOLI
ID SGBU_ECOLI STANDARD; PRT; 286 AA.
AC P37679;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative hexulose-6-phosphate isomerase (EC 5.---) (HUMPI).
GN SGBU OR B3582.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes."
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [2]
RP DISCUSSION OF SEQUENCE.
RA Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
RT "Novel phosphotransferases system genes revealed by bacterial genome
analysis: operons encoding homologues of sugar-specific permease
domains of the phosphotransferase system and pentose catabolic
enzymes."
RL Genome Sci. Technol. 1:53-75(1996).
CC -1- FUNCTION: ISOMERIZATION OF D-ARABINO-6-HEXULOSE 3-PHOSPHATE TO
D-FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
SGBH.
CC -1- SIMILARITY: BELONGS TO THE HUMPI FAMILY.
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CC EMBL; U00039; AAB18559.1; ALT_INIT.
DR EMBL; AE000435; AAC76606.1; ALT_INIT.
DR EcoGene; EG12286; sgbu.
DR InterPro; IPR004560; Hx16Piso_put.
DR TIGRFAMS; TIGR00542; hx16Piso_put; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 286 AA; 32455 MW; 4C849F575E937BF9 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 LDWSA 5
DB 48 LDWSA 52

RESULT 13
CYCG_RHOSH
ID CYCG_RHOSH STANDARD; PRT; 296 AA.
AC Q53143;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Diheme cytochrome C-type.
GN CYCG.
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=95362655; PubMed=7543472;
RA Flory J.E., Donohue T.J.;
RT "Organization and expression of the Rhodobacter sphaeroides cycFG
operon."
RL J. Bacteriol. 177:4311-4320(1995).
CC -1- FUNCTION: DIHEME C-TYPE CYTOCHROME, THAT IS PARTICULARLY EXPRESSED
WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C
SUBUNIT.
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Query Match 87.9%; Score 29; DB 1; Length 296;

Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 LDWSA 5
|
|
|
|
Db 241 LDWSA 245

RESULT 14

Y763_TREPA
ID Y763_TREPA STANDARD; PRT; 313 AA.
AC O83744;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0763.
GN TP0763.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Nichols;
RA MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388(1998).

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EMBL; AE001247; AAC65734.1; -
DR TIGR; TP0763; -
DR Hypothetical protein; Transmembrane; Complete proteome.
KW HYPOTHEMETICAL 42 64 POTENTIAL.
FT TRANSMEM 74 96 POTENTIAL.
SQ SEQUENCE 313 AA; 36155 MW; 9B5FC058146E0C58 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSAL 6
|
|
|
|
Db 109 DWSAL 113

RESULT 15

CXAL_XENLA
ID CXAL_XENLA STANDARD; PRT; 378 AA.
AC P16863;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gap junction alpha-1 protein (Connexin 43) (Cx43).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

SEQUENCE FROM N.A.

RP TISSUE-Ovary;
RX MEDLINE=90171034; PubMed=2155241;
RA Glimich R.L., Kumar N.M., Gilula N.B.;
RT "Differential regulation of the levels of three gap junction mRNAs in
RT xenopus embryos.";
RL J. Cell Biol. 110:597-605(1990).
CC -|- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
CC -|- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. HIGHEST LEVELS
CC FOUND IN EYE AND BRAIN.
CC -|- DEVELOPMENTAL STAGE: APPEARS DURING ORGANOCENESIS.
CC -|- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.

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EMBL; X17243; CAA35108.1; -
DR PIR; A34575; A34575.
DR InterPro; IPR000500; Connexin.
DR InterPro; IPR002261; Connexin43.
DR Pfam; PF00029; connexin; 1.
DR Pfam; PF03508; Connexin43; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 43 POTENTIAL.
FT DOMAIN 44 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 96 POTENTIAL.
FT DOMAIN 97 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 227 POTENTIAL.
FT DOMAIN 228 378 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 378 AA; 42830 MW; 6E59117B04A94FE4 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSAL 6
|
|
|
|
Db 2 DWSAL 6

Search completed: May 30, 2003, 15:48:59
Job time : 4.11842 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDWSAL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	516	4	US-09-277-262-2
2	30	90.9	1891	2	US-08-804-227C-12
3	30	90.9	1891	2	US-08-804-198-6
4	29	87.9	201	1	US-07-929-580B-5
5	29	87.9	223	1	US-07-708-885B-3
6	29	87.9	223	1	US-07-714-386-3
7	29	87.9	223	1	US-07-708-888A-3
8	29	87.9	297	4	US-09-172-952-30
9	29	87.9	345	3	US-08-858-003-34
10	29	87.9	345	3	US-09-078-166-34
11	29	87.9	345	4	US-08-997-467-34
12	29	87.9	1580	2	US-08-804-227C-11
13	29	87.9	1580	2	US-08-804-198-5
14	29	87.9	3729	2	US-08-804-227C-4
15	28	84.8	208	1	US-08-631-607-3
16	28	84.8	208	4	US-09-098-358B-3
17	28	84.8	1843	4	US-09-413-814-50
18	28	84.8	2595	4	US-09-036-987A-2
19	28	84.8	2595	4	US-09-370-700-2
20	28	84.8	3248	1	US-08-353-700-1
21	28	84.8	3248	5	PCT-US95-16216-1
22	27	81.8	29	4	US-09-082-279B-1276
23	27	81.8	29	4	US-09-315-304B-1276
24	27	81.8	35	4	US-09-082-279B-1427
25	27	81.8	35	4	US-09-315-304B-1427
26	27	81.8	45	3	US-09-040-285A-9
27	27	81.8	80	3	US-09-040-285A-3

28	27	81.8	209	3	US-09-040-285A-8	Sequence 8, Appli
29	27	81.8	229	3	US-09-040-285A-7	Sequence 7, Appli
30	27	81.8	319	4	US-09-044-796A-13	Sequence 13, Appli
31	27	81.8	319	4	US-09-725-460A-13	Sequence 13, Appli
32	27	81.8	360	1	US-08-456-923-21	Sequence 21, Appli
33	27	81.8	360	4	US-09-025-769B-293	Sequence 293, App
34	27	81.8	360	5	PCT-US93-01676A-2	Sequence 2, Appli
35	27	81.8	370	5	PCT-US93-01676A-4	Sequence 4, Appli
36	27	81.8	396	4	US-08-861-774E-90	Sequence 90, Appli
37	27	81.8	441	4	US-09-522-666-4	Sequence 4, Appli
38	27	81.8	452	4	US-09-277-262-4	Sequence 8, Appli
39	27	81.8	497	4	US-09-277-262-4	Sequence 4, Appli
40	27	81.8	680	2	US-08-674-351-2	Sequence 2, Appli
41	27	81.8	726	6	5208144-37	Patent No. 5208144
42	27	81.8	1024	4	US-09-522-666-2	Sequence 2, Appli
43	27	81.8	1049	4	US-09-522-666-6	Sequence 6, Appli
44	27	81.8	1346	3	US-09-320-878-4	Sequence 4, Appli
45	27	81.8	1346	4	US-09-105-537-37	Sequence 37, Appli

ALIGNMENTS

RESULT 1
US-09-277-262-2
; Sequence 2, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayilgou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-262-2

Query Match 90.9%; Score 30; DB 4; Length 516;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 231 LDWSSL 236

RESULT 2
US-08-804-227C-12
; Sequence 12, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Khstoss, Stuart A.
; APPLICANT: Rostock, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-227C-12

Query Match 90.9%; Score 30; DB 2; Length 1891;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 904 LDWAAL 909

RESULT 3
US-08-804-198-6
Sequence 6, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-6

Query Match 90.9%; Score 30; DB 2; Length 1891;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 904 LDWAAL 909

RESULT 4
US-07-929-580B-5
Sequence 5, Application US/07929580B
Patent No. 5426181
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Lee, Gene W.
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929.580B
FILING DATE: 19920814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/640.492
FILING DATE: 14-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Guy Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: LEE25\VLCEK-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-929-580B-5

Query Match 87.9%; Score 29; DB 1; Length 201;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 180 LDWAAL 185

RESULT 5
US-07-708-885B-3
Sequence 3, Application US/07708885B
Patent No. 5245017
GENERAL INFORMATION:
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
APPLICANT: Toth, Carol A.

APPLICANT: Thomas, Peter
TITLE OF INVENTION: Method for Isolating
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,885B
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zon, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
JOURNAL: J. of Biological Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-708-885B-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LDWSAL 6
Db 202 LDWQAL 207

RESULT 6
US-07-714-386-3
Sequence 3, Application US/07714386
Patent No. 5278290
GENERAL INFORMATION:
APPLICANT: Thomas, Peter
APPLICANT: Toth, Carol A.
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
TITLE OF INVENTION: Binding Protein for
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,386
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zon, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
JOURNAL: J. of Biological Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-714-386-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LDWSAL 6
Db 202 LDWQAL 207

RESULT 7
US-07-708-888A-3
Sequence 3, Application US/07708888A
Patent No. 5281697
GENERAL INFORMATION:
APPLICANT: Toth, Carol A.
APPLICANT: Thomas, Peter
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
TITLE OF INVENTION: CEA-Binding Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/708.888A
FILING DATE: 19910531
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zon, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
TITLE: C-reactive Protein
JOURNAL: Journal of Biological
JOURNAL: Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-708-888A-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 202 LDWQAL 207

RESULT 8
US-09-172-952-30
Sequence 30, Application US/09172952
Patent No. 6368793
GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172.952
CURRENT FILING DATE: 1998-10-14.
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 297
TYPE: PRT
ORGANISM: Yiar-Ec
US-09-172-952-30

Query Match 87.9%; Score 29; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSA 5
Db 59 LDWSA 63

RESULT 9
US-08-858-003-34
Sequence 34, Application US/08858003
Patent No. 6060234

GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaolan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858.003
FILING DATE: 16-MAY-1979
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40.943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6060234e
US-08-858-003-34

Query Match 87.9%; Score 29; DB 3; Length 345;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 43 LDWSVL 48

RESULT 10
US-09-078-166-34
Sequence 34, Application us/09078166
Patent No. 6063561
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaolan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park

STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,166
FILING DATE: 16-MAY-1979
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6063561e
US-09-078-166-34

Query Match 87.9%; Score 29; DB 3; Length 345;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 43 LDWSVL 48

RESULT 11
US-08-997-467-34
Sequence 34, Application US/08997467
Patent No. 6200813
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaocan
APPLICANT: Pereda-Lopez, Ana
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,467
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/858,003

FILING DATE: 16-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6200813e
US-08-997-467-34
Query Match 87.9%; Score 29; DB 4; Length 345;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 43 LDWSVL 48

RESULT 12
US-08-804-227C-11
Sequence 11, Application US/08804227C
Patent No. 5878991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rostock, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1580 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-227C-11

Query Match 87.9%; Score 29; DB 2; Length 1580;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6

Db 604 LDWSVL 609

RESULT 13
US-08-804-198-5
; Sequence 5, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rostock, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.198
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1580 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-5

Query Match 87.9%; Score 29; DB 2; Length 1580;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 604 LDWSVL 609

RESULT 14
US-08-804-227C-4
; Sequence 4, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rostock, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3729 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-804-227C-4

Query Match 87.9%; Score 29; DB 2; Length 3729;
Best Local Similarity 83.3%; Pred. No. 6.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 2135 LDWSVL 2140

RESULT 15
US-08-631-607-3
; Sequence 3, Application US/08631607
; Patent No. 5767252
; GENERAL INFORMATION:
; APPLICANT: Worley et al, Paul
; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631.607
FILING DATE: 08-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/086001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-631-607-3

Query Match 84.8%; Score 28; DB 1; Length 208;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
 |||
Db 183 LDWRAL 188

Search completed: May 30, 2003, 14:41:30
Job time : 7.03947 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDWSAL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	6	23	Mutated IKKbeta NE
2	33	100.0	6	23	NBD mutant peptide
3	33	100.0	756	23	Human IKKbeta muta
4	31	93.9	53	21	Region A of protei
5	31	93.9	53	22	Protein kinase der
6	31	93.9	77	22	3-phosphoinositide
7	31	93.9	315	22	AGC protein kinase
8	31	93.9	345	22	Drosophila melanog
9	31	93.9	385	22	AGC protein kinase
10	31	93.9	652	22	Drosophila melanog

11	31	93.9	984	21	AAV94736
12	31	93.9	984	23	AAQ15489
13	30	90.9	53	21	Arabidopsis thalia
14	30	90.9	57	21	Arabidopsis thalia
15	30	90.9	124	22	ABG67643
16	30	90.9	516	23	ABB79577
17	30	90.9	536	22	ABG22095
18	30	90.9	631	22	ABG22094
19	30	90.9	1891	18	AAW23720
20	30	90.9	1891	18	AAW22610
21	29	87.9	35	22	AAO08947
22	29	87.9	98	21	AAO00108
23	29	87.9	129	22	AAU43320
24	29	87.9	134	22	AAU48444
25	29	87.9	204	16	AAU47463
26	29	87.9	210	16	AAU47469
27	29	87.9	223	13	AAU29923
28	29	87.9	254	21	AAU52497
29	29	87.9	255	21	AAU52496
30	29	87.9	292	21	AAU52495
31	29	87.9	292	22	ABG52479
32	29	87.9	302	23	ABG49167
33	29	87.9	345	20	AAW87715
34	29	87.9	345	21	AAU12927
35	29	87.9	352	20	AAU35284
36	29	87.9	361	22	AAU49927
37	29	87.9	382	19	AAU23969
38	29	87.9	382	23	ABP61480
39	29	87.9	382	23	ABP61481
40	29	87.9	394	22	ABG62389
41	29	87.9	414	20	AAU37671
42	29	87.9	441	22	ABG60529
43	29	87.9	441	22	ABG60529
44	29	87.9	464	22	ABG60227
45	29	87.9	471	22	ABG70575

ALIGNMENTS

RESULT 1

ABB08735

ID ABB08735 standard; peptide; 6 AA.

XX ABB08735;

AC

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 13.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; auto-immune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive; osteopathic; cytotoxic; neutropenic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antisthmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antitumor; mutant; mutagen.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 5 /note= "Wildtype Trp substituted by Ala"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-USA0654.

XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYVA) UNIV YALE.
 XX May MJ, Ghosh S;
 PI WPI; 2002-179350/23.
 DR
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 XX Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 33; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 1 LDWSAL 6
 |||||
 |||||
 RESULT 2
 AAM48518
 ID AAM48518 standard; Peptide; 6 AA.
 XX
 AC AAM48518;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 13.
 XX

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antiviral; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Example 6; Page 48; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 33; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 1 LDWSAL 6
 |||||
 |||||
 RESULT 3
 ABB77299
 ID ABB77299 standard; protein; 756 AA.
 XX

AC ABB77299;
 XX
 DT 14-JUN-2002 (first entry)
 XX
 DE Human IKKbeta mutant W741A.
 XX
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 741 /note= "Wildtype Trp substituted by Ala"
 FT
 XX
 XX W0200183547-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYUA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 XX inflammatory disorders, osteoporosis and cancer, comprises contacting a
 XX cell with an anti-inflammatory compound comprising at least one NEMO
 XX binding domain -
 XX
 XX Example 11; Page -; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of I-kappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. O14920 (ABB77294).
 XX
 SQ Sequence 756 AA;
 Query Match 100.0%; Score 33; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 DB 737 LDWSAL 742
 |||||
 RESULT 4
 AAY94732
 ID AAY94732 standard; peptide; 53 AA.
 XX
 AC AAY94732;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Region A of protein kinase C related protein kinase 2.
 XX
 KW Substrate specificity; phosphoinositide-dependent protein kinase 1;
 KW PK1; protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
 KW mechanical tissue damage; ischaemic disease; stroke;
 KW myocardial infarction; antigenic peptide.
 XX
 OS Unidentified.
 OS
 PN W0200056864-A2.
 XX
 XX 28-SEP-2000.
 XX
 XX 17-MAR-2000; 2000WO-GB01004.
 XX
 XX 19-MAR-1999; 99GB-0006245.
 XX
 XX (UYDU-) UNIV DUNDEE.
 XX
 XX Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 XX
 XX WPI; 2000-647155/62.
 XX
 XX Altering substrate specificity of phosphoinositide-dependent protein
 XX kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 XX interacting polypeptide -
 XX
 XX Disclosure; Page 12; 103pp; English.
 XX
 CC This invention relates to a method for altering the substrate
 CC specificity of phosphoinositide-dependent protein kinase 1 (PK1), by
 CC exposing it to an interacting polypeptide. Included in the invention are
 CC a preparation comprising PK1 and an interacting polypeptide, PK1 with
 CC altered specificity is useful for phosphorylating a residue corresponding
 CC to the Ser/Thr residue of a substrate with the following peptide
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PK1 is also used for
 CC phosphorylating protein kinase C related protein kinase 2 (PRK2). The
 CC compound identified by methods of the invention that are capable of
 CC altering the substrate specificity of PK1 are useful for manufacturing a
 CC medicament for treating a patient who is in need of modulation of the
 CC insulin signalling pathway and/or PK1, PK2 or PK2 signalling. A
 CC compound that is capable of reducing the activity (i.e. the PK1 and/or
 CC the PK2 activity) of PK1 may be useful in treating cancer. PK1,
 CC e.g. via protein kinase B and/or SGK, may be capable of providing a

CC survival signal that protects cells from apoptosis induced in a variety
 CC of ways. Reduction of the activity of PK1 may promote apoptosis and may
 CC be useful in treating cancer. Conditions in which aiding apoptosis may be
 CC of benefit may also include resolution of inflammation. A compound
 CC capable of increasing the activity of PK1 may be useful in treating
 CC diabetes or obesity, or may be useful in inhibiting apoptosis. Increased
 CC activity of PK1 may lead to increased levels of leptin, which may lead
 CC to weight loss. The compounds may suppress apoptosis, which may aid cell
 CC survival during or following cell damaging processes and in treating
 CC disease in which apoptosis is involved. Examples of the diseases include,
 CC mechanical (including heat) tissue injury or ischaemic disease, for
 CC example stroke and myocardial infarction, or neural injury. The present
 CC sequence represents a region of protein kinase C related protein kinase
 CC 2 (PRK2) which interacts with PK1.

XX
 SQ Sequence 53 AA;
 Query Match 93.9%; Score 31; DB 21; Length 53;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db :|||||
 12 IDWSAL 17

RESULT 5
 AAB99802
 ID AAB99802 standard; Peptide; 53 AA.
 AC AAB99802;
 XX
 DT 20-SEP-2001 (first entry)
 DE Protein kinase derived interacting peptide #4.
 DE
 KW Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200144497-A2.
 PD 21-JUN-2001.
 XX
 PF 04-DEC-2000; 2000WO-GB04598.
 XX
 PR 02-DEC-1999; 99US-0168559.
 XX
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Alessi D, Biondi R;
 XX
 DR WPI; 2001-390252/41.
 XX
 PT Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -
 XX
 PS Disclosure; Page 25; 180pp; English.

XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing

CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AA44210 and AA44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 53 AA;
 Query Match 93.9%; Score 31; DB 22; Length 53;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db :|||||
 12 IDWSAL 17

RESULT 6
 AAB99793
 ID AAB99793 standard; Peptide; 77 AA.
 AC AAB99793;
 XX
 DT 20-SEP-2001 (first entry)
 DE 3-phosphoinositide-dependent protein kinase 1 binding peptide P1F.
 DE
 KW Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200144497-A2.
 PD 21-JUN-2001.
 XX
 PF 04-DEC-2000; 2000WO-GB04598.
 XX
 PR 02-DEC-1999; 99US-0168559.
 XX
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Alessi D, Biondi R;
 XX
 DR WPI; 2001-390252/41.
 XX
 PT Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -
 XX
 PS Disclosure; Page 22; 180pp; English.

XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing

CC protein kinase. Specifically, the patient has cancer or diabetes or is
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischaemic injury, including stroke. The compound or
CC composition is also useful for inhibiting the degree or rate of
CC phosphorylation by the protein kinase. The interacting polypeptide or
CC compound is useful in methods of stabilising a hydrophobic pocket-
CC containing protein kinase, where the protein kinase is exposed to the
CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
CC used in the exemplification of the present invention.
XX
SQ Sequence 77 AA;

Query Match 93.9%; Score 31; DB 22; Length 77;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 12 IDWSAL 17

RESULT 7
AAB99835
ID AAB99835 standard; Protein; 315 AA.

XX AC AAB99835;
XX DT 20-SEP-2001 (first entry)
XX DE AGC protein kinase family member PRK2 protein sequence.

XX KW Protein kinase; identification; hydrophobic pocket; interacting;
XX KW cancer; diabetes; inhibition; apoptosis; tissue injury;
XX KW ischaemic injury; stroke.

XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200144497-A2.

XX PD 21-JUN-2001.
XX PF 04-DEC-2000; 2000WO-GB04598.
XX PR 02-DEC-1999; 99US-0168559.

XX PA (UYDU-) UNIV DUNDEE.
XX PI Alessi D, Biondi R;

XX WPI; 2001-390252/41.

XX PT Identifying modulators of protein kinase (PK) activity, useful in
XX PT developing drugs for treating cancer or diabetes, by measuring the
XX PT ability of the compound to modulate or mimic the interaction of PK with
XX PT interacting polypeptides -

XX PS Disclosure; Fig 16; 180pp; English.

XX CC The present invention describes a method for identifying a compound that
XX CC modulates protein kinase activity. The method comprises measuring the
XX CC ability of the compound to inhibit, promote or mimic the interaction of
XX CC a hydrophobic pocket-containing protein kinase with an interacting
XX CC polypeptide. The interacting polypeptide interacts with the hydrophobic
XX CC pocket of the protein kinase and/or comprises the amino acid sequence
XX CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
XX CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
XX CC or polynucleotides from the present invention are useful in medicine,
XX CC particularly in the manufacture of a medicament for treating a patient
XX CC in need of modulation of signalling by a hydrophobic pocket-containing
XX CC protein kinase. Specifically, the patient has cancer or diabetes or is
XX CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue

CC injury or ischaemic injury, including stroke. The compound or
CC composition is also useful for inhibiting the degree or rate of
CC phosphorylation by the protein kinase. The interacting polypeptide or
CC compound is useful in methods of stabilising a hydrophobic pocket-
CC containing protein kinase, where the protein kinase is exposed to the
CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
CC used in the exemplification of the present invention.
XX
SQ Sequence 315 AA;

Query Match 93.9%; Score 31; DB 22; Length 315;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 250 IDWSAL 255

RESULT 8
ABB63738
ID ABB63738 standard; Protein; 345 AA.

XX AC ABB63738;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 18006.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL07841.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -

XX PS Disclosure; SEQ ID NO 18006; 2lpp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).

XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 345 AA;

Query Match 93.9%; Score 31; DB 22; Length 345;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 136 LDWSAI 141

RESULT 9
AAB99822
ID AAB99822 standard; Protein; 385 AA.

XX AC AAB99822;
XX DT 20-SEP-2001 (first entry)
XX XX

DE AGC protein kinase family member PRK2 protein sequence.

XX Protein kinase; identification; hydrophobic pocket; interacting;
KW cancer; diabetes; inhibition; apoptosis; tissue injury;
KW ischaemic injury; stroke.

XX OS Homo sapiens.
OS Synthetic.

XX WO200144497-A2.

XX 21-JUN-2001.

XX 04-DEC-2000; 2000WO-GB04598.

XX 02-DEC-1999; 99US-0168559.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Biondi R;

XX WPI; 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides -

PS Disclosure; Fig 15; 180pp; English.

XX The present invention describes a method for identifying a compound that
modulates protein kinase activity. The method comprises measuring the
ability of the compound to inhibit, promote or mimic the interaction of
a hydrophobic pocket-containing protein kinase with an interacting
polypeptide. The interacting polypeptide interacts with the hydrophobic
pocket of the protein kinase and/or comprises the amino acid sequence
Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
for developing pharmaceutical compounds or drugs. Compounds, polypeptides
or polynucleotides from the present invention are useful in medicine,
particularly in the manufacture of a medicament for treating a patient
in need of modulation of signalling by a hydrophobic pocket-containing
protein kinase. Specifically, the patient has cancer or diabetes or is
in need of inhibition of apoptosis, e.g. a patient suffering from tissue
injury or ischaemic injury, including stroke. The compound or
composition is also useful for inhibiting the degree or rate of
phosphorylation by the protein kinase. The interacting polypeptide or
compound is useful in methods of stabilising a hydrophobic pocket-
containing protein kinase, where the protein kinase is exposed to the
compound or polypeptide. AAB99822 to AAB99847 represent amino acid
sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
used in the exemplification of the present invention.

XX Sequence 385 AA;

Query Match 93.9%; Score 31; DB 22; Length 385;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 320 LDWSAL 325

RESULT 10
ABB59094
ID ABB59094 standard; Protein; 652 AA.

XX AC ABB59094;
XX DT 26-MAR-2002 (first entry)
XX XX

XX Drosophila melanogaster polypeptide SEQ ID NO 4074.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL03197.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

PS Disclosure; SEQ ID NO 4074; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins
(ABB57737-ABB72072).

XX The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 652 AA;

Query Match 93.9%; Score 31; DB 22; Length 652;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 447 LDWSAM 452

RESULT 11
AAI94736
ID AAI94736 standard; Protein; 984 AA.

XX AC AAI94736;

XX DT 29-JAN-2001 (first entry)
XX XX

DE Protein kinase C related protein kinase 2.
 XX Substrate specificity; phosphoinositide-dependent protein kinase 1;
 KW PDK1; protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
 KW mechanical tissue damage; ischemic disease; stroke;
 KW myocardial infarction; antigenic peptide.
 KW Unidentified.
 OS
 XX WO200056864-A2.
 PN
 XX 28-SEP-2000.
 PD
 XX
 XX 17-MAR-2000; 2000WO-CB01004.
 PF
 XX 19-MAR-1999; 99GB-0006245.
 XX (UYDU-) UNIV DUNDEE.
 PA
 XX Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 PI
 XX WPI; 2000-647155/62.
 DR
 XX Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide.
 PT
 XX Disclosure; Fig 11; 103pp; English.
 PS
 XX This invention relates to a method for altering the substrate
 CC specificity of phosphoinositide-dependent protein kinase 1 (PKD1), by
 CC exposing it to an interacting polypeptide. Included in the invention are
 CC a preparation comprising PKD1 and an interacting polypeptide, PKD1 with
 CC altered specificity is useful for phosphorylating a residue corresponding
 CC to the Ser/Thr residue of a substrate with the following peptide
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PKD1 is also used for
 CC phosphorylating protein kinase C related protein kinase 2 (PRK2). The
 CC compound identified by methods of the invention that are capable of
 CC altering the substrate specificity of PKD1 are useful for manufacturing a
 CC medicament for treating a patient who is in need of modulation of the
 CC insulin signalling pathway and/or PKD1, PKD2 or PRK2 signalling. A
 CC compound that is capable of reducing the activity (i.e. the PKD1 and/or
 CC the PKD2 activity) of PKD1 may be useful in treating cancer. PKD1, e.g.
 CC via protein kinase B and/or SGK, may be capable of providing a survival
 CC signal that protects cells from apoptosis induced in a variety of ways.
 CC Reduction of the activity of PKD1 may promote apoptosis and may be useful
 CC in treating cancer. Conditions in which aiding apoptosis may be benefit
 CC may also include resolution of inflammation. A compound capable of
 CC increasing the activity of PKD1 may be useful in treating diabetes or
 CC obesity, or may be useful in inhibiting apoptosis. Increased activity of
 CC PKD1 may lead to increased levels of leptin, which may lead to weight
 CC loss. The compounds may suppress apoptosis, which may aid cell survival
 CC during or following cell damaging processes and in treating disease in
 CC which apoptosis is involved. Examples of the diseases include, mechanical
 CC (including heat) tissue injury or ischaemic disease, for example stroke
 CC and myocardial infarction, or neural injury. The present sequence
 CC represents a protein kinase C related protein kinase 2 amino acid
 CC sequence, used in the course of the invention.
 SX
 SQ Sequence 984 AA;
 Query Match 93.9%; Score 31; DB 21; Length 984;
 Best Local Similarity 83.3%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 919 IDWSAL 924
 RESULT 13
 AAG56197
 ID AAG56197 standard; Protein; 53 AA.
 XX
 AC AAG56197;
 XX
 DT 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 72196.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS

XX AAO15489;
 AC
 XX 03-OCT-2002 (first entry)
 DT
 XX Human serin-threonin-kinase PRK2.
 DE
 XX Human; DHAM-kinase inhibitor; guanylate kinase 1; PRK2;
 KW deregulated in hyperactive macrophage kinase inhibitor; GUK1;
 KW serin-threonin-kinase; PAK2; inflammatory condition;
 KW chronic inflammatory airway disease; chronic bronchitis;
 KW chronic obstructive pulmonary disease; COPD.
 XX
 OS Homo sapiens.
 XX WO200252036-A2.
 PN
 XX 04-JUL-2002.
 PD
 XX 15-DEC-2001; 2001WO-EPL4844.
 PF
 XX 22-DEC-2000; 2000US-257854P.
 XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
 PA
 XX Jung B, Mueller S, Kraut N;
 PI
 XX WPI; 2002-583570/62.
 DR N-PSDB; AAL44147.
 DR
 XX Determining activators or inhibitors of 'deregulated in hyperactive
 PT macrophage' (DHAM)-kinase for treating chronic inflammatory airway
 PT diseases, by measuring DHAM-kinase function after it is contacted with
 PT a test substance
 PT
 XX Claim 8; Page 41-47; 48pp; English.
 PS
 XX The invention comprises a method for determining whether a substance is
 CC an activator or an inhibitor of a DHAM-kinase (deregulated in hyperactive
 CC macrophage kinase). DHAM-kinases used in the invention include guanylate
 CC kinase 1 (GUK1), serin-threonin-kinase PAK2 and serin-threonin-kinase
 CC PRK2. The method of the invention is useful for identifying substances
 CC that influence inflammatory conditions of chronic inflammatory airway
 CC diseases (e.g. chronic bronchitis or chronic obstructive pulmonary
 CC disease - COPD). The present amino acid sequence represents the human
 CC serin-threonin-kinase PRK2.
 XX
 SQ Sequence 984 AA;
 Query Match 93.9%; Score 31; DB 23; Length 984;
 Best Local Similarity 83.3%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 919 IDWSAL 924
 RESULT 13
 AAG56197
 ID AAG56197 standard; Protein; 53 AA.
 XX
 AC AAG56197;
 XX
 DT 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 72196.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS

XX	EP1033405-A2.	PR	01-JUL-1999;	99US-0141842.
XX	06-SEP-2000.	PR	01-JUL-1999;	99US-0142154.
XX	25-FEB-2000; 2000EP-0301439.	PR	02-JUL-1999;	99US-0142055.
XX	25-FEB-1999;	PR	06-JUL-1999;	99US-0142390.
XX	05-MAR-1999;	PR	08-JUL-1999;	99US-0142803.
XX	09-MAR-1999;	PR	09-JUL-1999;	99US-0142920.
XX	23-MAR-1999;	PR	12-JUL-1999;	99US-0142977.
XX	25-MAR-1999;	PR	13-JUL-1999;	99US-0143542.
XX	29-MAR-1999;	PR	14-JUL-1999;	99US-0143624.
XX	01-APR-1999;	PR	15-JUL-1999;	99US-0144005.
XX	06-APR-1999;	PR	16-JUL-1999;	99US-0144085.
XX	08-APR-1999;	PR	19-JUL-1999;	99US-0144086.
XX	16-APR-1999;	PR	19-JUL-1999;	99US-0144331.
XX	19-APR-1999;	PR	19-JUL-1999;	99US-0144332.
XX	21-APR-1999;	PR	19-JUL-1999;	99US-0144333.
XX	23-APR-1999;	PR	19-JUL-1999;	99US-0144334.
XX	28-APR-1999;	PR	19-JUL-1999;	99US-0144335.
XX	30-APR-1999;	PR	20-JUL-1999;	99US-0144352.
XX	04-MAY-1999;	PR	20-JUL-1999;	99US-0144632.
XX	05-MAY-1999;	PR	20-JUL-1999;	99US-0144884.
XX	06-MAY-1999;	PR	21-JUL-1999;	99US-0144814.
XX	07-MAY-1999;	PR	21-JUL-1999;	99US-0145086.
XX	11-MAY-1999;	PR	21-JUL-1999;	99US-0145088.
XX	14-MAY-1999;	PR	22-JUL-1999;	99US-0145085.
XX	14-MAY-1999;	PR	22-JUL-1999;	99US-0145087.
XX	14-MAY-1999;	PR	22-JUL-1999;	99US-0145089.
XX	18-MAY-1999;	PR	22-JUL-1999;	99US-0145192.
XX	19-MAY-1999;	PR	23-JUL-1999;	99US-0145145.
XX	20-MAY-1999;	PR	23-JUL-1999;	99US-0145218.
XX	21-MAY-1999;	PR	23-JUL-1999;	99US-0145224.
XX	24-MAY-1999;	PR	26-JUL-1999;	99US-0145276.
XX	25-MAY-1999;	PR	27-JUL-1999;	99US-0145913.
XX	27-MAY-1999;	PR	27-JUL-1999;	99US-0145918.
XX	01-JUN-1999;	PR	27-JUL-1999;	99US-0145919.
XX	03-JUN-1999;	PR	28-JUL-1999;	99US-0145951.
XX	04-JUN-1999;	PR	02-AUG-1999;	99US-0146386.
XX	07-JUN-1999;	PR	02-AUG-1999;	99US-0146388.
XX	08-JUN-1999;	PR	02-AUG-1999;	99US-0146389.
XX	10-JUN-1999;	PR	03-AUG-1999;	99US-0147038.
XX	10-JUN-1999;	PR	04-AUG-1999;	99US-0147204.
XX	14-JUN-1999;	PR	04-AUG-1999;	99US-0147302.
XX	16-JUN-1999;	PR	05-AUG-1999;	99US-0147192.
XX	16-JUN-1999;	PR	05-AUG-1999;	99US-0147260.
XX	17-JUN-1999;	PR	06-AUG-1999;	99US-0147303.
XX	18-JUN-1999;	PR	06-AUG-1999;	99US-0147416.
XX	18-JUN-1999;	PR	09-AUG-1999;	99US-0147493.
XX	18-JUN-1999;	PR	09-AUG-1999;	99US-0147935.
XX	18-JUN-1999;	PR	10-AUG-1999;	99US-0148171.
XX	18-JUN-1999;	PR	11-AUG-1999;	99US-0148319.
XX	18-JUN-1999;	PR	12-AUG-1999;	99US-0148341.
XX	18-JUN-1999;	PR	13-AUG-1999;	99US-0148565.
XX	18-JUN-1999;	PR	13-AUG-1999;	99US-0148684.
XX	18-JUN-1999;	PR	16-AUG-1999;	99US-0149368.
XX	18-JUN-1999;	PR	17-AUG-1999;	99US-0149175.
XX	18-JUN-1999;	PR	18-AUG-1999;	99US-0149426.
XX	18-JUN-1999;	PR	20-AUG-1999;	99US-0149722.
XX	18-JUN-1999;	PR	20-AUG-1999;	99US-0149723.
XX	18-JUN-1999;	PR	20-AUG-1999;	99US-0149929.
XX	18-JUN-1999;	PR	23-AUG-1999;	99US-0149902.
XX	18-JUN-1999;	PR	23-AUG-1999;	99US-0149930.
XX	18-JUN-1999;	PR	25-AUG-1999;	99US-0150366.
XX	18-JUN-1999;	PR	26-AUG-1999;	99US-0150884.
XX	18-JUN-1999;	PR	27-AUG-1999;	99US-0151065.
XX	21-JUN-1999;	PR	27-AUG-1999;	99US-0151066.
XX	21-JUN-1999;	PR	27-AUG-1999;	99US-0151080.
XX	23-JUN-1999;	PR	30-AUG-1999;	99US-0151303.
XX	23-JUN-1999;	PR	31-AUG-1999;	99US-0151438.
XX	24-JUN-1999;	PR	01-SEP-1999;	99US-0151930.
XX	28-JUN-1999;	PR	07-SEP-1999;	99US-0152363.
XX	29-JUN-1999;	PR	10-SEP-1999;	99US-0153070.
XX	30-JUN-1999;	PR	13-SEP-1999;	99US-0153758.
XX		PR	15-SEP-1999;	99US-0154018.

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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 90.9%; Score 30; DB 21; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 30 VDWSAL 35

RESULT 14
AAG56196
ID AAG56196 standard; Protein; 57 AA.
XX AC
XX AAG56196;
XX DT 18-OCT-2000 (first entry)
XX DE
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 72195.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132566.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
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 Db 34 VDWSAL 39

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 KW pharmaceutical.
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR

DR N-PSDB; ABL11746.
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 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 29721; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
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 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 Db 49 LDWSAV 54
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds.
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Title: US-09-643-260-12

Perfect score: 36

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Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	36	100.0	8	9	US-09-847-946A-92
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7	36	100.0	9	9	US-09-847-946A-91
8	36	100.0	9	9	US-09-847-946A-94
9	36	100.0	9	9	US-09-847-946A-97
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21	88.9	32	88.9	9	9	US-09-847-946A-80	Sequence 80, Appl
22	88.9	32	88.9	9	9	US-09-847-946A-83	Sequence 83, Appl
23	88.9	32	88.9	9	9	US-09-847-946A-86	Sequence 86, Appl
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26	88.9	32	88.9	10	9	US-09-847-946A-85	Sequence 85, Appl
27	88.9	32	88.9	11	9	US-09-847-946A-79	Sequence 79, Appl
28	88.9	32	88.9	69	10	US-09-864-761-36612	Sequence 36612, A
29	88.9	32	88.9	71	9	US-09-969-730-172	Sequence 172, App
30	88.9	32	88.9	72	9	US-09-774-639-171	Sequence 171, App
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35	86.1	31	86.1	8	9	US-09-847-946A-30	Sequence 30, Appl
36	86.1	31	86.1	8	9	US-09-847-946A-38	Sequence 38, Appl
37	86.1	31	86.1	9	9	US-09-847-946A-29	Sequence 29, Appl
38	86.1	31	86.1	9	9	US-09-847-946A-32	Sequence 32, Appl
39	86.1	31	86.1	9	9	US-09-847-946A-35	Sequence 35, Appl
40	86.1	31	86.1	9	9	US-09-847-946A-36	Sequence 36, Appl
41	86.1	31	86.1	10	9	US-09-847-946A-31	Sequence 31, Appl
42	86.1	31	86.1	10	9	US-09-847-946A-34	Sequence 34, Appl
43	86.1	31	86.1	11	9	US-09-847-946A-28	Sequence 28, Appl
44	86.1	31	86.1	11	9	US-09-847-946A-132	Sequence 132, App
45	86.1	31	86.1	11	9	US-09-847-946A-140	Sequence 140, App

ALIGNMENTS

RESULT 1
US-09-847-940B-12
; Sequence 12, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847, 940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
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; TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-12

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Db 1 LDYSLW 6

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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-12

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QY 1 LDYSWL 6
Db 1 LDYSWL 6

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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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US-09-847-946A-95

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-847-946A-99
; Sequence 99, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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US-09-847-946A-99

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QY 1 LDYSWL 6
Db 1 LDYSWL 6

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US-09-847-946A-92
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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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US-09-847-946A-92

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; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
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US-09-847-946A-100

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Qy 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 7

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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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US-09-847-946A-91

Query Match 100.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 8

US-09-847-946A-94

; Sequence 94, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-94

Query Match 100.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 9

US-09-847-946A-97
; Sequence 97, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-97

Query Match 100.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
Db 3 LDYSWL 8

RESULT 10

US-09-847-946A-98
; Sequence 98, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-98

Query Match 100.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
Db 2 LDYSWL 7

RESULT 11

US-09-847-946A-93
; Sequence 93, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-93

Query Match 100.0%; Score 36; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6

Db 2 LDYSWL 7

RESULT 12

US-09-847-946A-96
; Sequence 96, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-96

Query Match 100.0%; Score 36; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
Db 3 LDYSWL 8

RESULT 13

US-09-847-946A-90
; Sequence 90, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-90

Query Match 100.0%; Score 36; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 LDFS WL 6

QY 1 LDY SWL 6
|||||
Db 3 LDY SWL 8Search completed: May 30, 2003, 15:53:19
Job time : 11.4605 secs

RESULT 14

US-09-847-940B-11
; Sequence 11, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-11

Query Match 88.9%; Score 32; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY SWL 6
|||||
Db 1 LDFS WL 6

RESULT 15

US-09-847-946A-11
; Sequence 11, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-11

Query Match 88.9%; Score 32; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY SWL 6
|||||

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds
(without alignments)
83.741 Million cell updates/sec

Title: us-09-643-260-12
Perfect score: 36
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.4	241	16 Q98D63	Q98D63 rhizobium 1
2	34	94.4	282	16 Q932C8	Q932C8 staphylococ
3	34	94.4	282	16 O06551	O06551 mycobacteri
4	33	91.7	237	11 Q9JMF2	Q9JMF2 mus musculu
5	33	91.7	263	11 Q9CRS3	Q9CRS3 mus musculu
6	33	91.7	392	11 Q99KP5	Q99KP5 mus musculu
7	32	88.9	93	12 O70791	O70791 rice yellow
8	32	88.9	107	2 O68455	O68455 ancylobacte
9	32	88.9	153	16 Q8XBY6	Q8XBY6 escherichia
10	32	88.9	168	16 Q91265	Q91265 pseudomonas
11	32	88.9	193	12 Q99FU7	Q99FU7 human echov
12	32	88.9	195	5 Q18653	Q18653 caenorhabdi
13	32	88.9	230	10 Q945X8	Q945X8 theobroma c
14	32	88.9	244	10 Q945Y3	Q945Y3 theobroma c
15	32	88.9	248	4 Q96J10	Q96J10 homo sapien
16	32	88.9	250	10 Q945X9	Q945X9 theobroma c

17	32	88.9	251	16 Q9R8S3	Q9R8S3 bacillus ha
18	32	88.9	255	10 Q945Z3	Q945Z3 theobroma c
19	32	88.9	255	10 Q945Y5	Q945Y5 theobroma c
20	32	88.9	255	10 Q945Y4	Q945Y4 theobroma c
21	32	88.9	259	16 Q8Z6N5	Q8Z6N5 salmonella
22	32	88.9	271	17 Q978V7	Q978V7 thermoplas
23	32	88.9	278	6 Q9XIA8	Q9XIA8 oryctolagus
24	32	88.9	302	16 Q8X8Q1	Q8X8Q1 escherichia
25	32	88.9	312	10 Q9AYF3	Q9AYF3 oryza sativ
26	32	88.9	315	13 Q91838	Q91838 coturnix co
27	32	88.9	349	5 Q17692	Q17692 caenorhabdi
28	32	88.9	379	16 Q8Z935	Q8Z935 salmonella
29	32	88.9	382	2 Q86661	Q86661 actinobacil
30	32	88.9	386	16 Q84474	Q84474 chlamydia t
31	32	88.9	391	16 P95247	P95247 mycobacteri
32	32	88.9	407	2 Q55047	Q55047 shigella so
33	32	88.9	414	2 Q9F738	Q9F738 shigella so
34	32	88.9	414	2 Q9S0V1	Q9S0V1 plesiomonas
35	32	88.9	414	11 Q9CXT6	Q9CXT6 mus musculu
36	32	88.9	415	16 Q8VJK7	Q8VJK7 mycobacteri
37	32	88.9	422	2 Q70023	Q70023 streptomyce
38	32	88.9	440	5 Q16963	Q16963 caenorhabdi
39	32	88.9	507	3 Q9HGR6	Q9HGR6 mucor circi
40	32	88.9	526	8 Q9T9G6	Q9T9G6 pupa strigo
41	32	88.9	527	17 Q8TVW7	Q8TVW7 methanopyru
42	32	88.9	566	10 Q9C926	Q9C926 arabidopsis
43	32	88.9	608	16 Q98G18	Q98G18 rhizobium l
44	32	88.9	621	17 Q976P4	Q976P4 sulfolobus
45	32	88.9	652	5 Q9N3C0	Q9N3C0 caenorhabdi

ALIGNMENTS

RESULT 1				
Q98D63	Q98D63	PRELIMINARY;	PRT;	241 AA.
AC	Q98D63			
DT	01-OCT-2001 (TREMBLrel. 18, Created)			
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Putative hydrolase, ripening-related protein-like.			
GN	MLR4841.			
OS	Rhizobium loti (Mesorhizobium loti).			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Phyllobacteriaceae; Mesorhizobium.			
OX	NCBI_TaxID=381;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MAFF303099;			
RX	MEDLINE=21082930; PubMed=11214968;			
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,			
RA	Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,			
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,			
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,			
RA	Takeuchi C., Yamada M., Tabata S.;			
RT	*Complete genome structure of the nitrogen-fixing symbiotic bacterium			
RT	Mesorhizobium loti.;			
RL	DNA Res. 7:331-338(2000).			
DR	EMBL: AP003005; BAB51408.1;			
DR	InterPro: IPR001454; Hlgnase/hydrolase.			
DR	Pfam: PF00702; Hydrolase; 1.			
KW	Hydrolase; Complete proteome.			
SO	SEQUENCE 241 AA; 27332 MW; 6AB5B55907CCC27A CRC64;			

Query Match				
Best Local Similarity 94.4%; Score 34; DB 16; Length 241;				
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1	LDYSWL	6	
Db	90	IDYSWL	95	

```

RESULT 2
Q932C8      PRELIMINARY;      PRT;      282 AA.
AC Q932C8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein SAV0804.
GN SAV0804.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=159878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cul L., Oguchi A., Aoki K.-I., Negai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003360; BAB56966.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 282 AA; 33281 MW; 3529EF85F1B1A6 CRC64;

Query Match      94.4%; Score 34; DB 16; Length 282;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDYSWL 6
      |||||
DB      132 LDYSWI 137

RESULT 3
O06551      PRELIMINARY;      PRT;      282 AA.
AC O06551;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical 30.9 kDa protein (O-methyltransferase, putative).
GN OMT OR RV1153C OR WTC165.20C OR MTL187.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV;
RA MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

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RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z95584; CAB09012.1;
DR EMBL; AE006996; AAK45444.1;
DR TIGR; MTL187;
DR Tuberculist; RV1153C;
DR InterPro; IPR003455; DUF142.
DR Pfam; PF02409; DUF142; 1.
KW Hypothetical protein; Transferase; Methyltransferase;
KW Complete proteome.
SQ SEQUENCE 282 AA; 30887 MW; 41760C508774154A CRC64;

Query Match      94.4%; Score 34; DB 16; Length 282;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDYSWL 6
      |||||
DB      142 LDYSWM 147

RESULT 4
Q9JMF2      PRELIMINARY;      PRT;      237 AA.
AC Q9JMF2;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Unknown protein (Fragment).
GN 3322402L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RX MEDLINE=20145471; PubMed=10679242;
RA Inoue S., Sano H., Ohta M.;
RT "Growth suppression of Escherichia coli by induction of expression of
RT mammalian genes with transmembrane or Atpase domains."
RL Biochem. Biophys. Res. Commun. 268:553-561(2000).
DR EMBL; AB030185; BAA92758.1;
DR MGD; MGI:1921273; 3322402L07RIK.
FT NON_TER
SQ SEQUENCE 237 AA; 26633 MW; B0928A9C7A41D377 CRC64;

Query Match      91.7%; Score 33; DB 11; Length 237;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDYSWL 6
      :|||||
DB      167 VDYSWL 172

RESULT 5
Q9CRS3      PRELIMINARY;      PRT;      263 AA.
AC Q9CRS3;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE 3322402L07RIK protein (Fragment).
GN 3322402L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

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RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX  MEDLINE=21085660; PubMed=11217851;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA  Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
DR  EMBL; AK014383; BAB29312.1; -
DR  MGD; MGI:1921273; 3322402L07Rik.
FT  NON_TER
SQ  SEQUENCE 263 AA; 30115 MW; 33280187EAD43392 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 263;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 126 VDYSWL 131

RESULT 6
ID Q99KP5 PRELIMINARY; PRT; 392 AA.
AC Q99KP5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to cyclin I.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004071; AAH04071.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Cyclin; Repeat; WD repeat.
SQ SEQUENCE 392 AA; 44527 MW; 4B2E5CBA3A22075A CRC64;

Query Match 91.7%; Score 33; DB 11; Length 392;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 384 VDYSWL 389

RESULT 7
O70791
ID Q8XBY6 PRELIMINARY; PRT; 153 AA.
AC Q8XBY6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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ID Q70791 PRELIMINARY; PRT; 93 AA.
AC Q70791;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein.
GN 6.
OS Rice yellow stunt virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Nucleorhabdovirus.
OX NCBI_TaxID=59380;
RN [1]
RP SEQUENCE FROM N.A.
RA Fang R., Luo Z., Zhao H.;
RT "Novel structure of the rice yellow stunt virus genome: a plant
RT rhabdovirus encodes seven genes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011257; BAA25159.1; -
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 10543 MW; A10CC3BD41F88305 CRC64;

Query Match 88.9%; Score 32; DB 12; Length 93;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 63 IDYSWI 68

RESULT 8
O68455 PRELIMINARY; PRT; 107 AA.
ID O68455;
AC O68455;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Haloacid dehalogenase (Fragment).
OS Ancylobacter aquaticus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Hyphomicrobium group; Ancylobacter.
OX NCBI_TaxID=100;
RN [1]
RP SEQUENCE FROM N.A.
RA Fortin N., Fulthorpe R.R., Allen D.G., Greer C.W.;
RT "Molecular analysis of bacterial isolates and total community DNA from
RT kraft pulp mill effluent treatment systems.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043240; AAC08952.1; -
DR HSP; Q60099; 1A06.
DR InterPro; IPR001454; Hlgnase/hydrlase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00413; HADHALOGNASE.
FT NON_TER
FT NON_TER 107
SQ SEQUENCE 107 AA; 12177 MW; 2BF77D4354B5D0C8 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 107;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 6 LEYSWL 11

RESULT 9
O8XBY6 PRELIMINARY; PRT; 153 AA.
ID O8XBY6;
AC O8XBY6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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CC -1- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY. ECF SUBFAMILY.
DR EMBL; AE004631; AAG03438.1; -.
DR InterPro; IPR000838; Sigma70_ECF.
DR Pfam; PF00776; Sigma70_ECF; 1.
DR KW DNA-binding; DNA-directed RNA polymerase; Sigma factor;
KW Transcription regulation; Complete proteome.
SQ SEQUENCE 168 AA; 19000 MW; 39473D9620E33FFD CRC64;

Query Match      88.9%; Score 32; DB 16; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

QY      2 DYSWL 6
      |||||
Db      18 DYSWL 22

RESULT 11
Q99FU7 PRELIMINARY; PRT; 193 AA.
ID Q99FU7 PRELIMINARY; PRT; 193 AA.
AC Q99FU7 PRELIMINARY; PRT; 193 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VP1 (Fragment).
OS Human echovirus 4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OC NCBI_TaxID=35295;
OX [1]
RP SEQUENCE FROM N.A.
RN STRAIN=2278/81;
RC MEDLINE=21015391; PubMed=11130885;
RA Norder H., Bjerregaard L., Magnus L.O.;
RT "Homotypic echoviruses share aminoterminal VP1 sequence homology
RT applicable for typing.";
RL J. Med. Virol. 63:35-44(2001).
DR EMBL; AF295452; AAK13340.1; -.
DR HSP; O91734; 1EVL.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
DR NON_TER 1
FT NON_TER 193
SQ SEQUENCE 193 AA; 21278 MW; 50F3E86B5D7D8539 CRC64;

Query Match      88.9%; Score 32; DB 12; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

QY      2 DYSWL 6
      |||||
Db      158 DYSWL 162

RESULT 12
Q18653 PRELIMINARY; PRT; 195 AA.
ID Q18653 PRELIMINARY; PRT; 195 AA.
AC Q18653;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 22.7 kDa protein.
OS C46A5.8.
OC Caenorhabditis elegans.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
OX [1]
RP SEQUENCE FROM N.A.
RN STRAIN-BRISTOL N2;
RC MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for

```


RT Investigating biology. The C. elegans Sequencing Consortium. ;
 RL Science 282:2012-2018(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Johnson D., Stellyes L.;
 RT "The sequence of C. elegans cosmid C46A5";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U61948; AAB03148.1; -;
 KW Hypothetical protein.

SQ SEQUENCE 195 AA; 22682 MW; 9EC3B3B2D3BE056B CRC64;
 Query Match 88.9%; Score 32; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 Db 74 DYSWL 78

RESULT 13
 Q945X8 PRELIMINARY; PRT; 230 AA.
 ID Q945X8;
 AC Q945X8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NBS/LRR resistance protein-like protein (Fragment).
 OS Theobroma cacao (Cacao) (Cocoa).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Theobroma.
 OX NCBI_TaxID=3641;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuhn D.N., Crucet K., Schnell R.J., Heath M.A.;
 RT "Development of Resistance Gene Homologs as Useful Genetic Markers in
 RT Theobroma cacao";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402764; AAL01031.1; -;
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00931; NB-ARC; 1.
 FT NON_TER 1 1
 FT NON_TER 230 230
 SQ SEQUENCE 230 AA; 26762 MW; 7407A8AAE4C1EB61 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 Db 132 DYSWL 136

RESULT 14
 Q945Y3 PRELIMINARY; PRT; 244 AA.
 ID Q945Y3;
 AC Q945Y3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NBS/LRR resistance protein-like protein (Fragment).
 OS Theobroma cacao (Cacao) (Cocoa).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Query Match 88.9%; Score 32; DB 10; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 Db 132 DYSWL 136

RESULT 15
 Q96J10 PRELIMINARY; PRT; 248 AA.
 ID Q96J10;
 AC Q96J10;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Unknown (Protein for IMAGE:3448071) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RC TISSUE-PLACENTA;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006816; AAH06816.1; -;
 DR NON_TER 1 1
 FT NON_TER 248 248
 SQ SEQUENCE 248 AA; 28319 MW; 403D242313357D1E CRC64;

Query Match 88.9%; Score 32; DB 4; Length 248;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 Db 240 IDYSWI 245

Search completed: May 30, 2003, 14:39:00
 Job time : 15.7632 secs

OC eurosids II; Malvales; Malvaceae; Theobroma.
 OX NCBI_TaxID=3641;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuhn D.N., Crucet K., Schnell R.J., Heath M.A.;
 RT "Development of Resistance Gene Homologs as Useful Genetic Markers in
 RT Theobroma cacao";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402759; AAL01026.1; -;
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00931; NB-ARC; 1.
 FT NON_TER 1 1
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 28331 MW; 537754BB2935806D CRC64;

Query Match 88.9%; Score 32; DB 10; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 Db 131 DYSWL 135

RESULT 15
 Q96J10 PRELIMINARY; PRT; 248 AA.
 ID Q96J10;
 AC Q96J10;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Unknown (Protein for IMAGE:3448071) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RC TISSUE-PLACENTA;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006816; AAH06816.1; -;
 DR NON_TER 1 1
 FT NON_TER 248 248
 SQ SEQUENCE 248 AA; 28319 MW; 403D242313357D1E CRC64;

Query Match 88.9%; Score 32; DB 4; Length 248;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 Db 240 IDYSWI 245

Search completed: May 30, 2003, 14:39:00
 Job time : 15.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds
(without alignments)
79.803 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSLW 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	91.7	404	1	ADMR_HUMAN
2	32	88.9	94	1	VLXS_BPAPS
3	32	88.9	229	1	HAD2_PSESP
4	32	88.9	253	1	HAD_XANAU
5	32	88.9	259	1	SSAT_SALTY
6	32	88.9	302	1	ABGR_ECOLI
7	32	88.9	313	1	IRFL_CHICK
8	32	88.9	400	1	AAT_RHILP
9	32	88.9	524	1	VGLG_RABVV
10	32	88.9	684	1	XYNA_CALSR
11	32	88.9	735	1	FT_ERWCH
12	32	88.9	1039	1	GUNB_CALSA
13	31	86.1	200	1	YB15_HAEIN
14	31	86.1	431	1	UL78_HCMVA
15	31	86.1	745	1	IKKA_HUMAN
16	31	86.1	745	1	IKKA_MOUSE
17	31	86.1	756	1	IKKB_MOUSE
18	31	86.1	757	1	IKKB_MOUSE
19	31	86.1	757	1	IKKB_RAT
20	30	83.3	225	1	YBIB_BACSU
21	30	83.3	460	1	GUNC_CLOJO
22	30	83.3	460	1	GUNC_CLOCE
23	30	83.3	638	1	60IM_COXBU
24	30	83.3	728	1	UVRC_STRCO
25	30	83.3	868	1	NIBQ_YEAST
26	30	83.3	1029	1	YFC5_YEAST
27	30	83.3	1091	1	ACYL_MOUSE
28	30	83.3	1100	1	ACYL_RAT
29	30	83.3	1101	1	ACYL_HUMAN
30	29	80.6	167	1	YMH6_CAEEL
31	29	80.6	191	1	YCEI_ECOLI
32	29	80.6	217	1	YVEE_BACSU
33	29	80.6	224	1	DEH2_MORSP

34	29	80.6	224	1	HAD2_PSEPU
35	29	80.6	227	1	HAD1_PSEPU
36	29	80.6	227	1	HAD_PSEFL
37	29	80.6	232	1	HAD_PSESP
38	29	80.6	233	1	MTGA_NEIMA
39	29	80.6	252	1	RLA_ARCFU
40	29	80.6	252	1	YHFQ_ECOLI
41	29	80.6	261	1	YHFQ_ECOLI
42	29	80.6	267	1	EBAG_FLASP
43	29	80.6	298	1	ICIA_VIBCH
44	29	80.6	301	1	Y664_METJA
45	29	80.6	349	1	OMPA_BUCAI
	29	80.6	352	1	XYNA_DICTH

ALIGNMENTS

RESULT 1

ID	ADMR_HUMAN	STANDARD;	PRT;	404 AA.
AC	O15218;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	15-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Adrenomedullin receptor (AM-R).			
GN	ADMR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98042541; PubMed=9367907;			
RA	Haenze J., Dittich K., Dotsch J., Rascher W.;			
RT	"Molecular cloning of a novel human receptor gene with homology to the rat adrenomedullin receptor and high expression in heart and immune system.";			
RL	Biochem. Biophys. Res. Commun. 240:183-188(1997).			
CC	- - FUNCTION: RECEPTOR FOR ADRENOMEDULLIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE (BY SIMILARITY).			
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE, IMMUNE SYSTEM, ADRENAL GLAND AND LIVER.			
CC	- - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST RESEMBLANCE WITH THE RDC1 ORPHAN RECEPTOR.			
CC	-----			
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CC	-----			
DR	EMBL; Y13583; CAA73910.1; -			
DR	Gene; HGNC:13708; ADMR.			
DR	MIM; 605307; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm.1; 1			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.			
DR	PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 58 79 1 (POTENTIAL).			
FT	DOMAIN 80 90 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 91 113 2 (POTENTIAL).			
FT	DOMAIN 114 127 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 128 149 3 (POTENTIAL).			
FT	DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 171 193 4 (POTENTIAL).			
FT	DOMAIN 194 217 EXTRACELLULAR (POTENTIAL).			

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FT TRANSMEM 218 239 5 (POTENTIAL).
FT DOMAIN 240 258 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 259 280 6 (POTENTIAL).
FT DOMAIN 281 299 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 300 320 7 (POTENTIAL).
FT DOMAIN 321 404 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 202 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 404 AA; 45323 MW; EF187ECFDF2DC6C1 CRC64;

Query Match 91.7%; Score 33; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 115 LDYTWL 120

RESULT 2
VLVS_BPAPS STANDARD; PRT; 94 AA.
AC Q9T177;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Putative lysis protein S (P11).
GN 11.
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC unclassified Podoviridae.
OX NCBI_TaxID=106199;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95420383; PubMed=10489345;
RA van der Wijk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
RL the secondary endosymbiont of acyrthosiphon pisum.";
RL Virology 262:104-113(1999).
CC -1- FUNCTION: ESSENTIAL FOR LYSIS OF THE BACTERIAL CELL WALL BY
CC DISRUPTING THE CELL MEMBRANE, THEREBY GIVING HYDROLYTIC ENZYMES
CC ACCESS TO THE CELL WALL (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LAMBDA PHAGE S PROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF157835; AAF03954.1;
CC PHAGE Lysis protein.
CC SEQUENCE 94 AA; 10589 MW; C3EE1A3181150120 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6
DB 66 DYSWL 70

RESULT 3
HAD2_PSESP STANDARD; PRT; 229 AA.
AC P24070;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

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DE 2-haloalkanoic acid dehalogenase II (EC 3.8.1.2) (L-2-haloacid
DE dehalogenase II) (Halocarboxylic acid halidohydrolase II) (DEHCII).
OS Pseudomonas sp. (strain CBS3).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139597; PubMed=1995594;
RA Schneider B., Mueller R., Frank R., Lingens F.;
RT "Complete nucleotide sequences and comparison of the structural genes
RT of two 2-haloalkanoic acid dehalogenases from Pseudomonas sp. strain
RT CBS3.";
RL J. Bacteriol. 173:1530-1535(1991).
CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O -> (R)-2-hydroxyacid +
CC halide.
CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
CC FAMILY.
CC -----
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CC -----
CC EMBL; M62909; AAA25833.1;
CC PIR; B38452; B38452.
CC HSP; O53464; 12RN.
CC InterPro; IPR001454; Hlg_nase/hydrolase.
CC Pfam; PF00702; Hydrolase; 1.
CC PRINTS; PR00413; HADHALOGENASE.
CC KW Hydrolase.
CC ACT SITE 10 10 NUCLEOPHILE (BY SIMILARITY).
CC SEQUENCE 229 AA; 25712 MW; A77AA63C97DD40AB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 229;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 45 LEYSWL 50

RESULT 4
HAD_XANAU STANDARD; PRT; 253 AA.
AC Q60099; Q56757;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid
DE dehalogenase) (Halocarboxylic acid halidohydrolase).
GN dhlB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Hyphomicrobium group; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
RC STRAIN=GJ10;
RX MEDLINE=92078101; PubMed=1744048;
RA van der Ploeg J., van Hall G., Janssen D.B.;
RT "Characterization of the haloacid dehalogenase from Xanthobacter
RT autotrophicus GJ10 and sequencing of the dhlB gene.";
RL J. Bacteriol. 173:7925-7933(1991).
RN [2]
RP SEQUENCE OF 1-122 FROM N.A.
RC STRAIN=GJ10;
RX MEDLINE=96066306; PubMed=7580000;
RA van der Ploeg J., Janssen D.B.;
RT "Sequence analysis of the upstream region of dhlB, the gene encoding

```

RT haloalkanoic acid dehalogenase of Xanthobacter autotrophicus GJ10.";
RL Biodegradation 6:257-263(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) AND REVISION TO 84.
RC STRAIN-GJ10;
RX MEDLINE=98070500; PubMed=9407083;
RA Ridder I.S., Rozeboom H.J., Kalk K.H., Janssen D.B., Dijkstra B.W.;
RT "Three-dimensional structure of L-2-haloacid dehalogenase from
RT Xanthobacter autotrophicus GJ10 complexed with the substrate-analogue
RT formate.";
RL J. Biol. Chem. 272:33015-33022(1997).
CC -1- FUNCTION: CATALYZES THE HYDROLYTIC DEHALOGENATION OF SMALL L-2-
CC HALOALKANOIC ACIDS TO YIELD THE CORRESPONDING D-2-HYDROXYALKANOIC
CC ACIDS. ACTIVE WITH 2-HALOGENATED CARBOXYLIC ACIDS AND CONVERTS
CC ONLY THE L-ISOMER OF 2-CHLOROPROPIONIC ACID WITH INVERSION OF
CC CONFIGURATION TO PRODUCE D-LACTATE. OPTIMAL ACTIVITY IS BETWEEN PH
CC 9-10, AND MAXIMAL ACTIVITY SEEN AT PH 9.5.
CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
CC halide.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; M81691; AAA27590.1; -;
DR EMBL; X86084; CAA60039.1; -;
DR PDB; 1A06; 28-JAN-98.
DR InterPro; IPR001454; Hlgase/hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00413; HADHALOGNASE.
DR Hydrolase; 3D-structure.
FT ACT_SITE 8 8 NUCLEOPHILE.
FT CONFLICT 84 84 D -> G (IN REF. 1 AND 2).
SQ SEQUENCE 253 AA; 27469 MW; E2AB8DEED37A5716 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 253;
Best Local Similarity 83.3%; Pred. NO. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 43 LEYSWL 48
|:|||||

RESULT 5
SSAT_SALTY STANDARD; PRT; 259 AA.
ID SSAT_SALTY STANDARD; PRT; 259 AA.
AC P96068;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Secretion system apparatus protein ssat.
GN SSAT OR STM1421.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2;
RX MEDLINE=97285756; PubMed=9140973;
RA Hensel M., Shea J.E., Raupach B., Monack D., Falkow S., Gleeson C.,
RA Kubo T., Holden D.W.;
RT "Functional analysis of ssat and the ssak/U operon, 13 genes encoding
RT components of the type III secretion apparatus of Salmonella
RT pathogenicity Island 2.";

RL Mol. Microbiol. 24:155-167(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -1- FUNCTION: PART OF A TYPE III SECRETION SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.
CC -----
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CC -----
DR EMBL; X99944; CAA68201.1; -;
DR EMBL; X808761; AAL20345.1; -;
DR StGene; SG10717; ssat.
DR InterPro; IPR002010; Bac_export_1.
DR Pfam; PF01311; Bac_export_1; 1.
DR PRINTS; PR00953; TYPE3IMRPROT.
DR Transport; Protein transport; Transmembrane; Complete proteome.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 35 55 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
FT TRANSMEM 127 147 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 214 234 POTENTIAL.
SQ SEQUENCE 259 AA; 29218 MW; 8E5F0734991373DD CRC64;

Query Match 88.9%; Score 32; DB 1; Length 259;
Best Local Similarity 100.0%; Pred. NO. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 67 DYSWL 71
|:|||||

RESULT 6
ABGR_ECOLI STANDARD; PRT; 302 AA.
ID ABGR_ECOLI STANDARD; PRT; 302 AA.
AC P77744;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative transcriptional regulator abgr.
GN ABGR OR B1339.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]

SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RC MEDLINE-97251357; PubMed-9097039;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sanei G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
 RA Takeuchi K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
 RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 [3]
 RN CHARACTERIZATION.
 RC STRAIN-BN101;
 RC MEDLINE-99047572; PubMed-9829935;
 RA Hussein M.J., Green J.M., Nichols B.P.;
 RT "Characterization of mutations that allow p-aminobenzoyl-glutamate
 utilization by Escherichia coli.";
 RL J. Bacteriol. 180:6260-6269(1998).
 CC -1- FUNCTION: COULD BE THE REGULATOR OF THE ABG OPERON.
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
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 DR EMBL; AE000232; AAC74421.1;
 DR EMBL; D90772; BAA14941.1;
 DR EMBL; D90773; BAA14944.1;
 DR EcoGene; EG13353; abgR.
 DR InterPro; IPR000847; HTH_LysR.
 DR InterPro; IPR005119; LysR_subst.
 DR Pfam; PF00126; HTH_1;
 DR Pfam; PF03466; LysR_substrate; 1.
 DR PRINTS; PR00039; HTHLYSR.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
 KW Transcription regulation; DNA-binding; Complete proteome.
 FT DNA_BIND 22 41 H-T-H MOTIF (POTENTIAL).
 SQ SEQUENCE 302 AA; 34058 MW; 57C83FA6DF8ABA66 CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 302;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDYSW 5
 Db 191 LDYSW 195
 RESULT 7
 ID IRF1_CHICK STANDARD; PRT; 313 AA.
 AC Q90876;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interferon regulatory factor 1 (IRF-1).
 GN IRF1.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-95241453; PubMed-7536924;
 RA Jungwirth C., Rebbert M., Ozato K., Degen H.J., Schultz U.,

David I.B.;
 RA "Chicken interferon consensus sequence-binding protein (ICSBP) and
 RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
 RT conservation in the IRF gene family";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).
 CC -1- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
 CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
 CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE IRF FAMILY.
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 DR EMBL; L39766; AAA62160.1;
 DR HSSP; P15314; 1IF1
 DR InterPro; IPR001346; IRF.
 DR Pfam; PF00605; IRF; 1.
 DR PRINTS; PR00267; INTERREGFCT.
 DR PRODOM; PD002355; IRF; 1.
 DR SMART; SM00348; IRF; 1.
 DR PROSITE; PS00601; IRF; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DNA_BIND 7 109 TRYPTOPHAN PENTAD REPEAT.
 SQ SEQUENCE 313 AA; 36009 MW; 0895FA3736FA7463 CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 313;
 Best Local Similarity 83.3%; Pred. No. 53;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDYSWL 6
 Db 295 LDYSWL 300
 RESULT 8
 ID AAT_RHILP STANDARD; PRT; 400 AA.
 AC O86459;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPA).
 GN ASPC OR AATA.
 OS Rhizobium leguminosarum (biovar phaseoli).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Rhizobium.
 CC NCBI_TaxID=385;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-8002;
 RA Allaway D.;
 RT "Sequence of an aspartate aminotransferase from Rhizobium
 RT leguminosarum.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
 CC L-glutamate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
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CC -----
DR EMBL; AJ006709; CAA07198.1; -.
DR HSP; Q56232; IBKG.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR004839; AminoTransf1/2.
DR InterPro; IPR004838; NhrTransf_1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Transferase; AminoTransferase; Pyridoxal phosphate.
FT BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 400 AA; 43752 MW; 1375BE0A72934304 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
Db 87 LDYSW 91

RESULT 9
VGLG_RABVV STANDARD; PRT; 524 AA.
AC Q08089;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Spike glycoprotein precursor.
GN G.
OS Rabies virus (strain Vnukovo-32).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=45418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95070778; PubMed=7979981;
RA Fodor I., Grabko V.I., Khozinski V.V., Selimov M.A.;
RT "Nucleotide and deduced amino acid sequences of the glycoprotein gene
of rabies virus vaccine strain Vnukovo-32.";
RL Arch. Virol. 135:451-459(1994).
CC -1- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.
CC IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE
CC HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL.
CC THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND
CC THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF
CC THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND VIRUS
CC BUDDING.
CC -1- SUBUNIT: HOMOTRIMER.
CC -----
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CC -----
DR EMBL; X71879; CAA50713.1; -.
DR InterPro; IPR001903; Rhabd_glycop.
DR Pfam; PF00974; Rhabd_glycop; 1.
KW Transmembrane; Envelope protein; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 524 SPIKE GLYCOPROTEIN.
FT TRANSMEM 460 476 BY SIMILARITY.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 524 AA; 58692 MW; 6DB36E50406CC16D CRC64;
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Query Match 88.9%; Score 32; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 137 DYSWL 141

RESULT 10
XYNA_CALSR STANDARD; PRT; 684 AA.
AC P40944;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XYNA.
OS Caldicellulosiruptor sp. (strain Rt88.4).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
OC Caldicellulosiruptor.
OX NCBI_TaxID=28238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97077616; PubMed=8920183;
RA Dwivedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
RT "Cloning, sequencing and overexpression in Escherichia coli of a
xylanase gene, xyna from the thermophilic bacterium Rt88.4 genus
Caldicellulosiruptor.";
RL Appl. Microbiol. Biotechnol. 45:86-93(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
DR EMBL; L18965; AAB42044.1; -.
DR PIR; S41788; S41788.
DR HSP; P10478; IXYZ.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF00331; Glyco_hydro_10; 1.
DR Pfam; PF02018; CBM_4_9; 2.
DR PRINTS; PR00134; GLHYDRLASE10.
DR PROSITE; PS00591; GLYCOSYL-HYDROL_F10; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 684 ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 490 490 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 598 598 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 684 AA; 79353 MW; 0AE575F4FB4BA5E6 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 650 DYSWL 654

RESULT 11
FCT_ERWCH STANDARD; PRT; 735 AA.
ID FCT_ERWCH
```

AC 047162;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Ferrichrysoactin receptor precursor.
 GN FCT.
 OS Erwinia chrysanthemi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Pectobacterium;
 OX NCBI_TaxID=556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3937;
 RA MEDLINE=96165286; PubMed=8576065;
 RA Sauvage C., Franca T., Expert D.;
 RT "Analysis of the Erwinia chrysanthemi ferrichrysoactin receptor
 RT gene: resemblance to the Escherichia coli fepA-fes bidirectional
 RT promoter region and homology with hydroxamate receptors.";
 RL J. Bacteriol. 178:1227-1231(1996).
 CC -!- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING
 CC CHRYSOACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE
 CC BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
 CC -!- SUBCELLULAR LOCATION: Outer membrane.
 CC -!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
 CC -----
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 CC -----
 DR EMBL; X87967; CAA61205.1; -
 DR HSP; P06971; 2FCP.
 DR InterPro: IPR000531; TonB_boxC.
 DR Pfam: PF00593; TonB_boxC; 1.
 DR PROSITE: PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; 1.
 KW Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
 KW Transport; TonB box.
 FT SIGNAL 1 38
 FT CHAIN 39 735
 FT SITE 45 52
 FT SITE 718 735
 FT DOMAIN 39 45
 FT TRANSMEM 46 54
 FT DOMAIN 55 82
 FT TRANSMEM 83 91
 FT DOMAIN 92 107
 FT TRANSMEM 108 116
 FT DOMAIN 117 124
 FT TRANSMEM 125 133
 FT DOMAIN 134 169
 FT TRANSMEM 170 178
 FT DOMAIN 179 179
 FT TRANSMEM 180 188
 FT DOMAIN 189 194
 FT TRANSMEM 195 203
 FT DOMAIN 204 222
 FT TRANSMEM 223 231
 FT DOMAIN 232 261
 FT TRANSMEM 262 270
 FT DOMAIN 271 286
 FT TRANSMEM 287 295
 FT DOMAIN 296 312
 FT TRANSMEM 313 321
 FT DOMAIN 322 328
 FT TRANSMEM 329 337
 FT DOMAIN 338 343
 FT TRANSMEM 344 352
 FT DOMAIN 353 378
 FT TRANSMEM 379 387

FT DOMAIN 388
 FT TRANSMEM 393
 FT DOMAIN 401
 FT TRANSMEM 402
 FT DOMAIN 412
 FT TRANSMEM 413
 FT TRANSMEM 424
 FT TRANSMEM 425
 FT TRANSMEM 433
 FT TRANSMEM 434
 FT TRANSMEM 448
 FT TRANSMEM 449
 FT TRANSMEM 457
 FT TRANSMEM 458
 FT TRANSMEM 461
 FT TRANSMEM 462
 FT TRANSMEM 470
 FT TRANSMEM 471
 FT TRANSMEM 495
 FT TRANSMEM 496
 FT TRANSMEM 505
 FT TRANSMEM 510
 FT TRANSMEM 518
 FT TRANSMEM 519
 FT TRANSMEM 538
 FT TRANSMEM 539
 FT TRANSMEM 547
 FT TRANSMEM 548
 FT TRANSMEM 552
 FT TRANSMEM 553
 FT TRANSMEM 561
 FT TRANSMEM 562
 FT TRANSMEM 569
 FT TRANSMEM 578
 FT TRANSMEM 599
 FT TRANSMEM 600
 FT TRANSMEM 609
 FT TRANSMEM 649
 FT TRANSMEM 650
 FT TRANSMEM 659
 FT TRANSMEM 674
 FT TRANSMEM 675
 FT TRANSMEM 684
 FT TRANSMEM 696
 FT TRANSMEM 704
 FT TRANSMEM 705
 FT TRANSMEM 707
 FT TRANSMEM 715
 FT TRANSMEM 716
 FT TRANSMEM 727
 FT TRANSMEM 735
 SQ SEQUENCE 735 AA; 81055 MW; 3C37073E4538DC3C CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 735;
 Best Local Similarity 83.3%; Pred. No. 1.2e-02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 DB 399 LDYKWL 404
 ID GUNB_CALSA STANDARD; PRT; 1039 AA.
 AC P10474;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Endoglucanase/exoglucanase B precursor [Includes: Endoglucanase
 DE (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Cellobiohydrolase); Exoglucanase (EC 3.2.1.91) (Exocellobiohydrolase)
 DE (1,4-beta-cellobiohydrolase)].
 GN CELB.
 OS Caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosiruptor.
 OX NCBI_TaxID=44001;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89098398; PubMed=2789517;
 RA Saul D.J., Williams L.C., Love D.R., Chamley I.W., Bergquist P.I.;
 RT "Nucleotide sequence of a gene from Caldocellum saccharolyticum
 RT encoding for exocellulase and endocellulase activity.";
 RL Nucleic Acids Res. 17:439-439(1989).
 CC -!- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL
 CC DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS
 CC AN ENDOGLUCANASE.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 CC in cellulose and cellotetraose, releasing cellobiose from the non-

reducing ends of the chains.
 -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULOSE FAMILY
 F (FAMILY 10 OF GLYCOSYL HYDROLASES).
 -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULOSE FAMILY
 A (FAMILY 5 OF GLYCOSYL HYDROLASES).

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 EMBL; X13602; CAA31936.1; -
 PIR; S02711; S02711.
 HSSP; Q06851; INBC.
 InterPro; IPR001956; CBD_3.
 InterPro; IPR001547; GH_5.
 InterPro; IPR001000; Glyco_hydro_10.
 Pfam; PF00150; cellulase; 1.
 Pfam; PF00331; Glyco_hydro_10; 1.
 Pfam; PF00942; CBM_3; 1.
 PRINTS; PR00134; GLHYDRLASE10.
 ProDom; PD001947; CBD_3; 1.
 ProSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
 ProSITE; PS00639; GLYCOSYL_HYDROL_F5; 1.
 Cellulose degradation; Hydrolase; Glycosidase; Repeat;
 KW Multifunctional enzyme; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 1039 ENDOGLUCANASE/EXOGLUCANASE B.
 FT DOMAIN 376 416 THR/PRO-RICH, TANDEM REPEATS OF T-P.
 FT DOMAIN 417 570 CELLULOSE-BINDING (BY SIMILARITY).
 FT DOMAIN 571 618 THR/PRO-RICH, TANDEM REPEATS OF T-P.
 FT ACT_SITE 177 177 PROTON DONOR (POTENTIAL).
 FT ACT_SITE 285 285 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 792 792 BY SIMILARITY.
 SQ SEQUENCE 1039 AA; 117641 MW; 0E0378171594DDAE CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 1039;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DYSWL 6
 Db 339 DYSWL 343

 RESULT 13
 YE15_HAEIN STANDARD; PRT; 200 AA.
 ID YE15_HAEIN
 AC P44187;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein H11415.
 GN H11415.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OC NCBI_TaxID=727;
 RN [1]
 SEQUENCE FROM N.A.
 RC SPRAIN-Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
 "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RD.";
 Science 269:496-512(1995).
 -1- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.

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 EMBL; U32821; AAC23066.1; -
 HSSP; P23951; 2BAA.
 TIGR; H11415; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 200 AA; 22895 MW; 42199FDDA4859FBB CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 200;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 61 LDYSWL 66

 RESULT 14
 UL78_HCMVA STANDARD; PRT; 431 AA.
 ID UL78_HCMVA
 AC P16751;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein UL78.
 GN UL78.
 OS Human cytomegalovirus (strain AD169).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OC NCBI_TaxID=10360;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=90269039; PubMed=2161319;
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Horsnell T., Hutchison C.A. III, Koutzarides T., Martignetti J.A.,
 RA Reddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 "Analysis of the protein-coding content of the sequence of human
 cytomegalovirus strain AD169.";
 Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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 EMBL; X17403; CAA35351.1; -
 PIR; S09841; S09841.
 InterPro; IPR000276; GPCR_Rhodpsn.
 ProSITE; PS0262; G_PROTEIN_RECEP_F1_2; UNKNOWN_1.
 KW Hypothetical protein; Transmembrane
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 111 131 POTENTIAL.
 FT TRANSMEM 153 173 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT TRANSMEM 279 299 POTENTIAL.

FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 431 AA; 47357 MW; 34668FE7F908C657 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 431;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||| ||
Db 180 LDYRWL 185

RESULT 15
IKKA_HUMAN
ID IKKA_HUMAN STANDARD; PRT; 745 AA.
AC O15111; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikappab kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).
GN IKKA OR CHUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an Ikappab kinase.";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive Ikappab kinase that activates the transcription
RT factor NF-kappaB.";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain.";
RL Cell. Mol. Biol. Res. 41:537-549(1995).
RN [6]
RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND
RP S-180.
RX MEDLINE=98188283; PubMed=9520446;

RA Ling L., Cao Z., Goeddel D.V.;
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
RT Ser-176.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
RN [7]
RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE=99413720; PubMed=10485710;
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
RA Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt
RT serine-threonine kinase.";
RL Nature 401:82-85(1999).
RN [8]
RP IKKA-IKKB BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of Ikappab kinase activity through
RT IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [9]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [10]
RP REVIEW
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
CC WHEN DEPHOSPHORYLATED.
CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
CC ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY
CC MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AF012890; AAC51662.1;
CC EMBL; AF009225; AAC51671.1;
CC EMBL; AF080157; AAC08996.1;
CC EMBL; U22512; AAC50713.1;
CC HSSP; Q63450; 1A06.
CC Genew; HGNC:1974; CHUK.
CC MIM; 600664;
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; ATP-binding;
CC KW

KW Phosphorylation. 302 PROTEIN KINASE.
FT DOMAIN 15 476 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 738 743 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PRK/AKT1).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
DECREASE OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
ACTIVITY.
FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
FT CONFLICT 543 543 E-> G (IN REF. 2).
FT CONFLICT 604 604 L-> R (IN REF. 5).
FT CONFLICT 679 680 TS -> AY (IN REF. 5).
FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
FT CONFLICT 686 687 TS -> DL (IN REF. 5).
SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 738 LDWSWL 743

Search completed: May 30, 2003, 15:48:58
Job time : 5.11842 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds
(without alignments)
87.500 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR73: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	94.4	282	2 B70555	probable omt prote
2	33	91.7	404	2 JC5784	adrenomedullin rec
3	32	88.9	122	2 S52840	haloalkanoic acid
4	32	88.9	153	2 F90704	hypothetical prote
5	32	88.9	153	2 A85555	hypothetical prote
6	32	88.9	168	2 A83390	probable sigma-70
7	32	88.9	195	2 T29815	hypothetical prote
8	32	88.9	229	2 B38452	2-haloacid dehalog
9	32	88.9	251	2 B84016	hypothetical prote
10	32	88.9	259	2 AG0696	probable type III
11	32	88.9	302	2 C90869	probable transcript
12	32	88.9	302	2 F83749	probable transcript
13	32	88.9	302	2 F64883	probable transcript
14	32	88.9	349	2 T15422	probable transcript
15	32	88.9	379	2 AG0542	hypothetical prote
16	32	88.9	386	2 H71511	conserved hypothet
17	32	88.9	391	2 A70663	probable 2-compone
18	32	88.9	414	2 T44513	probable PPF prote
19	32	88.9	440	2 T32190	hypothetical prote
20	32	88.9	524	2 S33419	hypothetical prote
21	32	88.9	684	2 S41788	glycoprotein G - r
22	32	88.9	694	2 A95251	endo-1,4-beta-xyla
23	32	88.9	694	2 F98115	antigen, cell wall
24	32	88.9	700	2 T30910	conserved hypothet
25	32	88.9	705	2 T34531	xylanase (EC 3.2.1
26	32	88.9	735	2 S57486	hypothetical prote
27	32	88.9	872	2 F75073	ferrichrysoabactin
28	32	88.9	915	2 A43802	ATP-dependent RNA
29	32	88.9	1039	2 S02711	cellulase (EC 3.2.

30 32 88.9 1209 2 T16663 hypothetical prote
31 32 88.9 1232 2 D64413 cobalamin biosynth
32 32 88.9 1319 2 S75705 hypothetical prote
33 32 88.9 1779 2 T31085 xylanase - Caldice
34 31 86.1 200 2 H64028 hypothetical prote
35 31 86.1 234 2 AF3543 phosphoglycolate p
36 31 86.1 282 2 T20203 hypothetical prote
37 31 86.1 431 2 S09841 hypothetical prote
38 31 86.1 618 2 D71055 probable indolepyr
39 31 86.1 745 1 I49101 conserved helix-lo
40 31 86.1 837 2 H82970 hypothetical prote
41 31 86.1 1010 2 D72203 hypothetical prote
42 30 83.3 61 2 D82732 hypothetical prote
43 30 83.3 144 2 A10698 probable pathogen
44 30 83.3 154 2 F90195 conserved hypothet
45 30 83.3 225 2 S39672 ywbb protein - Bac

ALIGNMENTS

RESULT 1

B70555
Probable omt protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: B70555
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A: Reference number: A70500; MUID:98295987; PMID:9634230
A: Accession: B70555
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-282 <COL>
A: Cross-references: GB:295584; GB:AL123456; NID:g3261774; PIDN:CAB09012.1; PID:e31712
A: Experimental source: strain H37RV
C: Geneticks:
A: Gene: omt

Query Match 94.4%; Score 34; DB 2; Length 282;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 142 LDYSWM 147

RESULT 2

JC5784
adrenomedullin receptor - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: JC5784
R: Haenze, J.; Dietrich, K.; Doetsch, J.; Rascher, W.
Biochem. Biophys. Res. Commun. 240, 183-188, 1997
A: Title: Molecular cloning of a novel human receptor gene with homology to the rat ad
A: Reference number: JC5784; MUID:98042541; PMID:9367907.
A: Accession: JC5784
A: Molecule type: mRNA
A: Residues: 1-404 <HAE>
A: Cross-references: GB:Y13583; NID:g2652933; PIDN:CAA73910.1; PID:g2652934
C: Superfamily: vertebrate rhodopsin
C: Keywords: glycoprotein; receptor; transmembrane protein
F: 58-79/Domain: transmembrane #status predicted <TM1>
F: 91-113/Domain: transmembrane #status predicted <TM2>
F: 128-149/Domain: transmembrane #status predicted <TM3>
F: 171-193/Domain: transmembrane #status predicted <TM4>
F: 218-239/Domain: transmembrane #status predicted <TM5>

F:260-280/Domain: transmembrane #status predicted <TM6>
F:301-320/Domain: transmembrane #status predicted <TM7>
F:28,37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.7%; Score 33; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
|||||

Db 115 LDYTWL 120
|||||

RESULT 3

S52840
haloalkanoic acid dehalogenase - Xanthobacter autotrophicus (fragment)
C:Species: Xanthobacter autotrophicus
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jan-2000
C:Accession: S52840

R:van der Ploeg, J.; Janssen, D.B.

submitted to the EMBL Data Library, April 1995

A:Description: Sequence analysis of the upstream region of dh1B, the gene encoding haloalkanoic acid dehalogenase

A:Reference number: S52838

A:Accession: S52840

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-122 <VAN>

A:Cross-references: EMBL:X86084; NID:g763396; PIDN:CAA60039.1; PID:g763399

C:Superfamily: Alkaligenes eutrophus phosphoglycolate phosphatase

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
|||||

Db 43 LEYSWL 48
|||||

RESULT 4

F90704
hypothetical protein ECs0606 [imported] - Escherichia coli (strain O157:H7, substrain R1)

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: F90704

R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F90704

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-153 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA834029.1; PID:g13360064; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECs0606

Query Match 88.9%; Score 32; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSW 5
|||||

Db 83 LDYSW 87
|||||

RESULT 5

A85555
hypothetical protein 20706 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A85555

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85555

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-153 <STO>

A:Cross-references: GB:AE005174; NID:gl2513450; PIDN:AAG54901.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: 20706

Query Match 88.9%; Score 32; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSW 5
|||||

Db 83 LDYSW 87
|||||

RESULT 6

A83390

probable sigma-70 factor, ECF subfamily PA2050 [imported] - Pseudomonas aeruginosa (s)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83390

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: A83390

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <STO>

A:Cross-references: GB:AE004631; GB:AE004091; NID:g9948050; PIDN:AAG05438.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2050

Query Match 88.9%; Score 32; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
|||||

Db 18 DYSWL 22
|||||

RESULT 7

T29815

hypothetical protein C46A5.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29815

R:Johnson, D.; Stellyes, L.

submitted to the EMBL Data Library, June 1996

A:Description: The sequence of C. elegans cosmid C46A5.

A:Reference number: Z20690

A:Accession: T29815

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-195 <JOH>

A:Cross-references: EMBL:U61948; PIDN:AAB03148.1; GSPDB:GN00022; CESP:C46A5.8

A:Experimental source: strain Bristol N2; clone C46A5

C:Genetics:

A:Gene: CESP:C46A5.8

A:Map position: 4

A; Introns: 93/3; 122/3

Query Match 88.9%; Score 32; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
|||||
Db 74 DYSWL 78

RESULT 8

B38452
2-haloacid dehalogenase (EC 3.8.1.2) II - *Pseudomonas* sp.

C; Species: *Pseudomonas* sp.

C; Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 24-Nov-1999

C; Accession: B38452

R; Schneider, B.; Mueller, R.; Frank, R.; Lingens, F.

J. Bacteriol. 173, 1530-1535, 1991

A; Title: Complete nucleotide sequences and comparison of the structural genes of two 2-haloacid dehalogenases from *Pseudomonas* sp.

A; Reference number: A38452; MUID:91139597; PMID:1995594

A; Accession: B38452

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-229 <SCH>

A; Cross-references: GB:M62909; GB:M37619; NID:g151249; PIDN:AAA25833.1; PID:g151250

C; Superfamily: Alkaligenes eutrophus phosphoglycolate phosphatase

C; Keywords: hydrolase

Query Match 88.9%; Score 32; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||||
Db 45 LEYSWL 50

RESULT 9

B84016

hypothetical protein BH2930 [Imported] - *Bacillus halodurans* (strain C-125)

C; Species: *Bacillus halodurans*

C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C; Accession: B84016

R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fujii, F.; Hirai, T.

Nucleic Acids Res. 28, 4317-4331, 2000

A; Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and its relationship to other members of the family Halobacteriaceae

A; Reference number: A83650; MUID:20512582; PMID:11058132

A; Accession: B84016

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-251 <STO>

A; Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06649.1; GSPDB:GN00154

A; Experimental source: strain C-125

C; Genetics:

A; Gene: BH2930

Query Match 88.9%; Score 32; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
|||||
Db 153 LDYSW 157

RESULT 10

AG0696

probable type III secretion protein ssat [Imported] - *Salmonella enterica* subsp. enterica serovar typhi

C; Species: *Salmonella enterica* subsp. enterica serovar typhi

A; Note: this species has also been called *Salmonella typhi*

C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C; Accession: AG0696

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar typhi

A; Reference number: AB0502; PMID:11677608

A; Accession: AG0696

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-259 <PAR>

A; Cross-references: GB:AL513382; PIDN:CAD01944.1; PID:g16502786; GSPDB:GN00176

C; Genetics:

A; Gene: ssat

Query Match 88.9%; Score 32; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
|||||
Db 67 DYSWL 71

RESULT 11

C90869

probable transcription regulator LYSR-type [Imported] - *Escherichia coli* (strain O157:H7)

C; Species: *Escherichia coli*

C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001

C; Accession: C90869

R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic relatedness to other *E. coli* serotypes

A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Accession: C90869

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-302 <HAY>

A; Cross-references: GB:BA000007; PIDN:BA035346.1; PID:g13361388; GSPDB:GN00154

A; Experimental source: strain O157:H7, substrain RMD 050952

C; Genetics:

A; Gene: Ecs1923

C; Superfamily: regulatory protein ilvY

Query Match 88.9%; Score 32; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
|||||
Db 191 LDYSW 195

RESULT 12

F85749

probable transcription regulator LYSR-type ydaK [Imported] - *Escherichia coli* (strain O157:H7)

C; Species: *Escherichia coli*

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C; Accession: F85749

R; Perne, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, M.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda, N.

Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: F85749

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-302 <STO>

A; Cross-references: GB:AE005174; NID:g12515416; PIDN:AAG56458.1; GSPDB:GN00145; UWGP:

A; Experimental source: strain O157:H7, substrain EDL933

C; Genetics:

A; Gene: ydaK

C:Superfamily: regulatory protein ilvY

Query Match 88.9%; Score 32; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
DB 191 LDYSW 195

RESULT 13

F64883

Probable transcription regulator ydaK - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F64883
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: AG4720; MUID:97426617; PMID:9278503

A:Accession: F64883

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-302 <BLAT>

A:Cross-references: GB:AE000232; GB:U00096; NID:g1787600; PIDN:AAC74421.1; PID:g1787601;
A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ydaK

C:Superfamily: regulatory protein ilvY

C:Keywords: DNA binding; transcription regulation

F:21-51/Region: regulatory protein lysR motif

Query Match 88.9%; Score 32; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
DB 191 LDYSW 195

RESULT 14

T15422

Hypothetical protein C06A8.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000

C:Accession: T15422

R:Leimbach, D.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C06A8.

A:Reference number: Z18348

A:Accession: T15422

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-349 <LEI>

A:Cross-references: EMBL:U39849; NID:g1055041; PID:g1055044; PIDN:AAA81047.1; CESP:C06A8

C:Genetics:

A:Gene: CESP:C06A8.6

A:Introns: 29/3; 202/3; 263/3; 316/3

C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match 88.9%; Score 32; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
DB 49 DYSWL 53

RESULT 15

AH0542

conserved hypothetical protein STY0359 [imported] - Salmonella enterica subsp. enteri
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C:Accession: AH0542

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AH0502; PMID:11677608

A:Accession: AH0542

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08784.1; PID:g16501600; GSPDB:GN00176

C:Genetics:

A:Gene: STY0359

C:Superfamily: Streptomyces coelicolor hypothetical protein SCE15.16c

Query Match 88.9%; Score 32; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
DB 275 DYSWL 279

Search completed: May 30, 2003, 14:52:54
Job time : 7.5921 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	91.7	404	1	US-08-696-770-2
2	33	91.7	404	2	US-09-015-557-2
3	32	88.9	230	2	US-08-637-759B-457
4	32	88.9	230	3	US-08-871-355A-457
5	32	88.9	230	4	US-09-201-945-457
6	32	88.9	351	3	US-08-591-685-7
7	32	88.9	375	3	US-08-591-685-11
8	32	88.9	404	2	US-08-282-197C-62
9	32	88.9	438	2	US-08-282-197C-59
10	32	88.9	1426	4	US-09-136-574A-43
11	31	86.1	745	2	US-08-887-518-3
12	31	86.1	745	2	US-09-023-321-3
13	31	86.1	745	2	US-08-890-853-4
14	31	86.1	745	2	US-09-032-475-3
15	31	86.1	745	2	US-09-099-125A-4
16	31	86.1	745	2	US-09-099-124A-4
17	31	86.1	745	4	US-09-032-476-4
18	31	86.1	745	4	US-08-890-854-4
19	31	86.1	745	4	US-09-023-324-4
20	31	86.1	745	4	US-09-168-629-2
21	31	86.1	745	4	US-08-910-820-10
22	31	86.1	745	4	US-08-810-131A-2
23	31	86.1	756	2	US-08-887-518-4
24	31	86.1	756	2	US-09-023-321-4
25	31	86.1	756	2	US-08-890-853-2
26	31	86.1	756	2	US-09-032-475-4
27	31	86.1	756	2	US-09-099-125A-2

Sequence 2, Appli
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Sequence 2, Appli
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Sequence 9, Appli
Sequence 46, Appli
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Sequence 45, Appli
Sequence 25, Appli
Sequence 32, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4008, Ap
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli

756 2 US-09-099-124A-2
756 4 US-09-032-476-2
756 4 US-08-890-854-2
756 4 US-09-023-324-2
756 4 US-09-168-629-15
756 4 US-08-910-820-9
172 2 US-08-853-659A-46
305 2 US-08-853-659A-47
398 2 US-08-853-659A-45
480 4 US-09-078-173A-25
480 4 US-09-537-357-32
807 4 US-09-081-345-2
879 1 US-08-306-546C-2
879 2 US-08-530-524A-2
1162 4 US-09-134-001C-4008
1212 4 US-09-090-535-1
1212 4 US-09-090-535-2
1212 4 US-09-090-535-3

ALIGNMENTS

RESULT 1
US-08-696-770-2
; Sequence 2, Application US/08696770
; Patent No. 5763218
; GENERAL INFORMATION:
; APPLICANT: Fujii, RYO
; APPLICANT: Hinuma, Shuji
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAK50001-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

US-08-696-770-2

Query Match 91.7%; Score 33; DB 1; Length 404;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSLW 6
 DB 115 LDYTWL 120

RESULT 2

US-09-015-557-2
 ; Sequence 2, Application US/09015557
 ; Patent No. 5932702
 ; GENERAL INFORMATION:
 ; APPLICANT: Fujii, Ryo
 ; APPLICANT: Hinuma, Shuji
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven
 ; APPLICANT: Soppet, Daniel
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/015,557
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/696,770
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Han, William T
 ; REGISTRATION NUMBER: 34,344
 ; REFERENCE/DOCKET NUMBER: TAK50001-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5219
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 404 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; US-09-015-557-2

Query Match 91.7%; Score 33; DB 2; Length 404;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSLW 6
 DB 115 LDYTWL 120

RESULT 3

US-08-637-759B-457
 ; Sequence 457, Application US/08637759B
 ; Patent No. 5876931
 ; GENERAL INFORMATION:
 ; APPLICANT: David William Holden
 ; TITLE OF INVENTION: Identification of Genes
 ; NUMBER OF SEQUENCES: 501
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; STREET: 1201 West Peachtree Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/637,759B
 ; FILING DATE: 03-MAY-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/02875
 ; FILING DATE: 11-DEC-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: RPMS 101
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404) 873-8794
 ; TELEFAX: (404) 873-8795
 ; INFORMATION FOR SEQ ID NO: 457:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-08-637-759B-457

Query Match 88.9%; Score 32; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 DB 67 DYSWL 71

RESULT 4

US-08-871-355A-457
 ; Sequence 457, Application US/08871355A
 ; Patent No. 6015669
 ; GENERAL INFORMATION:
 ; APPLICANT: David William Holden
 ; TITLE OF INVENTION: Identification of Genes
 ; NUMBER OF SEQUENCES: 501
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; STREET: 1201 West Peachtree Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/871,355A
;; FILING DATE: 09-JUN-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB95/02875
;; FILING DATE: 11-DEC-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: RPMS 101 CON
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 873-8794
;; TELEFAX: (404) 873-8795
;; INFORMATION FOR SEQ ID NO: 457:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 230 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-08-871-355A-457

Query Match 88.9%; Score 32; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
DB 67 DYSWL 71

RESULT 5
US-09-201-945-457
;; Sequence 457, Application US/09201945
;; Patent No. 6342215
;; GENERAL INFORMATION:
;; APPLICANT: David William Holden
;; TITLE OF INVENTION: Identification of Genes
;; NUMBER OF SEQUENCES: 501
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Patrea L. Pabst
;; STREET: 2800 One Atlantic Center
;; STREET: 1201 West Peachtree Street
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-3450
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/201,945
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/637,759
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: RPMS 101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 873-8794
;; TELEFAX: (404) 873-8795
;; INFORMATION FOR SEQ ID NO: 457:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 230 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-09-201-945-457

Query Match 88.9%; Score 32; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
DB 67 DYSWL 71

RESULT 6
US-08-591-685-7
;; Sequence 7, Application US/08591685
;; Patent No. 6083733
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Thermostable xylanases
;; NUMBER OF SEQUENCES: 13
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/591,685
;; FILING DATE:
;; CLASSIFICATION: 435
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 351 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-591-685-7

Query Match 88.9%; Score 32; DB 3; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
DB 317 DYSWL 321

RESULT 7
US-08-591-685-11
;; Sequence 11, Application US/08591685
;; Patent No. 6083733
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Thermostable xylanases
;; NUMBER OF SEQUENCES: 13
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/591,685
;; FILING DATE:
;; CLASSIFICATION: 435
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 375 amino acids
;; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-685-11

Query Match 88.9%; Score 32; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
Db 328 DYSWL 332

RESULT 8

US-08-282-197C-62
Sequence 62, Application US/08282197C
Patent No. 5871730

GENERAL INFORMATION:

APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
METHODS OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave., NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/282,197C

FILING DATE: 29-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050.0410000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 404 amino acids

TYPE: amino acid

TOPOLOGY: both

US-08-282-197C-62

Query Match 88.9%; Score 32; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
Db 328 DYSWL 332

RESULT 9

US-08-282-197C-59

Sequence 59, Application US/08282197C

Patent No. 5871730

GENERAL INFORMATION:

APPLICANT: Brzezinski, Ryszard

APPLICANT: Dery, Claude V

APPLICANT: Beaulieu, Carole

TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and

METHODS OF INVENTION: Methods of Use

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave., NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/282,197C

FILING DATE: 29-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050.0410000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 438 amino acids

TYPE: amino acid

TOPOLOGY: both

US-08-282-197C-59

Query Match 88.9%; Score 32; DB 2; Length 438;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6

Db 339 DYSWL 343

RESULT 10

US-09-136-574A-43

Sequence 43, Application US/09136574A

Patent No. 6294366

GENERAL INFORMATION:

APPLICANT: Farrington, Graham K.

Anderson, Paige

Gibbs, Moreland

Bergquist, Peter

Daniels, Roy

Morgan, Hugh W.

Williams, Diane P.

TITLE OF INVENTION: Compositions and Methods for

Treating Cellulose Containing Fabrics Using Truncated

Cellulase Enzyme Compositions

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House

STATE: PA

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,574A

FILING DATE: 19-Aug-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/932,571

;; FILING DATE: September 19, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bak, Mary E.
;; REGISTRATION NUMBER: 31,215
;; REFERENCE/DOCKET NUMBER: 1997US001/CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-540-9200
;; TELEFAX: 215-540-5818
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1426 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: NO. 6294366e
;; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-136-574A-43

Query Match 88.1%; Score 32; DB 4; Length 1426;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DY5WL 6
|||
Db 339 DY5WL 343

RESULT 11
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY5WL 6
|||
Db 738 LDY5WL 743
RESULT 12
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY5WL 6
|||
Db 738 LDY5WL 743

RESULT 13
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/890.853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSLW 6
Db 738 LDWSWL 743

RESULT 14

US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSLW 6
Db 738 LDWSWL 743

RESULT 15

US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goedel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.125A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890.853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSLW 6
Db 738 LDWSWL 743

Search completed: May 30, 2003, 14:41:29
Job time : 7.03947 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSLW 6

Scoring table: BLOSUM62.

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq101002.*

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- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	23	ABB08734
2	36	100.0	6	23	AA048517
3	36	100.0	6	23	AA048540
4	36	100.0	6	23	AA048592
5	36	100.0	7	23	AA048596
6	36	100.0	8	23	AA048589
7	36	100.0	8	23	AA048597
8	36	100.0	9	23	AA048588
9	36	100.0	9	23	AA048591
10	36	100.0	9	23	AA048594

11	36	100.0	9	23	AA048595	Anti-inflammatory
12	36	100.0	10	23	AA048590	Anti-inflammatory
13	36	100.0	10	23	AA048593	Anti-inflammatory
14	36	100.0	11	23	AA048587	Anti-inflammatory
15	36	100.0	756	23	ABB77297	Human IKKbeta muta
16	33	91.7	390	22	ABG00789	Novel human diagno
17	33	91.7	404	19	AAW59035	Human G-protein co
18	33	91.7	404	19	AAW51344	Human G-protein co
19	33	91.7	404	19	AAW34984	Human G-protein co
20	33	91.7	404	20	AA028463	Polyprotein encodi
21	33	91.7	404	22	AA078632	Human protein SQ
22	33	91.7	404	23	AA079260	Human ADAM protein
23	33	91.7	404	23	AA079261	Human ADAM variant
24	33	91.7	448	22	ABB12312	Human GPCR homolog
25	33	91.7	448	22	AA079616	Human protein SEQ
26	32	88.9	6	23	ABB08733	Mutated IKKbeta NE
27	32	88.9	6	23	AA048516	NBD mutant peptide
28	32	88.9	6	23	AA048539	Anti-inflammatory
29	32	88.9	6	23	AA048581	Anti-inflammatory
30	32	88.9	7	23	AA048585	Anti-inflammatory
31	32	88.9	8	23	AA048578	Anti-inflammatory
32	32	88.9	8	23	AA048586	Anti-inflammatory
33	32	88.9	9	23	AA048577	Anti-inflammatory
34	32	88.9	9	23	AA048580	Anti-inflammatory
35	32	88.9	9	23	AA048583	Anti-inflammatory
36	32	88.9	9	23	AA048584	Anti-inflammatory
37	32	88.9	10	23	AA048579	Anti-inflammatory
38	32	88.9	10	23	AA048582	Anti-inflammatory
39	32	88.9	11	23	AA048576	Anti-inflammatory
40	32	88.9	69	22	ABB30729	Peptide #3390 enco
41	32	88.9	69	22	ABB35904	Peptide #3410 enco
42	32	88.9	69	22	ABB21314	Protein #313 enco
43	32	88.9	69	22	AA056709	Human brain expres
44	32	88.9	69	22	AA069084	Human bone marrow
45	32	88.9	69	22	AA016922	Peptide #3356 enco

ALIGNMENTS

RESULT 1

ABB08734

ID ABB08734 standard; peptide; 6 AA.

XX ABB08734;

XX 14-JUN-2002 (first entry)

XX Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 12.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX autoimmune disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
XX osteoparitic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
XX antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
XX dermatological; antibacterial; antipsoriatic; antirheumatic;
XX antiarthritic; osteopathic; antiulcer; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 3 /note= "Wildtype Trp substituted by Tyr"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYA) UNIV YALE.
 XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 DR
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSLW 6
 Db 1 LDYSLW 6
 RESULT 2
 AAM48517
 ID AAM48517 standard; Peptide; 6 AA.
 AC AAM48517;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 12.
 DE
 XX

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA
 XX (UYA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findels MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Example 6; Page 48; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSLW 6
 Db 1 LDYSLW 6
 RESULT 3
 AAM48540
 ID AAM48540 standard; Peptide; 6 AA.
 XX

QY 1 LDYSWL 6
| | | | |
Db 1 LDYSWL 6

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
| | | | |
Db 1 LDYSWL 6

RESULT 5
AAM48596
ID AAM48596 standard; Peptide; 7 AA.
XX
XX AAM48596;
XX
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 99.

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX
XX WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappab activation, and for treating asthma, lung inflammation, psoriasis

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, neurotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 36; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
| | | | |
Db 1 LDYSWL 6

RESULT 6
AAM48589
ID AAM48589 standard; Peptide; 8 AA.
XX
XX AAM48589;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 92.

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX
XX WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappab activation, and for treating asthma, lung inflammation, psoriasis

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, neurotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 36; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 |||||

RESULT 7
 AAM48597
 ID AAM48597 standard; Peptide; 8 AA.
 AC AAM48597;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 100.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.

XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 36; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 Db 1 LDYSWL 6
 |||||

RESULT 8
 AAM48588
 ID AAM48588 standard; Peptide; 9 AA.
 AC AAM48588;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 91.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.

XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, The
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 D 1 LDYSWL 6
 RESULT 9
 AAM48591
 ID AAM48591 standard; Peptide; 9 AA.
 AC AAM48591;
 XX
 XX 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 94.
 KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYIA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 D 1 LDYSWL 6
 RESULT 10
 AAM48594
 ID AAM48594 standard; Peptide; 9 AA.
 AC AAM48594;
 XX
 XX 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 97.
 KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYIA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PT Novel antiinflammatory compound comprising membrane translocation

XX PT domain fused to NEMO binding sequence, useful for blocking nuclear

XX PT factor kappaB activation, and for treating asthma, lung inflammation,

XX PT psoriasis

XX PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotective,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 36; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6

Db 3 LDYSWL 8

RESULT 11

AAM48595

ID AAM48595 standard; Peptide; 9 AA.

XX AC AAM48595;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 98.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;

XX KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

XX KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

XX KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

XX KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

XX KW autoimmune disorder; multiple sclerosis; transplant rejection;

XX KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX XX 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV VALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

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PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis

XX PS Claim 6; Page 62; 88pp; English.

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CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 36; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6

Db 2 LDYSWL 7

RESULT 12

AAM48590

ID AAM48590 standard; Peptide; 10 AA.

XX AC AAM48590;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 93.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;

XX KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

XX KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

XX KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

XX KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

XX KW autoimmune disorder; multiple sclerosis; transplant rejection;

XX KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX 08-NOV-2001.
 XX
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 36; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDYSWL 6
 Db 2 LDYSWL 7
 |||||
 |||||
 RESULT 13
 AA48593
 ID AA48593 standard; Peptide; 10 AA.
 XX
 AC AA48593;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 96.
 DE
 XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anticallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
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 PS Claim 6; Page 62; 88pp; English.
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 XX The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 36; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDYSWL 6
 Db 3 LDYSWL 8
 |||||
 |||||
 RESULT 14
 AA48587
 ID AA48587 standard; Peptide; 11 AA.
 XX
 AC AA48587;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 90.
 DE
 XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anticallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW anti-rheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRACIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX
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 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 11 AA;
 XX
 XX Query Match 100.0%; Score 36; DB 23; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 3.7;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 XX
 XX RESULT 15
 XX ABB77297
 XX ID ABB77297 standard; protein: 756 AA.
 XX
 XX ABB77297;
 AC

XX 14-JUN-2002 (first entry)
 DT Human IKKbeta mutant W739Y.
 XX
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytotatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiasthmatic; anti-allergic;
 KW dermatological; antibacterial; antipsoriatic; anti-rheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 739 /note= "Wildtype Trp substituted by Tyr"
 FT
 FT
 FT
 XX WO200183547-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 XX Example 11; Page -; 82pp; English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arthritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis, in
 CC sunburn or aging. The compound may be used to replace corticosteroids in

CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. O14920 (ABB77294).

XX
 SQ Sequence 756 AA;

Query Match 100.0%; Score 36; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
 |||||
 Db 737 LDYSWL 742

Search completed: May 30, 2003, 14:49:57
 Job time : 19.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds
(without alignments)
58.060 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDFSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications, AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	9	US-09-847-940B-11
2	35	100.0	6	9	US-09-847-946A-11
3	35	100.0	6	9	US-09-847-946A-42
4	35	100.0	6	9	US-09-847-946A-84
5	35	100.0	7	9	US-09-847-946A-88
6	35	100.0	8	9	US-09-847-946A-81
7	35	100.0	8	9	US-09-847-946A-89
8	35	100.0	9	9	US-09-847-946A-80
9	35	100.0	9	9	US-09-847-946A-83
10	35	100.0	9	9	US-09-847-946A-86
11	35	100.0	9	9	US-09-847-946A-87
12	35	100.0	10	9	US-09-847-946A-82
13	35	100.0	10	9	US-09-847-946A-85
14	35	100.0	11	9	US-09-847-946A-79
15	33	94.3	265	10	US-09-881-752A-368
16	32	91.4	6	9	US-09-847-940B-12
17	32	91.4	6	9	US-09-847-946A-12
18	32	91.4	6	9	US-09-847-946A-95
19	32	91.4	7	9	US-09-847-946A-99

20	91.4	8	9	US-09-847-946A-92	Sequence 92, Appl
21	91.4	8	9	US-09-847-946A-100	Sequence 100, App
22	91.4	9	9	US-09-847-946A-91	Sequence 91, Appl
23	91.4	9	9	US-09-847-946A-94	Sequence 94, Appl
24	91.4	9	9	US-09-847-946A-97	Sequence 97, Appl
25	91.4	9	9	US-09-847-946A-98	Sequence 98, Appl
26	91.4	10	9	US-09-847-946A-93	Sequence 93, Appl
27	91.4	10	9	US-09-847-946A-96	Sequence 96, Appl
28	91.4	11	9	US-09-847-946A-90	Sequence 90, Appl
29	88.6	236	9	US-10-277-693A-11	Sequence 11, Appl
30	88.6	239	1	US-08-726-211-5	Sequence 5, Appl
31	88.6	239	9	US-10-101-482-12	Sequence 12, Appl
32	88.6	239	9	US-10-277-693A-10	Sequence 10, Appl
33	88.6	662	10	US-09-924-358-11	Sequence 11, Appl
34	85.7	6	9	US-09-847-940B-2	Sequence 2, Appl
35	85.7	6	9	US-09-847-946A-2	Sequence 33, Appl
36	85.7	7	9	US-09-847-946A-33	Sequence 37, Appl
37	85.7	8	9	US-09-847-946A-30	Sequence 30, Appl
38	85.7	8	9	US-09-847-946A-38	Sequence 38, Appl
39	85.7	9	9	US-09-847-946A-29	Sequence 29, Appl
40	85.7	9	9	US-09-847-946A-32	Sequence 32, Appl
41	85.7	9	9	US-09-847-946A-35	Sequence 35, Appl
42	85.7	9	9	US-09-847-946A-36	Sequence 36, Appl
43	85.7	10	9	US-09-847-946A-31	Sequence 31, Appl
44	85.7	10	9	US-09-847-946A-34	Sequence 34, Appl
45	85.7	10	9	US-09-847-946A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-11
; Sequence 11, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-11

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
Db 1 LDFSWL 6

RESULT 2
US-09-847-946A-11
; Sequence 11, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-11

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
| | | | |
DB 1 LDFS WL 6

RESULT 3
US-09-847-946A-42
; Sequence 42, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-42

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
| | | | |
DB 1 LDFS WL 6

RESULT 4
US-09-847-946A-84
; Sequence 84, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-84

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
| | | | |
DB 1 LDFS WL 6

RESULT 5
US-09-847-946A-88
; Sequence 88, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-88

Query Match 100.0%; Score 35; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
| | | | |
DB 1 LDFS WL 6

RESULT 6
US-09-847-946A-81
; Sequence 81, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-81

Query Match 100.0%; Score 35; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
DB 3 LDFSWL 8

RESULT 7

US-09-847-946A-89
; Sequence 89, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-89

Query Match 100.0%; Score 35; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
DB 1 LDFSWL 6

RESULT 8

US-09-847-946A-80

; Sequence 80, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-80

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
DB 1 LDFSWL 6

RESULT 9

US-09-847-946A-83
; Sequence 83, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-83

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
DB 1 LDFSWL 6

RESULT 10

US-09-847-946A-86
; Sequence 86, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-86

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFS WL 6
Db 3 LDFS WL 8

RESULT 11

US-09-847-946A-87
; Sequence 87, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-87

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFS WL 6

Db 2 LDFS WL 7

RESULT 12

US-09-847-946A-82
; Sequence 82, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-82

Query Match 100.0%; Score 35; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFS WL 6
Db 2 LDFS WL 7

RESULT 13

US-09-847-946A-85
; Sequence 85, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-85

Query Match 100.0%; Score 35; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;

Matches	6;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	LDFS WL 6													
Db	3	LDFS WL 8													

RESULT 14

US-09-847-946A-79
; Sequence 79, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-79

Query Match 100.0%; Score 35; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LDFS WL 6
Db	3	LDFS WL 8

RESULT 15

US-09-881-752A-368
; Sequence 368, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Comen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-368

Query Match 94.3%; Score 33; DB 10; Length 265;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Search completed: May 30, 2003, 15:53:18
Job time : 10.4605 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds
(without alignments)
29.231 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSRL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	88.6	21	1	US-08-798-897-13
2	31	88.6	21	2	US-08-978-523-13
3	31	88.6	23	2	US-08-337-646A-23
4	31	88.6	23	4	US-08-927-326-23
5	31	88.6	25	2	US-08-337-646A-29
6	31	88.6	25	4	US-08-927-326-29
7	31	88.6	154	1	US-08-077-848A-3
8	31	88.6	154	3	US-09-211-640-3
9	31	88.6	154	4	US-09-378-536-3
10	31	88.6	229	2	US-08-408-095-19
11	31	88.6	232	2	US-08-408-095-17
12	31	88.6	232	2	US-08-408-095-18
13	31	88.6	236	1	US-08-112-208C-11
14	31	88.6	236	1	US-08-248-819A-11
15	31	88.6	236	1	US-08-607-269-21
16	31	88.6	236	1	US-08-607-269-22
17	31	88.6	236	2	US-08-337-646A-11
18	31	88.6	236	2	US-08-856-531-11
19	31	88.6	236	2	US-08-856-034-11
20	31	88.6	236	4	US-09-127-048-9
21	31	88.6	236	4	US-08-927-326-11
22	31	88.6	236	5	PCT-US95-04600-21
23	31	88.6	236	5	PCT-US95-04600-22
24	31	88.6	236	1	US-08-333-565-51
25	31	88.6	239	1	US-08-112-208C-10
26	31	88.6	239	1	US-08-248-819A-10
27	31	88.6	239	1	US-08-248-819A-12

28	31	88.6	239	1	US-08-607-269-20	Sequence 20, Appl
29	31	88.6	239	1	US-08-471-058-12	Sequence 12, Appl
30	31	88.6	239	1	US-08-405-702A-12	Sequence 12, Appl
31	31	88.6	239	1	US-08-690-095-4	Sequence 4, Appl
32	31	88.6	239	2	US-08-465-485A-21	Sequence 21, Appl
33	31	88.6	239	2	US-08-661-479-51	Sequence 51, Appl
34	31	88.6	239	2	US-08-365-486A-15	Sequence 15, Appl
35	31	88.6	239	2	US-08-365-486A-17	Sequence 17, Appl
36	31	88.6	239	2	US-08-337-646A-10	Sequence 10, Appl
37	31	88.6	239	2	US-08-337-646A-12	Sequence 12, Appl
38	31	88.6	239	2	US-08-408-095-16	Sequence 16, Appl
39	31	88.6	239	2	US-08-856-531-10	Sequence 10, Appl
40	31	88.6	239	2	US-08-856-034-10	Sequence 10, Appl
41	31	88.6	239	3	US-08-471-057-12	Sequence 12, Appl
42	31	88.6	239	3	US-09-113-789-4	Sequence 4, Appl
43	31	88.6	239	3	US-09-080-285-21	Sequence 21, Appl
44	31	88.6	239	4	US-09-127-048-8	Sequence 8, Appl
45	31	88.6	239	4	US-08-927-326-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-13
; Sequence 13, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-798-897-13

Query Match 88.6%; Score 31; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DFSWL 6
Db 7 DFSWL 11

RESULT 2

US-08-978-523-13
; Sequence 13, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-978-523-13

Query Match 88.6%; Score 31; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFSWL 6
Db 7 DFSWL 11

RESULT 3

US-08-337-646A-23
; Sequence 23, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-337-646A-23

Query Match 88.6%; Score 31; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFSWL 6
Db 16 DFSWL 20

RESULT 4

US-08-927-326-23
; Sequence 23, Application US/08927326
; Patent No. 6184202
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,326
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,646
; FILING DATE: 10-NOV-1994
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-326-23

Query Match 88.6%; Score 31; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
DB 16 DFSWL 20

RESULT 5

US-08-337-646A-29
Sequence 29, Application US/08337646A
Patent No. 5856171

GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-337-646A-29

Query Match 88.6%; Score 31; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
DB 16 DFSWL 20

RESULT 6

US-08-927-326-29
Sequence 29, Application US/08927326
Patent No. 6184202

GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,646
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-326-29

Query Match 88.6%; Score 31; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
DB 16 DFSWL 20

RESULT 7

US-08-077-848A-3
Sequence 3, Application US/08077848A
Patent No. 5470955

GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California

;; COUNTRY: USA
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/077,848A
;; FILING DATE: 16-JUN-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haile, Ph.D., Lisa A.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: PD-2845
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 154 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: bcl-2alpha
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..154
;; US-08-077-848A-3

Query Match 88.6%; Score 31; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 126 DFSWL 130

RESULT 8
US-09-211-640-3
; Sequence 3, Application US/09211640
; Patent No. 6020466
; GENERAL INFORMATION:
; APPLICANT: Craig, Ruth W.
; TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,640
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,375
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: PD-2845

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 154 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: bcl-2alpha
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..154
;; US-09-211-640-3

Query Match 88.6%; Score 31; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 126 DFSWL 130

RESULT 9
US-09-378-536-3
; Sequence 3, Application US/09378536
; Patent No. 6200763
; GENERAL INFORMATION:
; APPLICANT: Craig, Ruth W.
; TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,536
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,848
; FILING DATE: 16-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: PD-2845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: bcl-2alpha
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..154

US-09-378-536-3

Query Match 88.6%; Score 31; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 126 DFSWL 130

RESULT 10

US-08-408-095-19
; Sequence 19, Application US/08408095
; Patent No. 5858678
; GENERAL INFORMATION:
; APPLICANT: Chinnadurai, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-19

Query Match 88.6%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 201 DFSWL 205

RESULT 11

US-08-408-095-17
; Sequence 17, Application US/08408095
; Patent No. 5858678
; GENERAL INFORMATION:
; APPLICANT: Chinnadurai, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-17

Query Match 88.6%; Score 31; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 204 DFSWL 208

RESULT 12

US-08-408-095-18
; Sequence 18, Application US/08408095
; Patent No. 5858678
; GENERAL INFORMATION:
; APPLICANT: Chinnadurai, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-18

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-18

Query Match 88.6%; Score 31; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
 DB 204 DFSWL 208

RESULT 13

US-08-112-208C-11
 ; Sequence 11, Application US/08112208C
 ; Patent No. 5691179
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/112,208C
 ; FILING DATE: 26-AUG-1993
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15726A-000610
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 236 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-112-208C-11

Query Match 88.6%; Score 31; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
 DB 208 DFSWL 212

RESULT 14

US-08-248-819A-11
 ; Sequence 11, Application US/08248819A
 ; Patent No. 5700638
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,819A
 FILING DATE: 25-NAY-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 236 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-248-819A-11

Query Match 88.6%; Score 31; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
 DB 208 DFSWL 212

RESULT 15

US-08-607-269-21
 ; Sequence 21, Application US/08607269
 ; Patent No. 5702897
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Sato, Takaaki
 ; TITLE OF INVENTION: Interaction of Proteins Involved in a
 ; TITLE OF INVENTION: Cell Death Pathway
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/607,269
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/226,876
 ; FILING DATE: 13-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 9882
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-607-269-21

Query Match 88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DFSWL 6
Db 208 DFSWL 212

Search completed: May 30, 2003, 14:41:28
Job time : 7.03947 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds
(without alignments)
40.589 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDFSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	23	Mutated IKKbeta NE
2	35	100.0	6	23	NBD mutant peptide
3	35	100.0	6	23	Anti-inflammatory
4	35	100.0	6	23	Anti-inflammatory
5	35	100.0	7	23	Anti-inflammatory
6	35	100.0	8	23	Anti-inflammatory
7	35	100.0	8	23	Anti-inflammatory
8	35	100.0	9	23	Anti-inflammatory
9	35	100.0	9	23	Anti-inflammatory
10	35	100.0	9	23	Anti-inflammatory

11	35	100.0	9	23	AAW48584	Anti-inflammatory
12	35	100.0	10	23	AAW48579	Anti-inflammatory
13	35	100.0	10	23	AAW48582	Anti-inflammatory
14	35	100.0	11	23	AAW48576	Anti-inflammatory
15	35	100.0	756	23	ABB77296	Human IKKbeta muta
16	33	94.3	144	21	AAW70582	Salmonella Pathoge
17	33	94.3	253	19	AAW11039	H. pylori ORF 06ae
18	33	94.3	265	19	AAW98384	H. pylori GHPO 128
19	32	91.4	6	23	ABB08734	Mutated IKKbeta NE
20	32	91.4	6	23	AAW48517	NBD mutant peptide
21	32	91.4	6	23	AAW48540	Anti-inflammatory
22	32	91.4	6	23	AAW48592	Anti-inflammatory
23	32	91.4	7	23	AAW48596	Anti-inflammatory
24	32	91.4	8	23	AAW48589	Anti-inflammatory
25	32	91.4	8	23	AAW48597	Anti-inflammatory
26	32	91.4	9	23	AAW48588	Anti-inflammatory
27	32	91.4	9	23	AAW48591	Anti-inflammatory
28	32	91.4	9	23	AAW48594	Anti-inflammatory
29	32	91.4	9	23	AAW48595	Anti-inflammatory
30	32	91.4	10	23	AAW48590	Anti-inflammatory
31	32	91.4	10	23	AAW48593	Anti-inflammatory
32	32	91.4	11	23	AAW48587	Anti-inflammatory
33	32	91.4	756	23	ABB77297	Human IKKbeta muta
34	31	88.6	23	20	AAW87823	Epitope of a Bcl-2
35	31	88.6	23	22	AAW74140	Bax epitope #10.
36	31	88.6	25	20	AAW87829	Epitope of a Bcl-2
37	31	88.6	25	22	AAW74146	Bax epitope #16.
38	31	88.6	42	21	AAW34347	Human secreted pro
39	31	88.6	87	22	ABG10985	Novel human diagno
40	31	88.6	106	22	AAW8387	Human immune/haema
41	31	88.6	106	23	ABP33839	Human DNA/RNA bind
42	31	88.6	229	17	AAW01021	Apoptosis-blocking
43	31	88.6	229	17	AAW94348	Human Bcl-2 mutant
44	31	88.6	232	17	AAW01019	Apoptosis-blocking
45	31	88.6	232	17	AAW01020	Apoptosis-blocking

ALIGNMENTS

RESULT 1
ABB08733
ID ABB08733 standard; peptide; 6 AA.
XX ABB08733;
XX AC ABB08733;
XX DT 14-JUN-2002 (first entry)
XX DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 11.
XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autolimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX OS Homo sapiens.
OS Synthetic.

2002/08/08

Key Location/Qualifiers
Misc-difference 3 /note= "Wildtype Trp substituted by Phe"
WO200183547-A2.
08-NOV-2001.
02-MAY-2001; 2001WO-US40654.

AA48539;
20-MAR-2002 (first entry)
Anti-inflammatory peptide SEQ ID NO 42.
Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
antiallergic; membrane translocation domain; NEMO binding domain; eczema;
cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
autoimmune disorder; multiple sclerosis; transplant rejection;
osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
ataxia telangiectasia; allergy; anaphylaxis; arthritis.
Synthetic.
WO200183554-A2.
08-NOV-2001.
02-MAY-2001; 2001WO-US14346.
02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
(PRAE-) PRAECIS PHARM INC.
(UYVA) UNIV YALE.
May MJ, Ghosh S, Findeis MA, Phillips K;
WPI; 2002-121889/16.
Novel antiinflammatory compound comprising membrane translocation
domain fused to NEMO binding sequence, useful for blocking nuclear
factor kappaB activation, and for treating asthma, lung inflammation,
psoriasis
Claim 6; Page 61; 88pp; English.
The invention relates to an antiinflammatory compound (especially
AA48628-AA48645), comprising a membrane translocation domain
(AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
amino acid residues, fused to a NEMO binding sequence
(AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
antibacterial, immunosuppressive, dermatological, neuroprotective,
nootropic, antiatherosclerotic, virucide and antiallergic activity. The
compounds act as selective inhibitors of cytokine-mediated NFkappaB
activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
the NEMO binding domain that results in inhibition of IKKbeta kinase
activation and subsequent decreased phosphorylation of IkappaB. The
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation or cancer, psoriasis, rheumatoid arthritis,
osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
burstis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
Alzheimer's disease; atherosclerosis; viral infections; and ataxia
telangiectasia. The compounds are also useful for treating
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
drug or food sensitivity, eczema, dermatitis, sunburn, aging and
arthritis.
Sequence 6 AA;
Query Match 100.0%; Score 35; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
Db 1 LDFSWL 6

RESULT 4
AA48581
ID AA48581 standard; Peptide; 6 AA.
XX AA48581;
AC AA48581;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 84.
XX
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
antiallergic; membrane translocation domain; NEMO binding domain; eczema;
cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
autoimmune disorder; multiple sclerosis; transplant rejection;
osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
ataxia telangiectasia; allergy; anaphylaxis; arthritis.
Synthetic.
WO200183554-A2.
08-NOV-2001.
02-MAY-2001; 2001WO-US14346.
02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
(PRAE-) PRAECIS PHARM INC.
(UYVA) UNIV YALE.
May MJ, Ghosh S, Findeis MA, Phillips K;
WPI; 2002-121889/16.
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psoriasis
Claim 6; Page 62; 88pp; English.
The invention relates to an antiinflammatory compound (especially
AA48628-AA48645), comprising a membrane translocation domain
(AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
amino acid residues, fused to a NEMO binding sequence
(AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
antibacterial, immunosuppressive, dermatological, neuroprotective,
nootropic, antiatherosclerotic, virucide and antiallergic activity. The
compounds act as selective inhibitors of cytokine-mediated NFkappaB
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the NEMO binding domain that results in inhibition of IKKbeta kinase
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osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
burstis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
Alzheimer's disease; atherosclerosis; viral infections; and ataxia
telangiectasia. The compounds are also useful for treating
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
drug or food sensitivity, eczema, dermatitis, sunburn, aging and
arthritis.
Sequence 6 AA;
Query Match 100.0%; Score 35; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
Db 1 LDFSWL 6

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
| | | | |
Db 1 LDFS WL 6

RESULT 5

AAM48585
ID AAM48585 standard; Peptide; 7 AA.

AC AAM48585;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 88.

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

PN WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

PI WPI; 2002-121889/16.

XX Novel antinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neutropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6

| | | | |
Db 1 LDFS WL 6

RESULT 6

AAM48578

ID AAM48578 standard; Peptide; 8 AA.

XX AAM48578;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 81.

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

PN WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neutropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 8 AA;
 Query Match 100.0%; Score 35; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
 Db 3 LDFS WL 8

RESULT 7
 AAM48586
 ID AAM48586 standard; Peptide; 8 AA.
 AC AAM48586;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 89.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 8 AA;
 Query Match 100.0%; Score 35; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
 Db 1 LDFS WL 6

RESULT 8
 AAM48577
 ID AAM48577 standard; Peptide; 9 AA.
 AC AAM48577;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 80.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
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 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma;
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6

DB 1 LDFS WL 6

RESULT 9

AAM48580

ID AAM48580 standard; Peptide; 9 AA.

XX AC AAM48580;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 83.

XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

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 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma;
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6

DB 1 LDFS WL 6

RESULT 10

AAM48583

ID AAM48583 standard; Peptide; 9 AA.

XX AC AAM48583;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 86.

XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYA) UNIV YALE.

XX May MJ, Ghosh S, Findels MA, Phillips K;

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XX DR WPI; 2002-121889/16.
XX PA
XX PT Novel antiinflammatory compound comprising membrane translocation
XX PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX PT factor kappaB activation, and for treating asthma, lung inflammation,
XX PT psoriasis
XX PS
XX PS Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AA48628-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC cytotatic, antipsoriatic, antirheumatic, dermatological, osteopathic,
CC antibacterial, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX SQ
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 35; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;
XX
XX QY 1 LDFSWL 6
XX Db 3 LDFSWL 8
XX
XX RESULT 11
XX AA48584
XX ID AA48584 standard; Peptide; 9 AA.
XX AC
XX AA48584;
XX
XX DT 20-MAR-2002 (first entry)
XX
XX DE Anti-inflammatory peptide SEQ ID NO 87.
XX
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX OS
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX PN 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.

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PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
XX PA (UYUA ) UNIV YALE.
XX
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
XX DR WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
XX PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX PT factor kappaB activation, and for treating asthma, lung inflammation,
XX PT psoriasis
XX
XX PS Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AA48628-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC cytotatic, antipsoriatic, antirheumatic, dermatological, osteopathic,
CC antibacterial, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX SQ
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 35; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;
XX
XX QY 1 LDFSWL 6
XX Db 2 LDFSWL 7
XX
XX RESULT 12
XX AA48579
XX ID AA48579 standard; Peptide; 10 AA.
XX AC
XX AA48579;
XX
XX DT 20-MAR-2002 (first entry)
XX
XX DE Anti-inflammatory peptide SEQ ID NO 82.
XX
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX OS
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX PN

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XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PF 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PR
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 35; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDFSWL 6
 Db 2 LDFSWL 7
 RESULT 13
 AA48582
 ID AA48582 standard; Peptide; 10 AA.
 XX
 AC AA48582;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 85.
 XX
 KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 35; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDFSWL 6
 Db 3 LDFSWL 8
 RESULT 14
 AA48576
 ID AA48576 standard; Peptide; 11 AA.
 XX
 AC AA48576;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 79.
 XX
 KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYUA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI: 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 11 AA;
 QY Query Match 100.0%; Score 35; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 |||||
 Db 3 LDFSWL 8
 RESULT 15
 ID ABB77296
 ID ABB77296 standard; protein; 756 AA.
 XX ABB77296;
 AC

XX 14-JUN-2002 (first entry)
 XX Human IKKbeta mutant W739F.
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiasthmatic; anti-allergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Misc-difference 739 /note= "Wildtype Trp substituted by Phe"
 XX WO200183547-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US40654.
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (UYUA) UNIV YALE.
 XX May MJ, Ghosh S;
 XX WPI: 2002-179350/23.
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX Example 11; Page -: 82pp; English.
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arthritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis, in
 CC sunburn or aging. The compound may be used to replace corticosteroids in

CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. O14920 (ABB77294).

XX
 SQ Sequence 756 AA;

Query Match 100.0%; Score 35; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFS WL 6

Db 737 LDFS WL 742

Search completed: May 30, 2003, 14:49:57
 Job time : 20.7529 secs